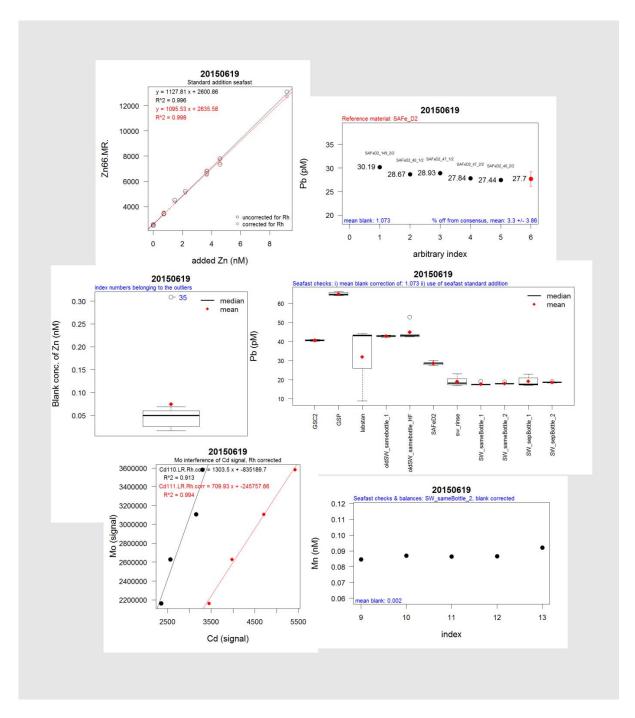
SEAFAST ICP-MS data, analysed in a snap

R script manual for the fast data analysis of trace metals extracted from seawater using a SEAFAST system and measured by ICP-MS

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1) Summary

The complete analysis of the trace metal data extracted from seawater by a SEAFAST system and measured by ICP-MS takes a lot of time using excel. This R script was developed to speed up this process so that all checks and balances and the resulting data can be assessed before the next set of samples are measured. This prevents that problems are detected in a later stage necessitating re-measurement of large quantities of samples. This R script allows correction for changes in the ICP-MS sensitivity using measurements of Rh added to the samples. It allows for the correction of the Cd data due to the interference of Mo using the ICP-MS. It visualizes the standard additions and provides a csv file with slopes and other data. It visualizes all checks and balances (separately treating ICP-MS and SEAFAST checks). It calculates the recovery efficiency of your SEAFAST column. It graphs the consensus reference values (e.g. SAFE, GEOTRACES, and any others to be added by the user) besides the measured results of reference samples. It calculates the final concentrations of all trace metals of interest of your environmental samples. If you don't want to correct your data for changes in ICP-MS sensitivity using Rh and the interference of Mo in the measurement of Cd you can turn these options off. It will take about 30 minutes to copy past the ICP-MS data in a series of separate csv files. Using the R script it will take you not more than 15 minutes to analyse the full data resulting in a perfect overview of all your checks and balances and a final dataset of your environmental samples.

2) General information:

The R script and the functions were written in R version 3.0.1 (2013-05-16), 32-bit under Windows. Sometimes function will not work in earlier versions because the R packages that are needed don't work there. For example, "library(string)" does not work in version R2.10.0. Please, if you use this R script send me your e-mail address (to micharijkenberg@yahoo.com.au) so that I can send you updates of the script when available. The use of this script is free but at your own risk.

The reference values provided with this script for the SAFE and GEOTRACES reference materials (version May 2013) originate from the GEOTRACES website (http://www.geotraces.org/science/intercalibration/322-standards-and-reference-materials).

3) Setting up the R working directory

- a. Create a folder
- b. place in here your latest R script (Script_icpmsDataAnalysis_310516.r)
- c. place in here your latest R Functions (Functions_ResultsICPMS_310516.r)
- d. place in here your csv file with reference values

(Trace Metal Reference Consensus Values.csv)

The R script is the script that you open and work in. The R Functions need to be in the same folder but you don't have to do anything with it other than activate it within your R script. The TraceMetalReferenceConsensusValues.csv will also be opened from within the R script. However, if you want to change anything in this file (e.g. add or change reference materials) you can do this in excel.

4) Setting up the data files

First we create a folder (other than the R work directory) where we place the excel file with the ICPMS data. In our case we name the folder after the date of the ICPMS run, e.g. 20150619. On a windows system you can use a number or a "text" to indicate the run. On an Apple system you need to use a number to indicate the run.

The main-datasheet

The excel file with ICPMS results (not Rh corrected) looks in our case like the example as shown in Figure 1 a. The first action is to add a column with an "index", see red arrow in Figure 1 b. This index will be copy pasted with subsets of the data so that all data stays retraceable to the original main-datasheet. This index is also necessary to allow identification of the right Rh correction for each sample data.

As some groups do not use Rh to correct for variation in ICPMS sensitivity and sample evaporation but for example Ga it is now possible to set the element that you use. However, throughout this manual Rh is used as example.

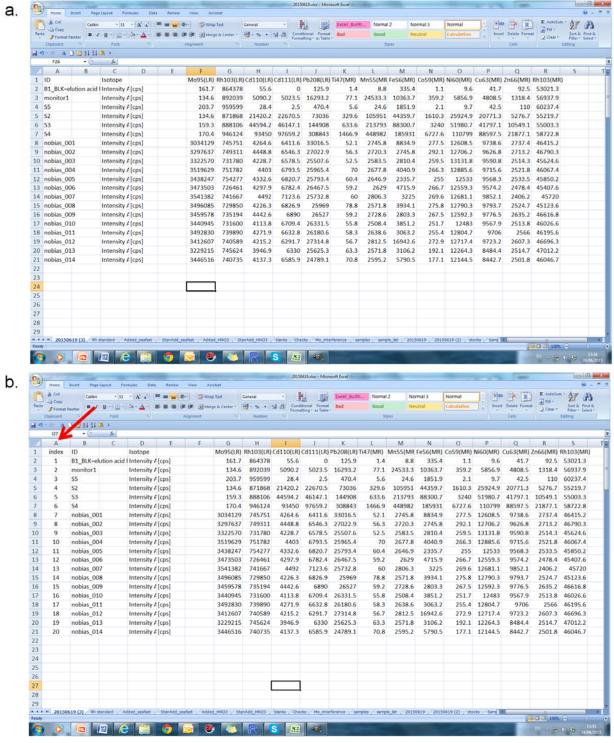


Figure 1. a) The main-datasheet in excel with data as it originates from the ICPMS. Please, note that shown is a truncated example used for illustration purposes and not a full run. B) First add a column "index" with numbers. This index will be copy pasted with subsets of the data so that all data stays retraceable in the original main data sheet.

"StandardElement" sub-datasheet (Rh, Ga or other element used)

We now construct a number of sub-datasheets with data from the main-datasheet. The first sub-datasheet is the "StandardElement" sub-datasheet. Rh is used as an example throughout this manual. This sub-datasheet contains three columns: i) the "index", ii) the Rh103(LR), and iii) the Rh103(MR), see Figure 2. The "index" column contains the index numbers as created in the first column of the main-datasheet and is a necessary column. Make sure that the header names of the necessary columns remain the same as in this manual. This sub-datasheet needs to be saved as "StandardElement.csv" in the same example folder "20150615".

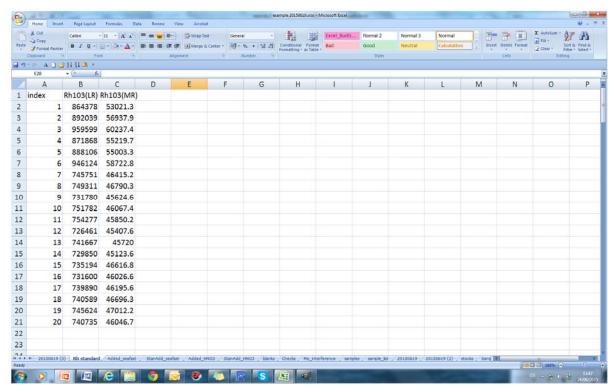


Figure 2. The StandardElement sub-datasheet.

"StanAdd_HNO3" sub-datasheet

The "StanAdd_HNO3" sub-datasheet contains the data of a standard addition to the HNO3 eluent. This data are only useful to relate the metal concentrations in the eluent blank to. This data is also used to calculate the percent recovery of the Seafast extracted metals. The necessary columns are: i) the "index", ii) "sample", iii) "repetition", and iv) "conc.order", see Figure 3. Make sure that the header names of the necessary columns remain the same as in this manual. The remaining columns contain the metal ICPMS data including the original header names (as long as they don't contain spaces or exotic symbols). The ICPMS trace metal data can be copy pasted from the main-datasheet into this sub-datasheet in any order after the first four columns, with any metal identity (header needs to start with an element code e.g. Fe and end with LR or MR mode between brackets, e.g. (LR), so at a minimum Cd(LR)) or in any number. The "index" column contains the index numbers as created in the first column of the main-datasheet. The "sample" column contains the sample names as given in the main-datasheet, the "repetition" column shows the repeated standard additions. In this case we did a standard addition in the beginning of the run and at the end. The "conc.order" column gives the order and the identity of the standard additions. A sub-datasheet with the standard addition concentrations will also be created (next). The sub-datasheet StanAdd HNO3 needs to be saved as "StanAdd HNO3.csv" in the same example folder "20150615".

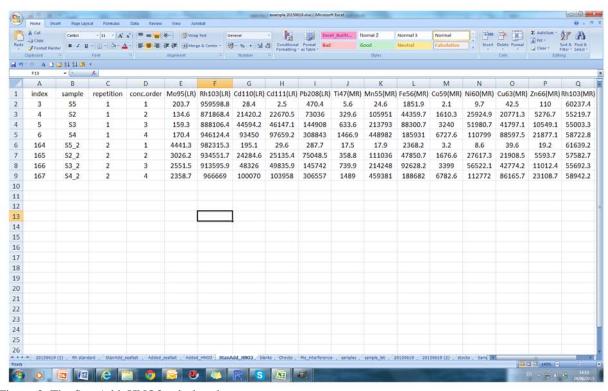


Figure 3. The StanAdd_HNO3 sub-datasheet.

"Added_HNO3" sub-datasheet

The "Added_HNO3" sub-datasheet contains the final concentrations of the standard additions to the HNO3 eluent for each metal, see Figure 4. The necessary column is: i) the "conc.order", it contains the order and identity of the standard additions. The numbers in this columns need to match the numbers in the "conc.order" column of the "StanAdd_HNO3" sub-datasheet. Make sure that the header names of the necessary columns remain the same as in this manual. The headers for the metals need to be their element name, e.g. "Fe". You can bring as many metal columns in as wished (no double though). It does not form a problem if it contains metals that you did not measure by IPMS or if it did not contain the metals that you did measure by ICPMS (however, these data will not be further used) in the seafast percent recovery calculations. The sub-datasheet Added_HNO3 needs to be saved as "Added_HNO3.csv" in the same example folder "20150615".

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Figure 4. The Added_HNO3 sub-datasheet.

"StanAdd_seafast" sub-datasheet

The "StanAdd_seafast" sub-datasheet contains the data of a standard addition to seawater samples to be used with the seafast, see Figure 5. This data will be used to calculate the concentration metals in the original seawater samples. The necessary columns are: i) the "index", ii) "sample", iii) "repetition", and iv) "conc.order", see Figure 5. Make sure that the header names of the necessary columns remain the same as in this manual. The remaining columns contain the metal ICPMS data including the original header names (as long as they don't contain spaces or exotic symbols). The ICPMS trace metal data can be copy pasted from the main-datasheet into this sub-datasheet in any order after the first four columns, with any metal identity (header needs to start with an element code e.g. Fe and end with LR or MR mode between brackets, e.g. (LR), so at a minimum Cd(LR)) or in any number. The "index" column contains the index numbers as created in the first column of the main-datasheet. The "sample" column contains the sample names as given in the main-datasheet, the "repetition" column shows the repeated standard additions. In this case we did a standard addition in the beginning of the run and at the end. The "conc.order" column gives the order and the identity of the standard additions. A sub-datasheet with the standard addition concentrations will also (next). The sub-datasheet StanAdd_seafast needs be created to saved "StanAdd seafast.csv" in the same example folder "20150615".

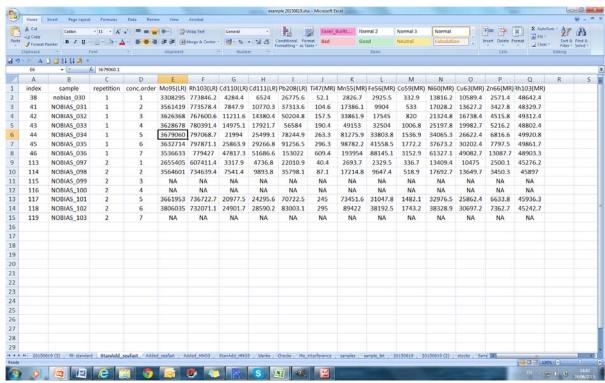


Figure 5. The StanAdd_seafast sub-datasheet.

"Added_seafast" sub-datasheet

The "Added_seafast" sub-datasheet contains the final concentrations of the standard additions for each metal to the seawater samples used with the seafast, see Figure 6. The necessary column is: i) the "conc.order", it contains the order and identity of the standard additions. The numbers in this columns need to match the numbers in the "conc.order" column of the "StanAdd_seafast" sub-datasheet. Make sure that the header names of the necessary columns remain the same as in this manual. The headers for the metals need to be their element name, e.g. "Fe". You can bring as many metal columns in as wished (no double though). It does not form a problem if it contains metals that you did not measure by IPMS or if it did not contain the metals that you did measure by ICPMS (however, these data will not be further used). The sub-datasheet Added_seafast needs to be saved as "Added_seafast.csv" in the same example folder "20150615".

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4	3	0.43	0.96	1.36	1.47	0.14	9.64	13.90	0.49	14.93	49.14	0.59
5	4	0.64	1.44	2.04	2.20	0.21	14.46	20.85	0.74	22.40	73.70	0.88
6	5	1.07	2.39	3.41	3.67	0.36	24.10	34.75	1.23	37.33	122.84	1.47
7	6	1.34	2.99	4.26	4.59	0.44	30.13	43.44	1.53	46.66	153.55	1.84
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Figure 6. The Added seafast sub-datasheet.

"Mo_interference" sub-datasheet

The "Mo_interference" sub-datasheet contains the data of a standard addition of Mo to seawater samples to be used to correct for Mo interference of the Cd measurement on the ICPMS, see Figure 7. This data will be used to determine the Mo interference of Cd and correct the Cd concentrations for it. If you are not interested in Cd you don't need this sub_datasheet. Also if you have Cd data you can chose not to correct for Mo interference. The necessary columns are: i) the "index", ii) "sample", iii) "Mo95(LR)", and iv) one of both Cd110(LR) or Cd111(LR), see Figure 7. Make sure that the header names of the necessary columns remain the same as in this manual. Make sure that the Cd isotope that you use is the same as the Cd isotope in your dataset. The "index" column contains the index numbers as created in the first column of the main-datasheet. The "sample" column contains the sample names as given in the main-datasheet. The sub-datasheet Mo_interference needs to be saved as "Mo_interference.csv" in the same example folder "20150615".

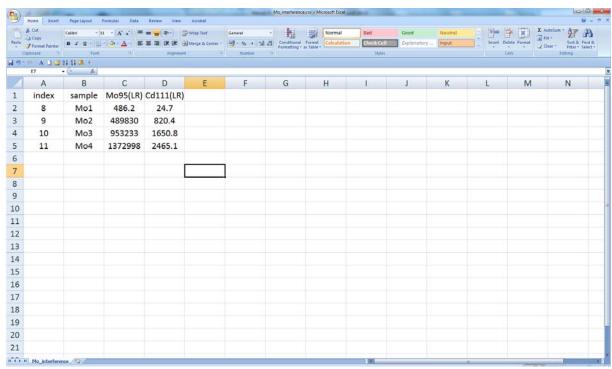


Figure 7. The Mo_interference sub-datasheet.

"blanks" sub-datasheet

The "blanks" sub-datasheet contains the data to determine the seafast blank, see Figure 8. This data will be used to correct all seawater trace metal data for the seafast blank. The necessary columns are: i) the "index", ii) "sample", and iii) "blank", see Figure 7. Make sure that the header names of the necessary columns remain the same as in this manual. The ICPMS trace metal data can be copy pasted from the main-datasheet into this sub-datasheet in any order after the first four columns, with any metal identity (header needs to start with an element code e.g. Fe and end with LR or MR mode between brackets, e.g. (LR), so at a minimum Cd(LR)) or in any number. The "index" column contains the index numbers as created in the first column of the main-datasheet. The "sample" column contains the sample names as given in the main-datasheet. The "blank" column gets and identifier for the type of blank you use. So you can do different blanks and group them by a common identifier in the "blank" column, see e.g. MQ_blank_SW and MQ_blank in Figure 8. Later you can chose which blank you will use to correct your data. The sub-datasheet blanks needs to be saved as "blanks.csv" in the same example folder "20150615".

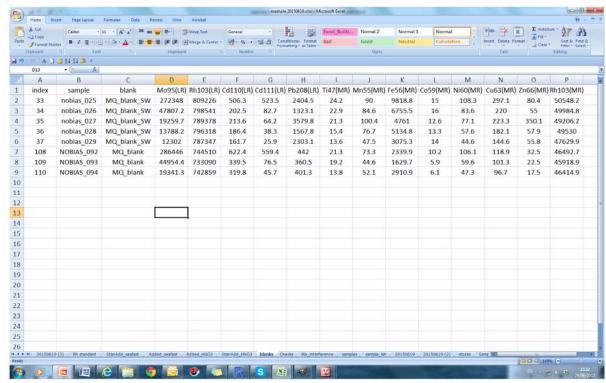


Figure 8. The blanks sub-datasheet.

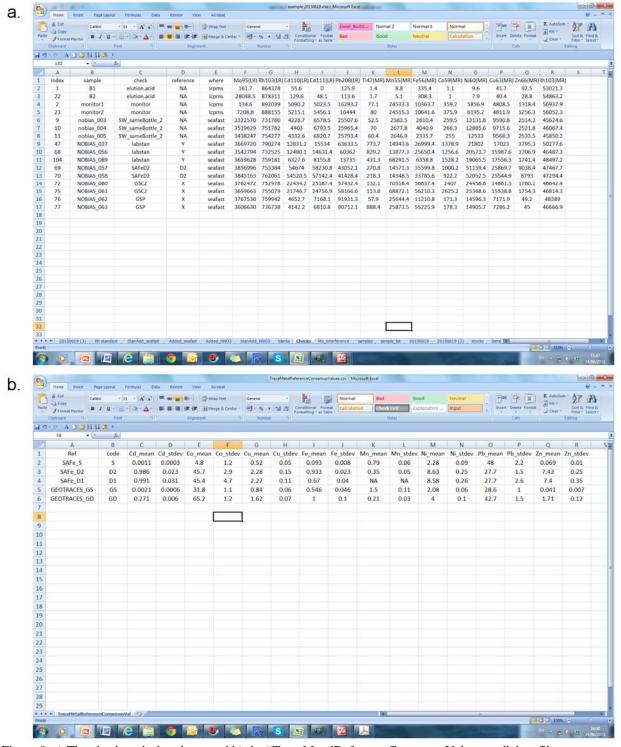
"checks" sub-datasheet

The "checks" sub-datasheet contains the data used to check different aspects, see Figure 9a. Figure 9a shows a checks sub-dataset checking the elution acid, a monitor to check the ICPMS, a check of reproducibility, a labstandard and several reference materials like SAFE. The necessary columns are: i) the "index", ii) "sample", iii) "check", iv) "reference", and v) "where", see Figure 9a. Make sure that the header names of the necessary columns remain the same as in this manual. The ICPMS trace metal data can be copy pasted from the maindatasheet into this sub-datasheet in any order after the first four columns, with any metal identity (header needs to start with an element code e.g. Fe and end with LR or MR mode between brackets, e.g. (LR), so at a minimum Cd(LR)) or in any number. The "index" column contains the index numbers as created in the first column of the main-datasheet. The "sample" column contains the sample names as given in the main-datasheet. The "check" column contains an identifier for the type of check and to group them. So you can do different checks and group them by a common identifier in the "check" column, see e.g. elution.acid and SafeD2 in Figure 9a. The "reference" column identifies the reference materials used. There is a code for the several SAFE and GEOTRACES reference samples that have consensus values attached (e.g. D2 for the SafeD2 sample see Figure 9a, other codes can be found and/or changed in the csv file with reference materials in the column "code", see Figure 9b). You can use a code like X, Y or Z or any other not used yet to indicate reference samples without consensus values like the lab standards or some of the newer official reference samples. The "where" column contains only the identifiers "seafast" and "icpms" to identify what is being checked. These identifiers are important as it determines which standard addition is used and which blanks or if blanks are used. The sub-datasheet checks needs to be saved as "checks.csv" in the same example folder "20150615".

The "TraceMetalReferenceConsensusValues.csv" file

The "TraceMetalReferenceConsensusValues.csv" file contains any know consensus values, see Figure 9b. The necessary columns are: i) the "Ref", and ii) "code". The "Ref" column identifies the reference material used. The "code" column provides an identifier that is also used in the "reference" column of the "check" sub-datasheet. You can change these codes if you want or you can add reference materials to it and add a new code. The

"TraceMetalReferenceConsensusValues.csv" needs to be saved in the same folder as the R script and the Functions script as this file will not change between different ICPMS runs.



 $Figure\ 9.\ a)\ The\ checks\ sub-data sheet,\ and\ b)\ the\ ``TraceMetalReferenceConsensusValues.csv"\ data\ file.$

"samples" sub-datasheet

The "samples" sub-datasheet contains the sample data, see Figure 10. This are the icpms data of the samples in which we wanted to measure the concentrations of the metals. The necessary columns are: i) the "index" and ii) "sample". Make sure that the header names of the necessary columns remain the same as in this manual. The ICPMS trace metal data can be copy pasted from the main-datasheet into this sub-datasheet in any order after the first four columns, with any metal identity (header needs to start with an element code e.g. Fe and end with LR or MR mode between brackets, e.g. (LR), so at a minimum Cd(LR)) or in any number. The "index" column contains the index numbers as created in the first column of the main-datasheet. The "sample" column contains the sample names as given in the main-datasheet. The sub-datasheet samples needs to be saved as "samples.csv" in the same example folder "20150615".

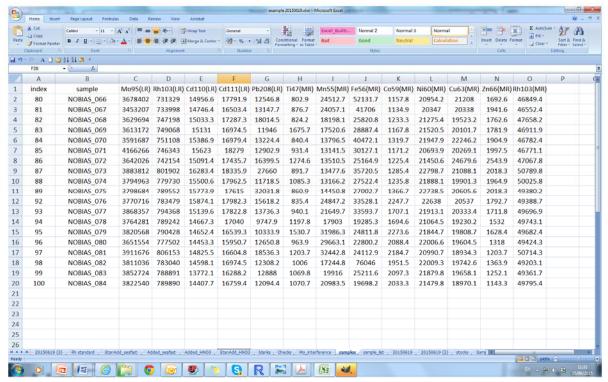


Figure 10. The samples sub-datasheet.

"sample_list" sub-datasheet

The "sample_list" sub-datasheet connects the sample name given to the seafast with the sample names, see Figure 11. This list will be used to implement the original sample names to the final results file. It is also used to implement the individual sample names into the figures with the reference material. This feature can be turned off by setting: sample.naming <- "no" in the script. So you cause the script without this sub-datasheet. The necessary columns are: i) the "seafast.name" and ii) "sample.name". The "seafast.name" column contains the sample names as given in the main-datasheet. The "sample.name" column contains the original sample names. Make sure that the header names of the necessary columns remain the same as in this manual. The sub-datasheet sample_list needs to be saved as "sample_list.csv" in the same example folder "20150615".

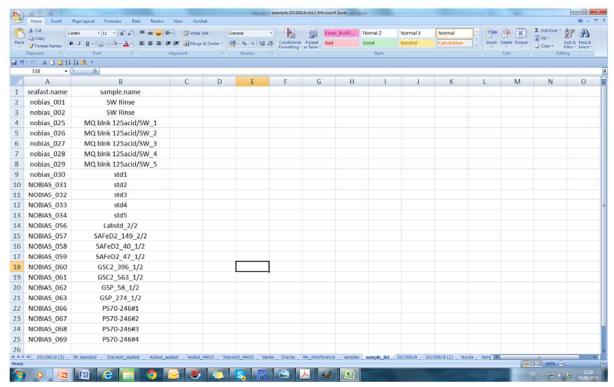


Figure 11. The sample_list sub-datasheet.

5) Using the R script

Here below I will explain how to use the R script using a number of computer screen shots. I will also show how the results look like. The red number refer to numbers in the figures. Please, note that don't have to change any coding to upload the different data files as long as you positioned them in your main directory (see explanation below). All results will be automatically located in this folder and re-opened from this folder. So do not change their locations.

Starting

- (1) If you use this script for the first time you will have to download a number of R packages. You only have to do this ones. Just remove the # and activate the line (run or cntrl R) and follow the instructions. After this you can replace the # (which prevents the line from being activated) because you do not need this line of code anymore.
- (2) This line just cleans the memory from anything that R has put in there. You don't need to re-run this all the time.
- (3) Part of the code depends on code written by others. To be able to use this script the libraries need to be activated when you start.
- (4) When you work in the basic R environment (not R studio or such) it is easiest to turn of the buffer so that you see the messages displayed in the R console that shows you how far you are with your analysis. It also provides extra information.
- (5) Some R code is different between Windows and Apple computers. Here you can indicate which system you use to run your script on. Basically the only difference in this script is that to create a figure a windows computer uses windows() and an Apple computer uses quartz () instead.
- (6) This line sets the working directory where your R script, your R Functions and your TraceMetalReferenceConsensusValues.csv file are located. You need to adapt this to your situation. Note, the example included and to use "/" instead of "\".
- (7) This line opens the R Functions script with the functions needed to analyse your data for use in your R script.

The general parameters are a number of parameters that you need to adapt if necessary and which stay the same throughout the remainder of the R script. So adapt them and you activate them once after you started. If you start working with a new data set you may have to change part of it again.

- (8) This vector shows the units used for each metal. You may have to change the location of the metals with respect to the vectors from nM (units.nM) to pM (units.pM) or visa versa depending on your own preferences.
- (9) Generally an element like Rh or Ga is used to correct for variations in the sensitivity of the ICPMS. If you add this element to the bulk eluting HNO3 solution before extracting the metals from the column it also corrects for solution evaporation between extraction and measurement on the ICPMS. At this line you can include the element that you use for this.
- (10) The **mainDir** directs the script to the folder with your data (the main-datasheet) and the sub-datasheet csv files. With this line the R script knows where to load the data from and where to save the results. The **name.run** is the name of your icpms run. It will appear in all file names (graphs and data) and as title in your figures.
- (11) The <u>fAcces.prev.files</u> function allows loading data that has been produced during a previous use of this script with a certain data set when the procedure was not completed. It

prevents you to have to rerun the part of the script that you used in a previous session with a certain data set.

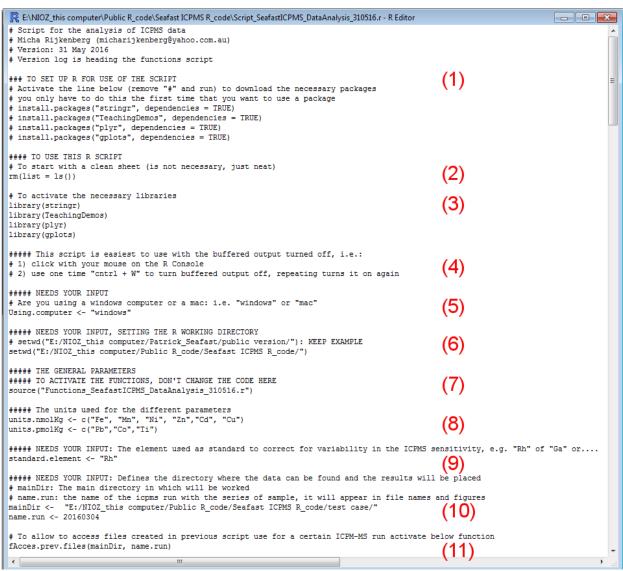


Figure 12. Start of the R script.

The fStElement.stand function

This function takes the standard element like for example Rh or Ga etc data and normalizes your metal data to the mean standard element concentration. Variation due to changes in ICPMS sensitivity or evaporation of the sample extract are than corrected for, see Figure 13. Rh is used as an example throughout this manual.

- (1) This line codes read in the data from the StandardElement.csv file that you created and shows you the headers and first five data points.
- (2) The codes save the graph as a tif file and shows the graph in your window. The: resolution.figures determines the resolution of the tif file
- cex determines the size of the symbols
- cex.lab determines the size of your axis titles
- cex.axis determines the size of the axis symbols
- (3) In our case we find sometimes different levels of Rh concentrations depending on the additions to the samples. You cannot just all normalize them to one Rh value. You have to do that for each group separate. Using the "line.high.lr", "line.low.lr", "line.high.mr", "line.low.mr" you can separate a maximum of three different Rh concentration groups for both the LR and the MR resolution. By changing the numbers behind them and re-running the function below you can fine tune the groups, see Figure 14. If you have only two Rh concentration groups you can put the "line.low" at 0 and if all samples had the same Rh concentration you can change "line.low" and "line.high" to 0 for both LR and MR. Sometimes it is impossible to neatly separate the groups. Try to do it as good as possible and adapt the final resulting csv file by hand for the samples that you were unable to place in the Rh concentration group where they belonged. After manual adaption of the csv file don't rerun the fRh.stand function anymore as it will change your adapted csv file again.
- (4) This line runs the function. It results in a tif file of the graph shown in Figure 14 and in a csv file with the mean Rh concentration for the different Rh groups and the two different resolutions LR and MR. The csv file needs to stay at the location where it was saved to as it will be used from there further on in the script.

Figure 13. The function needed to correct the data for changes in ICPMS sensitivity using Rh.

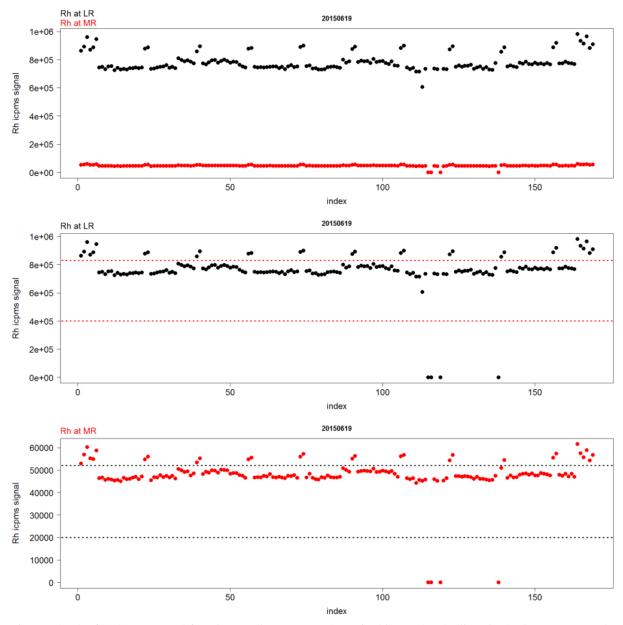


Figure 14. The fStElement.stand_function results (among others) in this graph. The lines in the lower two graphs visualize how you divided the groups with different Rh concentrations. You can manipulate this lines within the R script. The data will be normalized to the mean Rh concentration of the Rh concentration group that they belong to.

The fStandAdd.HNO3 and fStandAdd.seafast functions

These functions uses the "StanAdd_HNO3.csv", "StanAdd_seafast.csv", "Add_HNO3.csv" and "Add_seafast.csv" files for the standard additions in the HNO3 eluent and in seawater used with the seafast and provides the slopes for each metal of each standard addition and visualizes the results in graphs saved as tif files, see Figure 15 a,b. Variation due to changes in ICPMS sensitivity are corrected for using the Rh data.

- (1, 2 and 3) These lines read in the data from the files "StanAdd_HNO3.csv", "StanAdd_seafast.csv", "Add_HNO3.csv" and "Add_seafast.csv" and the results from the fRh.stand function to correct the data for changes in ICPMS sensitivity. In each case the header and five of the data rows will be shown.
- (4) The codes save the graph as a tif file and shows the graph in your window. The: resolution.figures determines the resolution of the tif file
- cex determines the size of the symbols
- cex.lab determines the size of your axis titles cex.axis determines the size of the axis symbols
- (5) This line determines if you want to have
- (5) This line determines if you want to have the data corrected for changes in ICPMS sensitivity (Standard.element.correction <- "yes") or not (Standard.element.correction <- "no").
- (6) These are the functions fStandAdd.HNO3 and fStandAdd.seafast that you need to run. It will result in graphs visualizing the standard additions and in a .csv file with the slope etc that will be used later to calculate the metal concentrations in your samples, see Figure 16. The HNO3 standard addition is only used for sample that are directly (without using the seafast) measured on the ICPMS and to calculate the recovery efficiency of each metal by the seafast system.

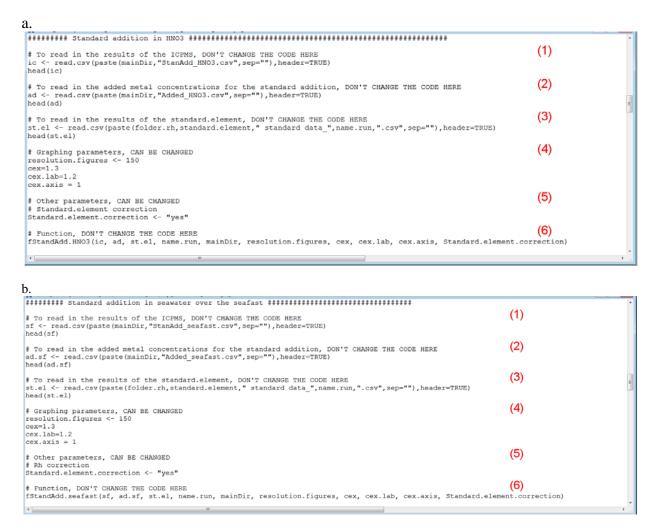


Figure 15 a,b. The functions fStandAdd.HNO3 and fStandAdd.seafast for the standard additions.

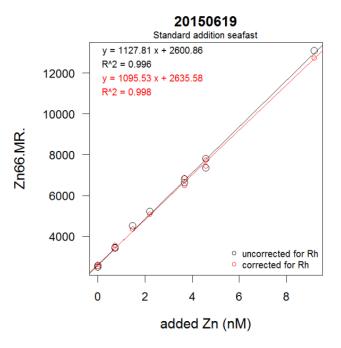


Figure 16. Example of a figure with the seafast standard addition of Zn.

The fMo.interference function

This function takes the data of a Mo standard addition to HNO3 eluent to determine the Mo interference on the Cd signal. This can be used to correct the Cd data for this interference, see Figure 17.

- (1, 2) These lines read in the data from the Mo_interference.csv file and the Rh results to correct the data for changes in the ICPMS sensitivity.
- (3) The codes save the graph as a tif file and shows the graph in your window. The: resolution.figures determines the resolution of the tif file
- cex determines the size of the symbols
- cex.lab determines the size of your axis titles
- cex.axis determines the size of the axis symbols
- (4) This line determines if you want to have the data corrected for changes in ICPMS sensitivity (Standard.element.correction <- "yes") or not (Standard.element.correction <- "no").
- (5) This line activates the fMo.interference function. It results in a csv file with the slope between changes in Mo and Cd used to correct the Cd data further on in the script. It also creates a graph as a tif file visualizing the relationship between Mo and Cd, see Figure 18.

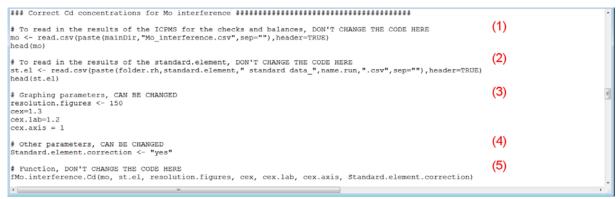


Figure 17. The function fMo.interference for the correction of the Cd signal by Mo interference.

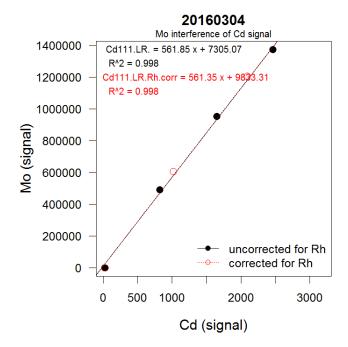


Figure 18. Example of the graph visualizing the Mo interference of the Cd signal.

The fBlank.Conc.Stats function

This function calculates the mean and median blanks for the different metals and visualizes them as boxplots saved as tif files where outliers are indicated by the index numbers as defined in the main-datasheet, see Figure 19. This so you can delete (replace by NA) these outliers from the blanks.csv file and re-run the function. In the remainder of the script the possibility is left open to either use the mean or the median to correct the metal data for the blank.

- (1, 2, 3, 4) These code lines open the "blanks.csv" file with the blank data, the file with the results of the seafast standard addition, the results of the Rh correction, and the results to correct the Cd data for Mo interference and it shows the headers and first five rows of each of these files.
- (5) The codes save the graph as a tif file and shows the graph in your window. The: resolution.figures determines the resolution of the tif file
- cex determines the size of the symbols
- cex.lab determines the size of your axis titles
- cex.axis determines the size of the axis symbols
- (6) This line determines if you want to have the data corrected for changes in ICPMS sensitivity (Standard.element.correction <- "yes") or not (Standard.element.correction <- "no"). You can also chose if you correct your Cd data for Mo interference (Mo.correction.Cd <- "yes") or not (Mo.correction.Cd <- "no").
- (7) This line activates the fBlank.Conc.Stats function. It results in a csv file with the with among others the mean and median blanks of the metals of interest. It also creates for each metal a graph as a tif file with a boxplot visualizing the data spread and any outliers. Outliers are identified in blue numbers by their index number, see Figure 20. This is the index number that has been added to the main-datasheet.

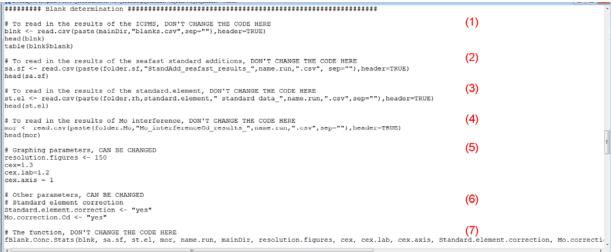


Figure 19. The function fBlank.Conc.Stats for calculation of mean and median blank values.

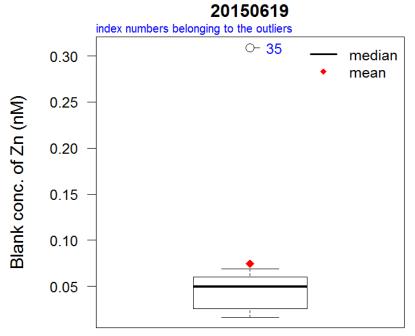


Figure 20. Example of the graph visualizing the spread in the Zn blank data with one outlier with index number 35 (you see how it increases the mean).

The fChecks.balances function

This function dela with the checks and balances for the seafast and the ICPMS, see Figure 21. It has several outputs:

- 1) Two csv files with metal concentrations of the seafast and icpms checks, respectively.
- 2) Boxplots as tif files summarizing all checks for each metal seperately, see Figure 22.
- 3) Dot plots as tif files for each metal and each check separate in separate folders for each check, see Figure 23
- 4) Dot plots with the reference samples including the consensus values when known or given, see Figure 24
- 5) csv file with the metal concentration of the reference samples
- 6) csv file with the percentage recovery efficiencies of the seafast. The percentage recovery efficiencies were calculated from the slope of the standard addition in the HNO3 elution acid and the standard addition of the seafast corrected for the preconcentration factor.
- (1) This line opens the data file with the data of the checks ("checks.csv")
- (2) This line opens the data file with the results of the seafast standard addition
- (3) This line opens the data file with the results of the standard addition in the HNO3 elution acid
- (4) This line opens the data file with the Rh results needed to correct the data for changes in ICPMS sensitivity (it also corrects for the evaporation of eluent).
- (5) This line opens the data file with results of the metal blanks. By defining: blank.type.name <- "MQ_blank_SW" (or another code from the column "blank" in "blanks.csv" that represents the blank data that you want to use to correct your metal data.
- (6) This line opens the file with reference sample consensus values
- "TraceMetalReferenceConsensusValues.csv". You can add new reference samples to this file yourself.
- (7) This line opens the data file with the results needed to correct the Cd data for Mo interference.
- (8) This line opens the data file with the original sample names connected to the seafast sample names "sample_list.csv". This allows the individual reference samples to be indicated in the graphs when multiple reference samples are used.
- (9) The codes save the graph as a tif file and shows the graph in your window. The: resolution.figures determines the resolution of the tif file
- cex determines the size of the symbols
- cex.lab determines the size of your axis titles
- cex.axis determines the size of the axis symbols
- (10) This set of lines provides you with some choices:

Standard.element.correction <- "yes" (or "no") determines if you want to have the data corrected for changes in ICPMS sensitivity using Rh. It also corrects for evaporation of the elution acid.

Mo.correction.Cd <- "yes" (or "no") determines if you want your Cd data to be corrected for Mo interference.

use.Blank <- "mean" (or "median") indicates if you want to use the mean or median of the blanks to correct your metal data.

Seafast.conc.factor <- 10/0.65 indicates the seafast concentration factor (10 ml seawater into 650 μ l HNO3 eluent). This factor is needed to calculate the seafast percentage recovery efficiency for each metal.

outliers.boxplot <- "yes" (or "no") The boxplots comparing all the checks and balances in one plot can be graphed with the outliers included. However, sometime this would affect the scale of the boxplot such that the boxplots become unreadable/useless. In this case you can choose for "no" and choose to not graph the outliers.

(11) sample.naming <- "yes" (or "no") indicates if you want to have the original sample naming of your reference material in the graphs with results of the reference samples. It makes it easier to identify the results of individual reference samples, see Figure 24.

(12) This line activates the function.

```
(1)
# To read in the results of the ICPMS for the checks and balances, DON'T CHANGE THE CODE HERE
et al. one results of the LUMN for the checks and balan
ck <- read.csv(paste(mainDir,"checks.csv",sep=""),header=TRUE)
head(ck)
table (ck$check)
                                                                                                                                                                                                             (2)
# To read in the results of the seafast standard additions, DON'T CHANGE THE CODE HERE
sa.sf <- read.csv(paste(folder.sf, "StandAdd_seafast_results_",name.run,".csv", sep=""),
head(sa.sf)</pre>
# To read in the results of the HNO3 standard additions, DON'T CHANGE THE CODE HERE sa.HNO3 <- read.csv(paste(folder.HNO3,"StandAdd_HNO3_results_",name.run,".csv", sep=""),header=TRUE) head(sa.HNO3)
                                                                                                                                                                                                             (4)
# To read in the results of the standard.element, DON'T CHANGE THE CODE HERE st.el <- read.csv(paste(folder.rh,standard.element," standard data_",name.run,".csv",sep=""),header=TRUE)
T NO LEGAL IN the results of the seafast blank, ONLY CHANGE "blank.type.name" to the name that you gave to the blablank.type.name <- "MQ blank"
blank <- read.csv(paste(folder.blank,"StatsData_blank_",blank.type.name,"_",name.run,".csv",sep=""),header=TRUE)
head(blank)
# To read in the results of the seafast blank, ONLY CHANGE "blank.type.name" to the name that you gave to the blank that you will use
                                                                                                                                                                                                             (6)
# To read in the reference material consensus values, DON'T CHANGE THE CODE HERE ref.mat <- read.csv("TraceMetalReferenceConsensusValues.csv",header=TRUE) head(ref.mat)
# To read in the results of Mo interference, DON'T CHANGE THE CODE HERE
mor <- read.csv(paste(folder.Mo,"Mo_interferenceCd_results_",name.run,".csv",sep=""),header=TRUE)
head(mor)
                                                                                                                                                                                                             (8)
# To read the sample coding, DON'T CHANGE THE CODE HERE
 coding <- read.csv(paste(mainDir, "sample_list.csv", sep=""), header=TRUE)
head(coding)
                                                                                                                                                                                                             (9)
# Graphing parameters, CAN BE CHANGED resolution.figures <- 150
cex.axis = 1
                                                                                                                                                                                                             (10)
# Other parameters, CAN BE CHANGED Standard.element.correction <- "yes Mo.correction.Cd <- "yes" use.Blank <- "median" # eit Seafast.conc.factor <- 10/0.65 outliers.boxplot <- "no"
                                             # either use "mean" or "median"
                                                                                                                                                                                                             (11)
# includes sample names in the graphs of the reference values, if you don't have a sample_list say "no"
 sample.naming <- "yes"
                                                                                                                                                                                                             (12)
the function, DON'T CHANGE THE CODE HERE fChecks.balances(ck, sa.sf, st.el, blank, ref.mat, mor, coding, sample.naming, name.run, mainDir, use.Blank, Seafast.conc.factor, outliers.boxp
```

Figure 21. The function fChecks.balances to deal with all seafast and ICPMS checks.

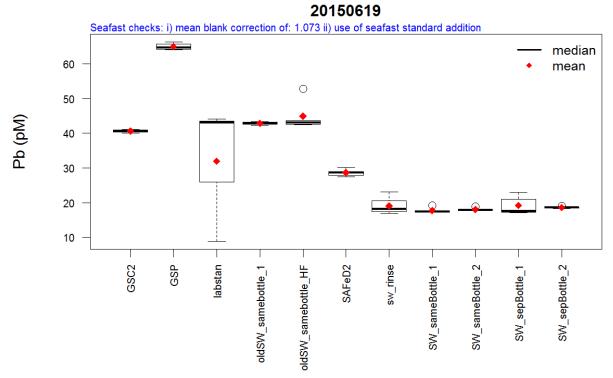


Figure 22. Example of a boxplot summarizing all seafast checks for Pb.

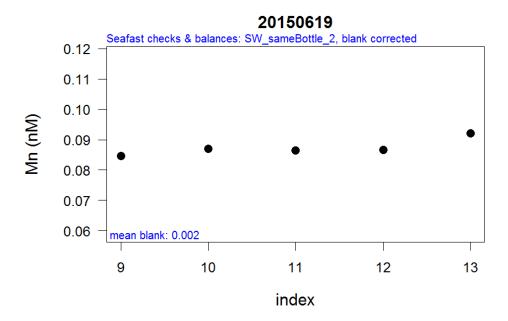


Figure 23. Example of a dotplot showing the check where repeated samples from the same bottle were extracted on the seafast for Mn.

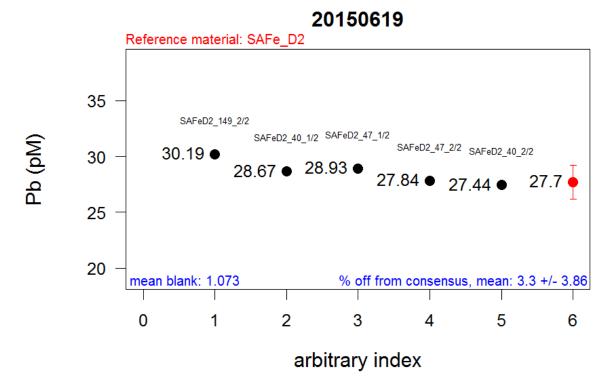


Figure 24. Example of a dotplot showing the results of the reference samples for Pb including the consensus value.

The fSample.concentrations and fSample.codes functions

The function fSample.concentrations calculates the final metal concentrations from the data in "samples.csv", see Figure 25. The output is a csv file with the concentrations and a series of dot plots as tif files showing the metal concentrations of the samples for each metal. The function fSample.codes does nothing else then to include the original the original sample names using input from "sample_list.cvs", see Figure 25.

- (1) This line opens the file with sample data "samples.csv"
- (2) This line opens the result of the seafast standard addition.
- (3) This line opens the results for the Rh correction to correct for sensitivity changes in the ICPMS and evaporation of elution acid.
- (4) This line opens the data file with results of the metal blanks. By defining: blank.type.name <- "MQ_blank_SW" (or another code from the column "blank" in "blanks.csv" that represents the blank data that you want to use to correct your metal data.
- (5) This line opens the data file with the results needed to correct the Cd data for Mo interference.
- (6) The codes save the graph as a tif file and shows the graph in your window. The: resolution.figures determines the resolution of the tif file
- cex determines the size of the symbols
- cex.lab determines the size of your axis titles
- cex.axis determines the size of the axis symbols
- (7) This set of lines provides you with some choices:

Standard.element.correction <- "yes" (or "no") determines if you want to have the data corrected for changes in ICPMS sensitivity using Rh. It also corrects for evaporation of the elution acid.

Mo.correction.Cd <- "yes" (or "no") determines if you want your Cd data to be corrected for Mo interference.

use.Blank <- "mean" (or "median") indicates if you want to use the mean or median of the blanks to correct your metal data.

- (8) This line activates the function.
- (9) This line opens the file with the concentrations of the trace metals as calculated using the previous function.
- (10) This line opens the data file with the original sample names connected to the seafast sample names "sample_list.csv". This allows the individual reference samples to be indicated in the graphs when multiple reference samples are used.
- (11) This line activates the function.

```
# To read in the results of the ICPMS for the checks and balances, DON'T CHANGE THE CODE HERE
fr <- read.csv(paste(mainDir,"samples.csv",sep=""),header=TRUE)</pre>
head(fr)
# To read in the results of the seafast standard additions, DON'T CHANGE THE CODE HERE
sa.sf <- read.csv(paste(folder.sf,"StandAdd_seafast_results_",name.run,".csv", sep=""),header=TRUE)
head(sa.sf)
# To read in the results of the standard.element, DON'T CHANGE THE CODE HERE
st.el <- read.csv(paste(folder.rh,standard.element," standard data ",name.run,".csv",sep=""),header=TRUE)
                                                                                                  (4)
# To read in the results of the seafast blank, DON'T CHANGE THE CODE HERE blank.type.name <- "MQ_blank_SW"
blank <- read.csv(paste(folder.blank,"StatsData_blank_",blank.type.name,"_",name.run,".csv",sep=""),header=TRUE)
                                                                                                  (5)
# To read in the results of Mo interference, DON'T CHANGE THE CODE HERE
mor <- read.csv(paste(folder.Mo,"Mo_interferenceCd_results_",name.run,".csv",sep=""),header=TRUE)
                                                                                                  (6)
# Graphing parameters, CAN BE CHANGED
resolution.figures <- 150
cex=1.3
cex.axis = 1
# Other parameters, CAN BE CHANGED
Standard.element.correction <- "no"
use.Blank <- "mean"
                      # either use "mean" or "median"
Mo.correction.Cd <- "no"
# the function, DON'T CHANGE THE CODE HERE
fsample.concentrations(fr, sa.sf, st.el, blank, mor, name.run, mainDir, use.Blank, resolution.figures, cex. cex.lab, cex.
(9)
# To read the final concentration results, DON'T CHANGE THE CODE HERE
samples <- read.csv(paste(folder.samples, "Sample concentrations_", name.run, ".csv", sep=""), header=TRUE)
head(samples)
                                                                                                  (10)
# To read the sample coding, DON'T CHANGE THE CODE HERE
coding <- read.csv(paste(mainDir,"sample_list.csv",sep=""),header=TRUE)
head(coding)
# Function, DON'T CHANGE THE CODE HERE
fsample.codes(samples, coding)
```

Figure 25. The function fSample.concentrations and fSample.codes to calculate the metal concentrations of the environmental samples and to add the original sample coding.