SAMS

Spectral Analysis and Management System

Version 2.0

User's Manual

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April, 2003

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1 Introduction

The Spectral Analysis and Management System (SAMS) is used to manage field spectra databases and analyses. SAMS 2.0, a new version of SAMS originally written by Michael O'Neill in 1999, adds new options to import, organize, visualize, manipulate, and export spectral data. The new version is a stand-alone Java application requiring a Java Runtime Environment (JRE).

Features include: import/export options in various formats, signature groupings, metadata management, common operations on single or multiple signatures, drag-and-drop, and a richer set of plotting capabilities. SAMS 2.0 does not require Matlab and runs on multiple platforms (Windows, Linux, and UNIX). Databases are interchangeable among these platforms.

Main concepts

Database

Spectra files are organized in databases. Each database is managed by SAMS as an independent entity and can have its own spectra metadata definition. Use SAMS to create new database(s), open existing database(s), import spectra files into an existing database, and delete database(s).

Signature

Defined as an ordered sequence of real points, a *signature*, $s = [(x_1, y_1), (x_2, y_2), \ldots, (x_n, y_n)]$ where x_i is a *wavelength value* and y_i is the *reflectance value* at wavelength, x_i. When importing signatures, SAMS usually assumes values are measured in nanometers. It will make any necessary rearrangement so that $x_1 < x_2 < \ldots < x_n$ holds.

After a database has been created, the user imports a number of spectra files in a recognized format. This operation is called *importation of signatures*. Recognized formats are (Appendix A):

- ASD[1] (binary and ASCII variants)
- GER[2]
- ASCII
- ENVI[3] Standard file.

SAMS can read multiple files at once which facilitates importing a lot of files. Files can be from:

- a given directory

[1] ASD, Analytical Spectral Devices.

[2] GER, Geophysical & Environmental Research Corporation.

[3] ENVI, *Environment for Visualizing Images*.

- the system clipboard
- drag-and-drop operations.

Grouping

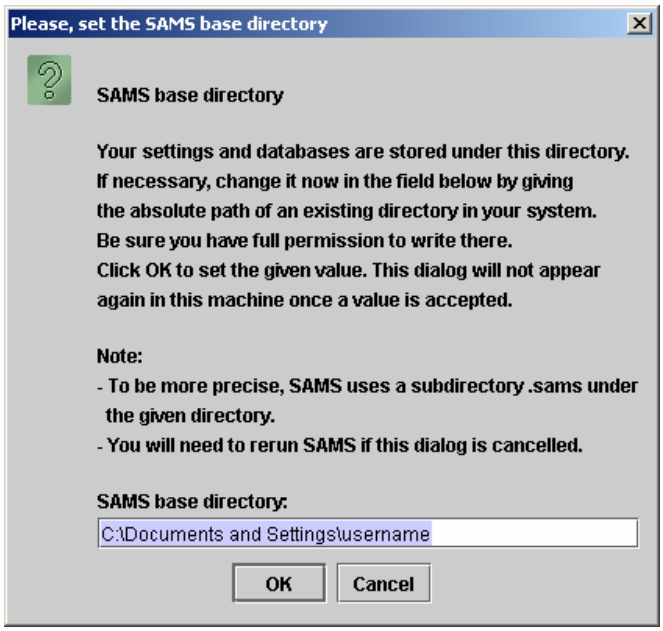
Groups of signatures can be created manually with user-defined criteria or, sometimes, automatically by SAMS.

2 Installation

A Java Runtime Environment (JRE version 1.4 or newer) properly installed on your machine is the only requirement for SAMS. JRE can be downloaded from: http://java.sun.com/j2se/1.4/download.html.

- Go to: http://www.cstars.ucdavis.edu/software/sams/.
- Follow the instructions for installation.

The first time it is run, SAMS will ask you to set the *base directory* where settings and databases will be stored. This dialog box appears:



Typically you use your *home directory* according to your operating system,[4] but you can use a directory of your choosing.

[4] Typically "c:\Documents and Settings\username" on Windows systems, and "/home/username" on UNIX or Linux systems.

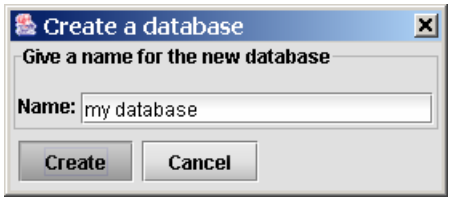
This path setting is very useful if you are running SAMS from different machines and want to access the same data through a networked drive or directory. The dialog box appears only once for a given machine/OS.

3 Getting started – a brief tour

This brief tour assumes you have a number of spectra files in a recognized format (Appendix A).

3.1 Creating a database

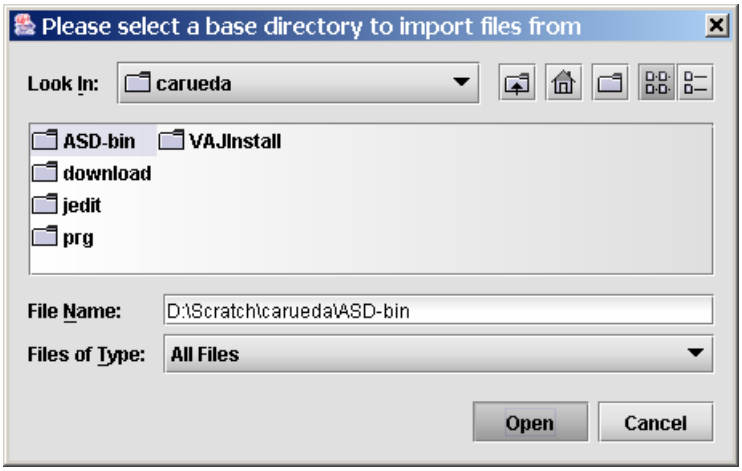
Use the option **`Database -> New`**.



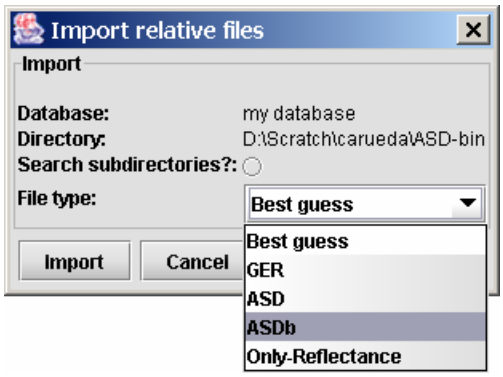
Assign a short, descriptive name. SAMS will add a new entry in its list of databases.

3.2 Importing signatures

Use the option **`Database -> Import signatures from -> Directory`**.



Select a base directory. SAMS will ask you for some options to perform the operation.



Search subdirectories? Check to scan all files in the directory and its subdirectories.

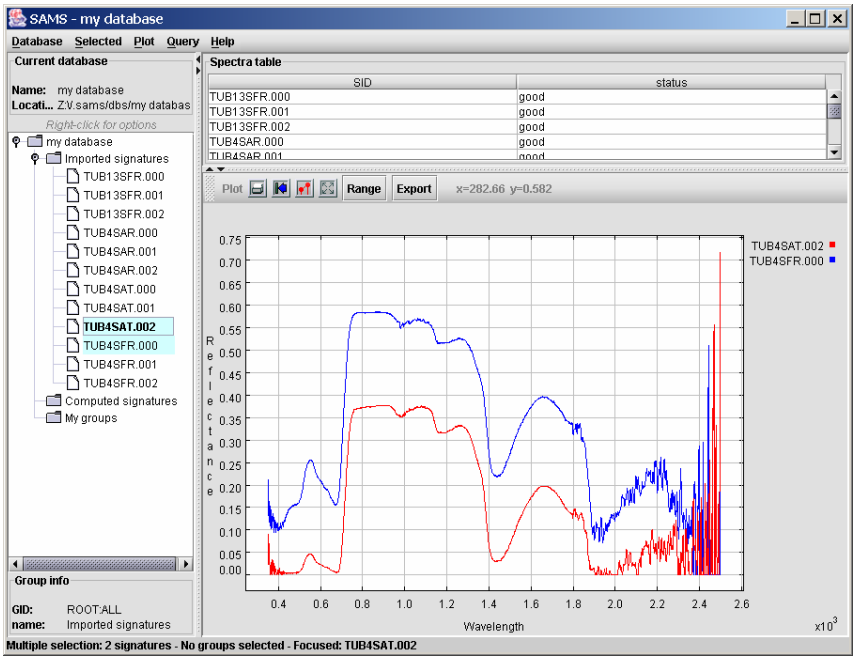
File type. Choose these options to import files of these formats:[5]

- **GER**. GER.
- **ASD**. ASD ASCII format.
- **ASDb**. ASD binary format.
- **Only-Reflectance**. ASCII files with at least one column (reflectance values).
- **Best guess**. Select for unknown format, or for files with different formats. SAMS will attempt to automatically recognize each file.

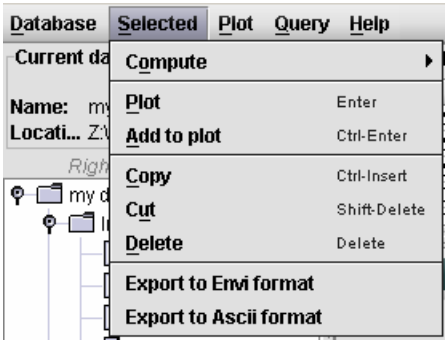
3.3 Browsing spectra

Use your mouse to select some signatures in the left window.

[5] Appendix A describes the currently recognized formats.

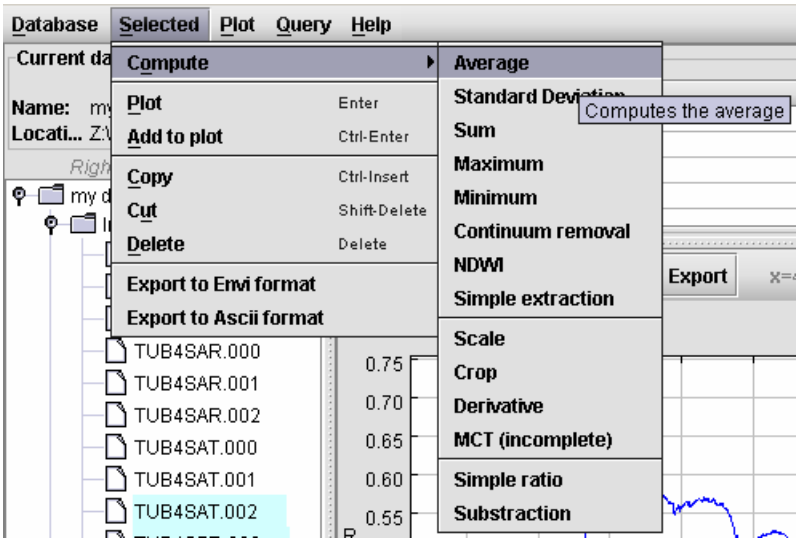


SAMS includes a **Selected** menu containing these options:

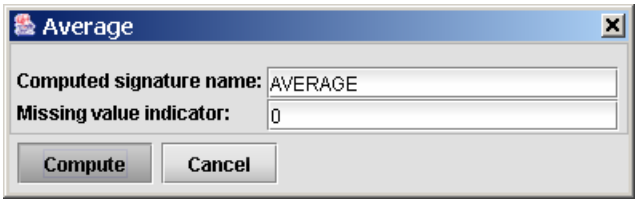


3.4 Performing an operation – an example

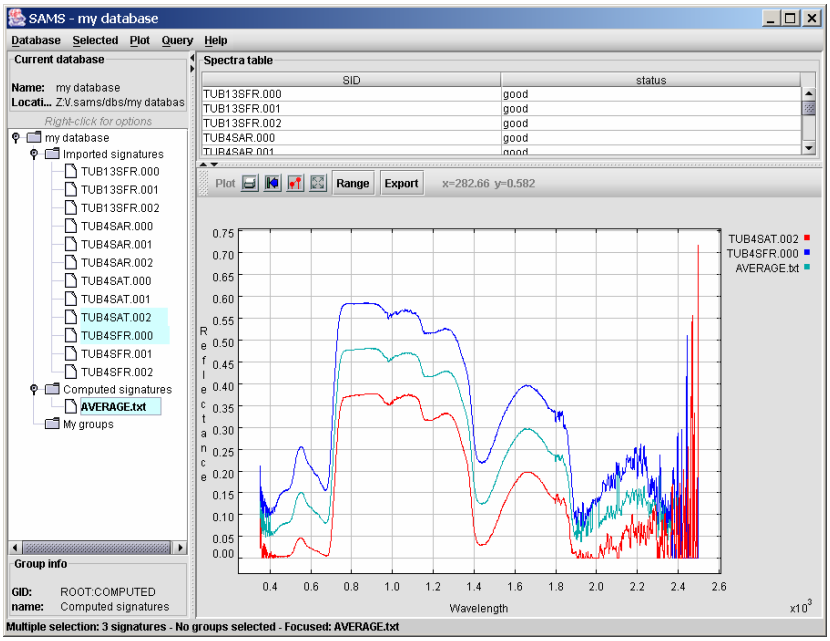
Average the current selected signatures: **`Selected -> Compute -> Average`**.



SAMS will ask you to enter a name and a **missing value indicator**:



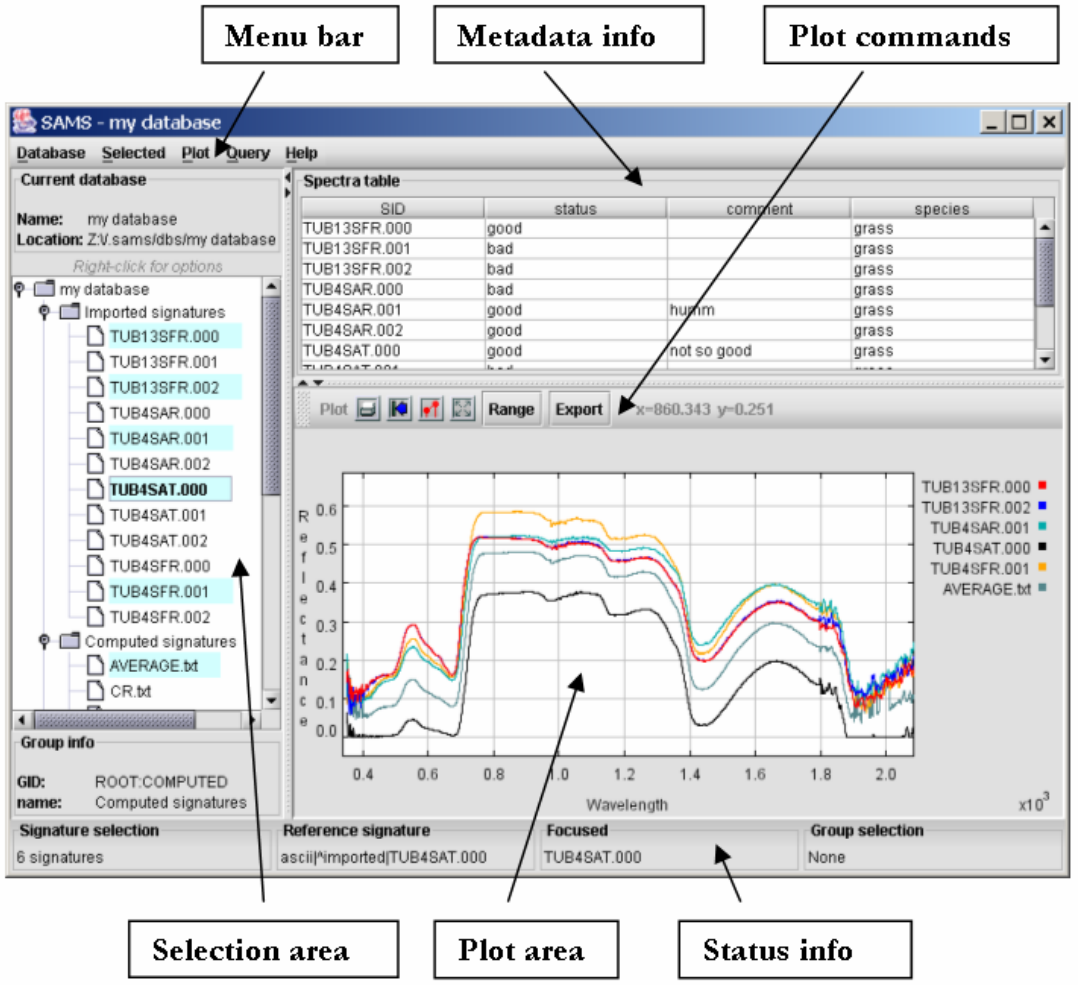
AVERAGE automatically becomes a member of the **Computed signatures** special group:



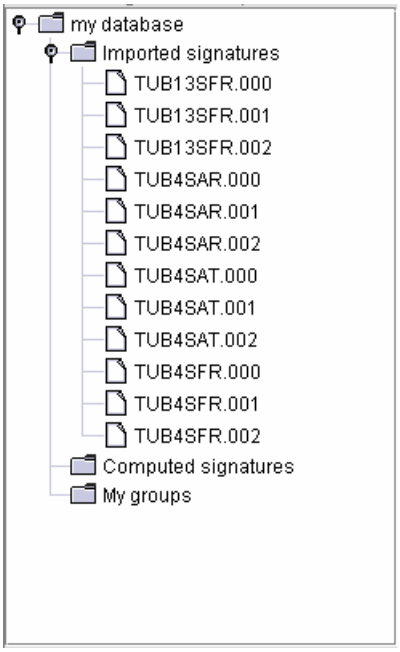
Clicking on this signature while holding down the **Ctrl** key adds it to the plot.

4 Overview

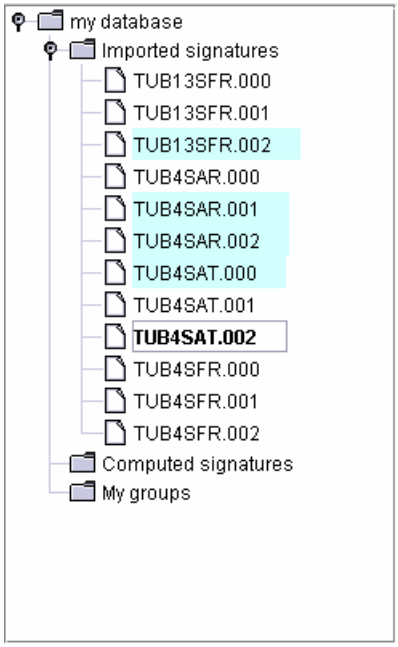
4.1 Graphical interface



4.2 Selection area and group management



Use your mouse and/or keyboard to operate in this area. Each entry corresponds to a signature. None, one, or more signatures can be selected at a time. Most SAMS commands act on the current selection.



Above, four highlighted signatures were selected by clicking while holding down the **`Ctrl`** key.

Only one *focused* element (surrounded by a square) can be selected at a time. To change the *focused* element, hold down the **Ctrl** key and use the navigational keys (Up and Down arrows, Page-up, Page-down, Home, End).

The *focused* element is used as the reference signature for reference-based operations when the command **Alt-Enter** is used.

There are three main groups in a SAMS database.

- Imported signatures
- Computed signatures
- My groups

These groups are created automatically with every database and cannot be deleted.

4.2.1 Imported signatures

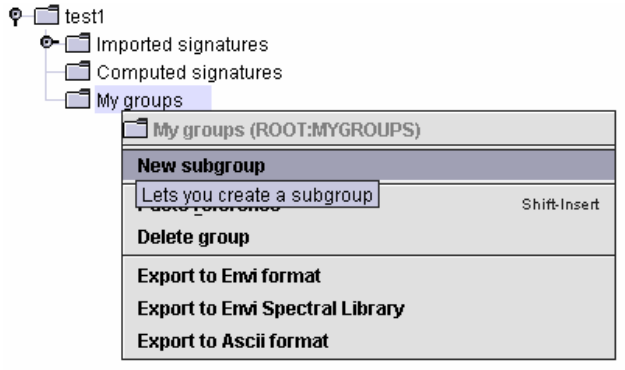
All imported signatures are in the **Imported signatures** group.

4.2.2 Computed signatures

All signatures resulting from an operation, as described in Section 5, are in the **Computed signatures** group.

4.2.3 My groups

Define as many groups as you want by right-clicking on **My groups** and using the pop-up menu.

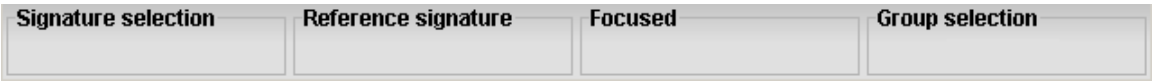


Populate the group by copying and pasting.

4.2.4 Automatic groupings

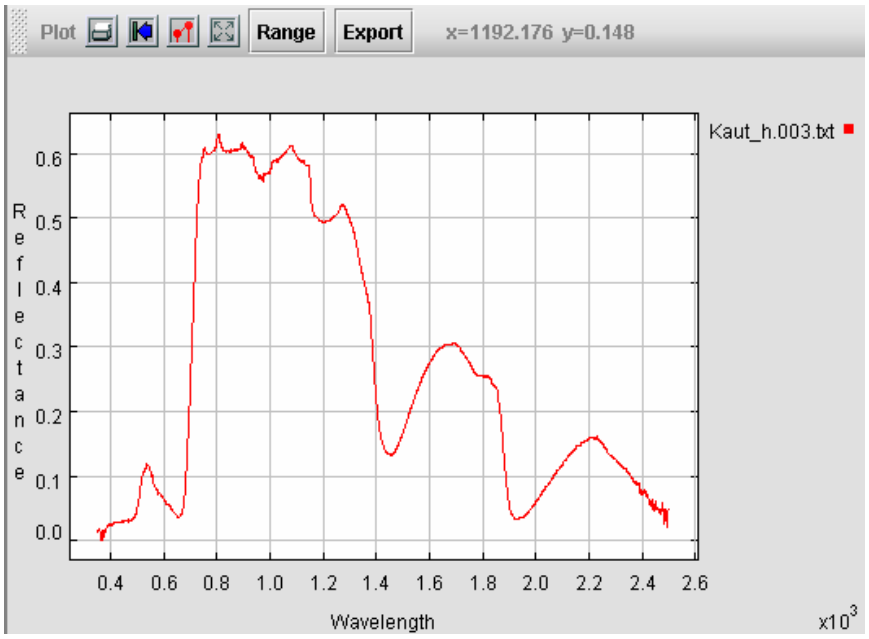
SAMS can generate groups automatically. See section 6.1.9 for options.

4.3 Status info



- **Signature selection -** number of selected signatures (or its name, if only one signature is selected).
- **Reference signature -** name of current signature (used as reference for reference-based operations).
- **Focused –** name of current focused element (either a group or a signature). If it is a signature, pressing **Alt-Enter** will make this element the reference.
- **Group selection -** number of selected groups (or group's name if only one group is selected).

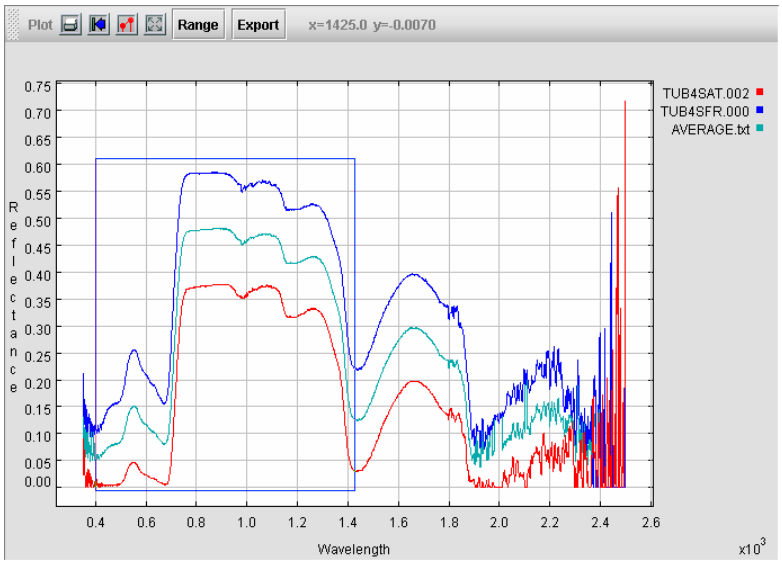
4.4 Plot area



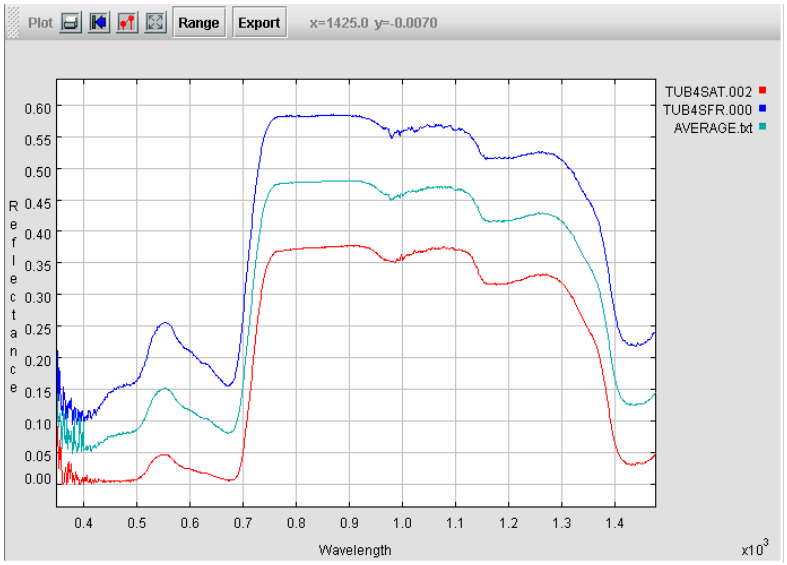
Includes buttons for common plot operations (see Section 6.3). Also shows the mouse location in X-Y coordinates.

Mouse interaction

To zoom in, drag the left mouse button down and to the right to draw a box around an area that you want to see in detail.

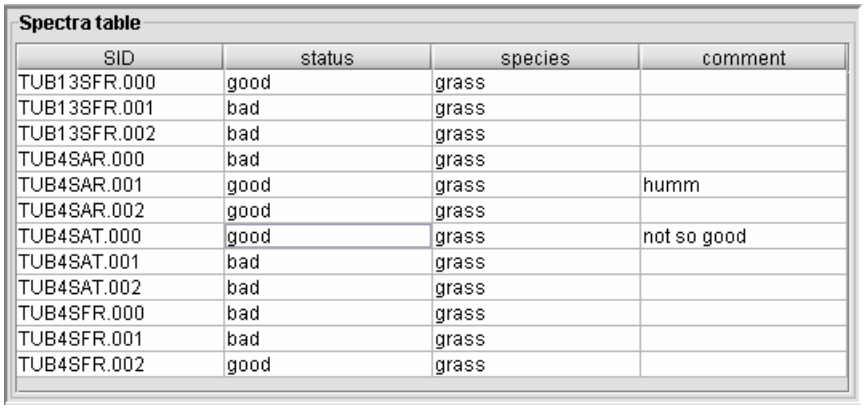


SAMS enlarges the area in the box.



To zoom out, drag the left mouse button up and to the right. To just fill the drawing area with the available data, use the fill command **`Plot -> Range -> Full scale`**.

4.5 Metadata



Spectra table

SID	status	species	comment
TUB13SFR.000	good	grass	
TUB13SFR.001	bad	grass	
TUB13SFR.002	bad	grass	
TUB4SAR.000	bad	grass	
TUB4SAR.001	good	grass	humm
TUB4SAR.002	good	grass	
TUB4SAT.000	good	grass	not so good
TUB4SAT.001	bad	grass	
TUB4SAT.002	bad	grass	
TUB4SFR.000	bad	grass	
TUB4SFR.001	bad	grass	
TUB4SFR.002	good	grass	

Metadata associated with each signature is shown in the above table. Although each SAMS database has a default set of associated attributes, you can define new attributes, too. Choose **`Database -> Edit metadata structure`**. Attributes are specific to each database. See Section 6.1.7.

4.6 Keyboard shortcuts

Most frequent commands have keyboard shortcuts as follows.

Key stroke	*Action*	*See*
`Ctrl-N`	Create new database	6.1.1
`Ctrl-O`	Open existing database	6.1.2
`Ctrl-S`	Save current database	6.1.3
`Ctrl-W`	Close current database	6.1.4
`Ctrl-Q`	Quit SAMS	6.1.10
`Alt-Enter`	Sets the "reference" signature	6.2.4
`Enter`	Plot only selected signatures	6.2.2
`Ctrl-Enter`	Plot selected signatures while keeping the already plotted ones	6.2.3
`Ctrl-P`	Print plot	6.3.5
`Ctrl-Insert`	Copy selected signatures to internal clipboard	6.2.5
`Shift-Delete`	Cut selected signatures to internal clipboard	6.2.6
`Delete`	Delete selected signatures	6.2.7

5 Signature operations

In SAMS a signature operation f can be:

- one-to-one, $f(s) \rightarrow s'$
- many-to-one, $f(s_1, s_2, ..., s_n) \rightarrow s'$
- reference-based, $f_r(s) \rightarrow s'$

Signature operations are applied to the current selection where $s_1, s_2, ..., s_n$ are selected signatures.

5.1 Notation

Operations are described in this manual according to the following notations:

$s_1, s_2, ..., s_n$	Current selected signatures.
r	Current reference signature.
$s = [(w_1, r_1), (w_2, r_2), \ldots, (w_m, r_m)]$	A defined signature.
$s(w_k) = s(k) = r_k$	A reflectance value, r_k, at wavelength, w_k, or, equivalently, at wavelength index, k.
$s(w)$	A point value of signature, s, at an arbitrary wavelength, w, in $[w_1, w_m]$. If necessary, this value $s(w)$ is computed by linear interpolation between nearest neighbors.
s'	A signature resulting from an operation.

5.2 One-to-one operations

$$f(s) \rightarrow s'$$

A one-to-one operation takes one signature and produces one signature. SAMS will apply the operation n times to generate n resulting signatures.

5.2.1 Scale

Given a scalar value, a, SAMS will compute s' from s by multiplying each ordinate point by a: $s'(w_k) = a \times s(w_k)$.

5.2.2 Crop

Given two wavelength values, a and b, SAMS will make a copy $s'(w_k)$ of $s(w_k)$ for wavelengths, w_k, such that $a \le w_k \le b$.

5.2.3 Smooth

Given a Savitzky-Golay filter[6] $c = [c_{-n_L}, ..., c_0, ..., c_{+n_R}]$ (see Appendix B for available filters), and two wavelength values, a and b, SAMS will create s' by applying the filter on s over the interval $[a, b]$:

$$s'(w_k) = \sum_{j=-n_L}^{j=+n_R} c_j \times s(w_{k+j})$$

for wavelengths, w_k, where $a \le w_k \le b$.

5.2.4 Derivative

SAMS calculates s' by taking the first discrete derivative of s:

$$s'(w_k) = \frac{s(w_{k+1}) - s(w_k)}{w_{k+1} - w_k}.$$

Before taking the derivative, SAMS automatically can apply a Savitzky-Golay smoothing filter to s.

5.2.5 Jump correction

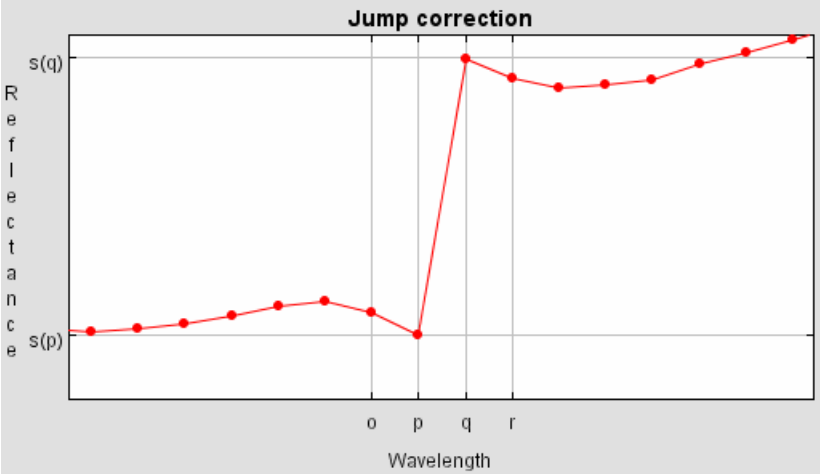
Given a wavelength, b, where a jump in s values occurs (a break-point), SAMS will perform an algorithm to adjust the values for wavelengths, $w_k > b$ (or $w_k < b$), so s' will not have a jump.

In the interval of modification, $s'(w_k)$ will differ from $s(w_k)$ by a correction value, c, that can be applied either multiplicatively or additively: This operation can be used to correct spectra recorded by an instrument which was calibrated incorrectly in a limited section of its spectral range.

$$s'(w_k) = \begin{cases} c \times s(w_k) & \text{if multiplicative correction} \\ s(w_k) - c & \text{if additive correction} \end{cases}$$

The correction, c, is calculated as follows.

[6] Press, W.H. *et al*, 1992. *Numerical Recipes in C, Second Edition.* Cambridge University Press. pp. 650-655. Original reference is Savitzky A., and Golay, M.J.E. 1964. *"Smoothing and differentiation of data by simplified least squares procedure."* Analytical Chemistry, vol. 36, pp. 1627-1639.

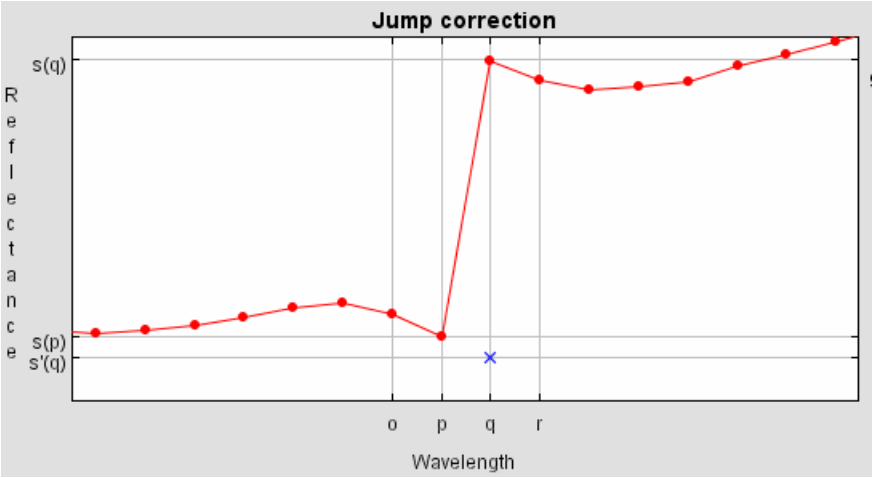


Let o, p, q, and r be indices of four consecutive points of interest, with a break-point, b, lying between w_p and w_q. SAMS will calculate the first tangent, t_1, from points o and p and the second tangent, t_2, from points q and r. The average tangent, $t = (t_1 + t_2)/2$, will be used to estimate the value at point, q, according to the following equation:

$$t = \frac{s'(q) - s(p)}{w_q - w_p}.$$

Solving for $s'(w_q)$, the estimated value, we have:

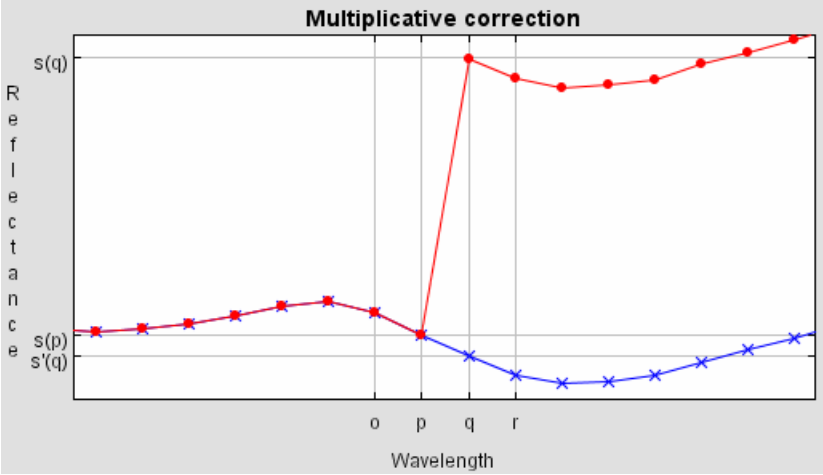
$$s'(q) = \frac{(t_1 + t_2)(w_q - w_p)}{2} + s(p).$$



So the correction will be

$$c = \begin{cases} s'(q)/s(q) & \text{for multiplicative correction} \\ s(q) - s'(q) & \text{for additive correction} \end{cases}$$

A multiplicative correction was applied to the right of the break point in this graph:



5.2.6 Change wavelength unit

Given a conversion factor, c, SAMS computes s' as a copy of s such that $s'(k) = s(k)$, but where wavelengths are multiplied by c:

$w_k' = c \times w_k$.

For example, if wavelength values are measured in nanometers, then a conversion factor of 0.001 will convert them to microns.

5.3 Many-to-one operations

$$f(s_1, s_2, ..., s_n) \rightarrow s'$$

Two types of many-to-one operations exist:

- In *aggregate* operations, SAMS outputs one signature from point-wise operations on selected signatures. Averages and standard deviations are examples.
- In a *constructed* signature, SAMS computes single values from corresponding input signature operations (e.g. *NDWI* in Section 5.3.7 and *absorption feature analysis* in Section 5.3.6). Although the resulting signatures are not necessarily "real" signatures, SAMS treats them as such.

5.3.1 Conform requirement

For aggregate many-to-one operations, all selected signatures $s_1, s_2, ..., s_n$ are expected to *conform* to each other by:

- having the same length, m
- being sampled at the same wavelengths: $s_i(w_k) = s_j(w_k)$ for all i, j in $[1, n]$ and all k in $[1, m]$.

SAMS alerts you if this requirement is not satisfied.

5.3.2 Average

Calculates point-wise average of selected signatures:

$$s'(w_k) = \frac{1}{n}\sum_{i=1}^{n} s_i(w_k).$$

5.3.3 Standard deviation

Takes point-wise square root of sample variance of selected signatures

$$s'(w_k) = \left(\frac{1}{n-1}\sum_{i} [s_i(w_k) - \overline{s}_i(w_k)]^2 \right)^{1/2}$$

where $\overline{s}(w_k)$ is the average at wavelength, w_k.

5.3.4 Minimum

Gives point-wise minimum of selected signatures

$$s'(w_k) = \min_i s_i(w_k).$$

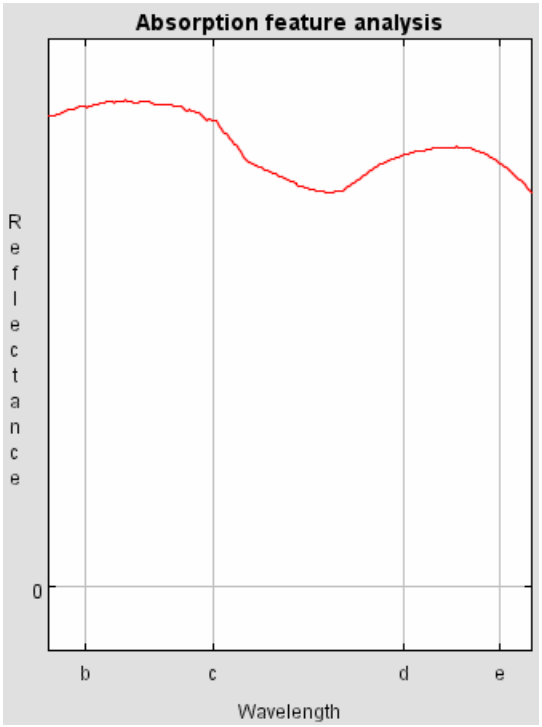
5.3.5 Maximum

Gives point-wise maximum of selected signatures

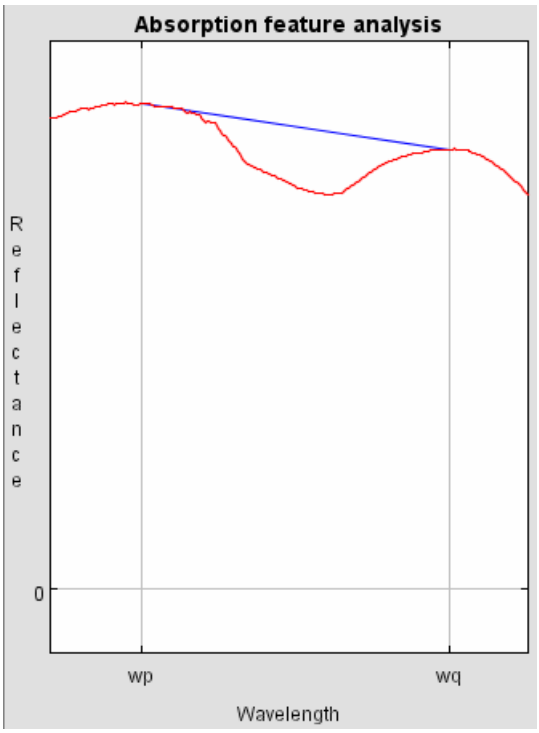
$$s'(w_k) = \max_i s_i(w_k).$$

5.3.6 Absorption feature analysis

This construction quantifies the magnitude of an absorption feature over selected signatures. Given two wavelength intervals, $[b,c]$ and $[d,e]$, SAMS constructs $s' = [(1,a_1),(2,a_2),...,(n,a_n)]$ by computing each value, a_i, from signature, s_i, as follows.



First SAMS identifies the local maxima within each interval. For this example, wavelength, w_p, in $[b,c]$ and wavelength, w_q, in $[d,e]$ are the maxima.



SAMS computes a_i as one minus the ratio between the area under the function in the interval $[w_p, w_q]$ and the area under the straight line segment connecting the maxima:

$$a_i = 1 - \frac{\text{area under curve in } [w_p, w_q]}{\text{area under line segment connecting } s_i(w_p) \text{ and } s_i(w_q)}.$$

5.3.7 NDWI

This construction uses wavelengths in nanometers. SAMS constructs $s' = [(1, a_1), (2, a_2), ..., (n, a_n)]$, where each value, a_i, is the NDWI[7] of signature, s_i:

$$a_i = \frac{s_i(860\text{nm}) - s_i(1240\text{nm})}{s_i(860\text{nm}) + s_i(1240\text{nm})}.$$

5.3.8 Simple extraction

This construction extracts a single reflectance value at a given wavelength, b, from each of the signatures selected. SAMS creates the signature $s' = [(1, a_1), (2, a_2), ..., (n, a_n)]$ where $a_i = s_i(b)$.

[7] Gao, B.C. 1996: NDWI: *A normalised difference water index for remote sensing of vegetation liquid water from space*. Remote Sensing of Environment. 58, pp. 257-266.

5.3.9 Sum

Calculates a point-wise sum of selected signatures.

$$s'(w_k) = \sum_i s_i(w_k) .$$

5.4 Reference-based operations

$$f_r(s) \rightarrow s'$$

A reference-based operation is a binary operation, $f(s,r)$, whose second argument is taken as a reference. So, it can be written $f_r(s)$ and be treated as a one-to-one operation (see above). The command to establish the reference signature is **Alt-Enter**.

SAMS includes these reference-based operations:

5.4.1 Simple ratio

Calculates a point-wise ratio between selected signature, s, and reference, r:

$$s'(w_k) = \begin{cases} \dfrac{s(w_k)}{r(w_k)} & r(w_k) \neq 0 \\ 0 & r(w_k) = 0 \end{cases} .$$

5.4.2 Subtraction

Takes a point-wise difference between selected signature, s, and reference, r:

$$s'(w_k) = s(w_k) - r(w_k) .$$

5.4.3 Normalize

Uses point-wise scaling according to reflectance ratio at a given wavelength, b:

$$s'(w_k) = \begin{cases} \dfrac{r(b)}{s(b)} \times s(w_k) & s(b) \neq 0 \\ s(w_k) & s(b) = 0 \end{cases} .$$

5.5 Operations on groups

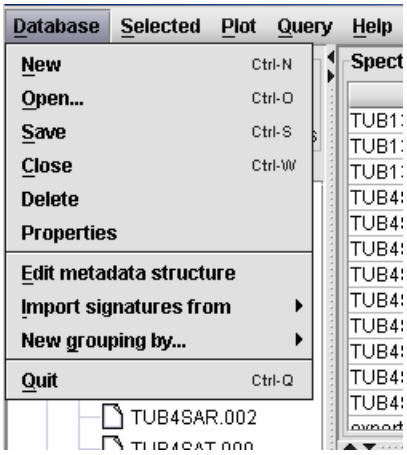
SAMS can apply a many-to-one operation on a selection of groups. SAMS performs an operation on a group's signature members and assigns the resulting name signature from the name of the group and the suffix given in the dialog box.

If any signatures are selected at the same time as groups, SAMS ignores them since group selection takes precedence over signature selection. To apply an operation to selected signatures, make sure no groups are selected.

6 Reference

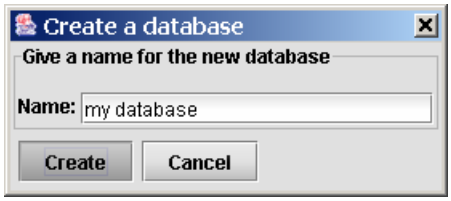
This section gives descriptions of options available from the menu bar and pop-up menus.

6.1 *Database* menu



6.1.1 New (Ctrl-N)

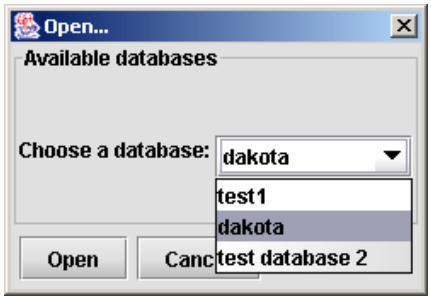
Creates a new database.



SAMS adds a new entry in its list of databases and lets you assign a short, descriptive name.

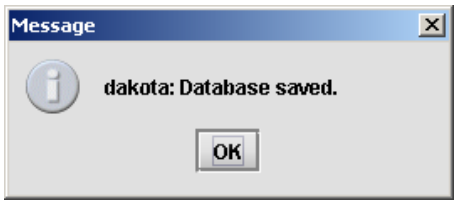
6.1.2 Open (Ctrl-O)

Opens a database and first saves and closes any other already-open database.



6.1.3 Save (Ctrl-S)

Saves database. SAMS confirms. It also saves automatically when you close a database or quit the program.



6.1.4 Close (Ctrl-W)

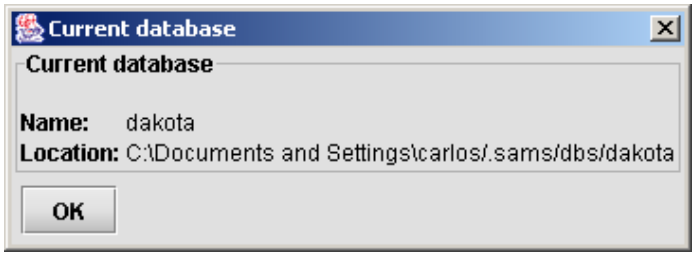
Saves and closes database.

6.1.5 Delete

Deletes database. SAMS asks for confirmation.

6.1.6 Properties

Shows database properties. Specifically, it shows:

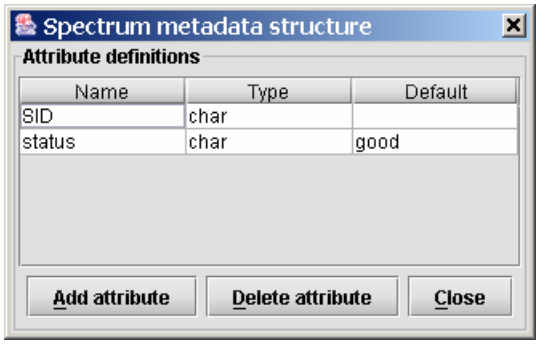


- database name
- directory under which data are stored.

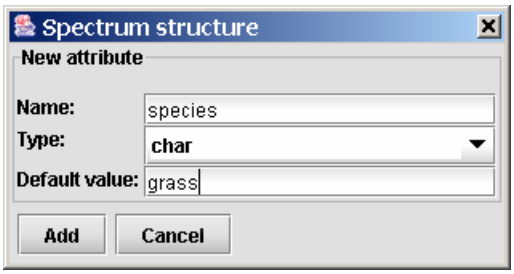
Find the directory under **`<base directory>/.sams/dbs/.`** [SAMS created **`<base directory>`** as a user-defined setting the first time it was run. See Section 2.]

6.1.7 Edit metadata structure

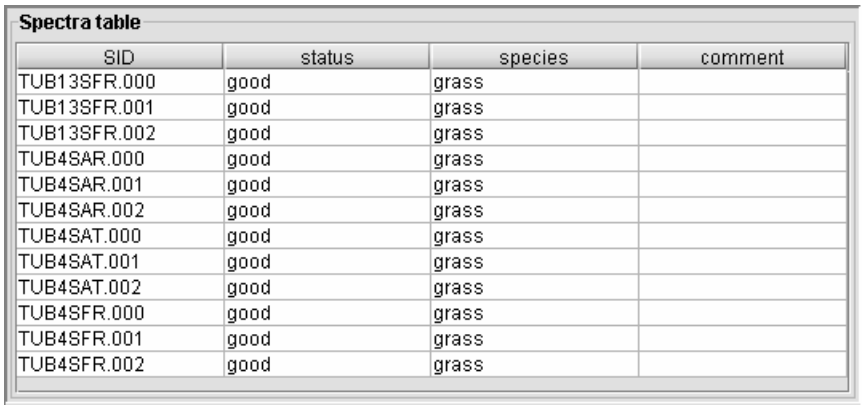
Modifies metadata associated with database. SAMS opens a window of default attributes.



Click on the **`Add attribute`** button.



Add *species* and *comment* attributes. SAMS will update your database as shown.



To change an attribute, click on the cell in the spectra table and make changes. *Humm* and *not so good* were added to the **comment** column in this table. Add as many attributes as you need.

Spectra table

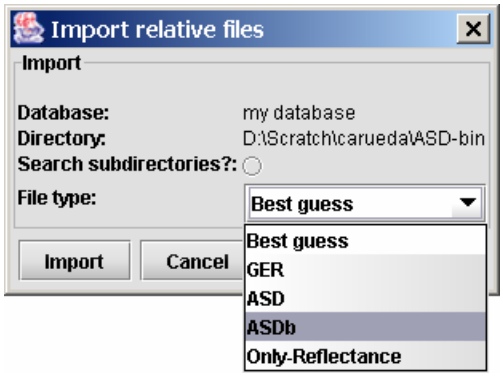
SID	status	species	comment
TUB13SFR.000	good	grass	
TUB13SFR.001	bad	grass	
TUB13SFR.002	bad	grass	
TUB4SAR.000	bad	grass	
TUB4SAR.001	good	grass	humm
TUB4SAR.002	good	grass	
TUB4SAT.000	good	grass	not so good
TUB4SAT.001	bad	grass	
TUB4SAT.002	bad	grass	
TUB4SFR.000	bad	grass	
TUB4SFR.001	bad	grass	
TUB4SFR.002	good	grass	

6.1.8 Import signatures from

Opens a submenu. Use it to import signatures into a database from different sources.

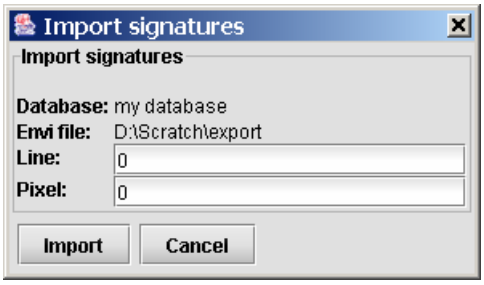
6.1.8.1 Directory

Specifies a directory to have SAMS search for spectra files.



6.1.8.2 ENVI Standard file

Reads an ENVI standard file in BIP format after you specify which location to read.



6.1.8.3 ASCII file

Reads multiple signatures from an ASCII file. See Appendix A.

6.1.8.4 System clipboard

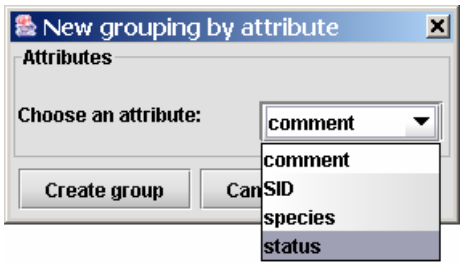
Pastes copied spectra files from the system clipboard. Use this option as an alternative to drag-and-drop.

6.1.9 New grouping by…

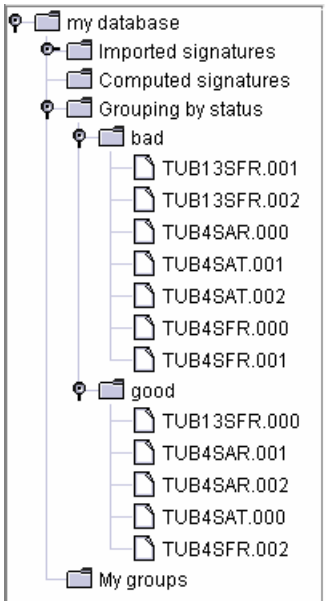
Opens a submenu with options to make automatic groupings.

6.1.9.1 Attribute value

Creates a group for each value of an attribute.



In this example:

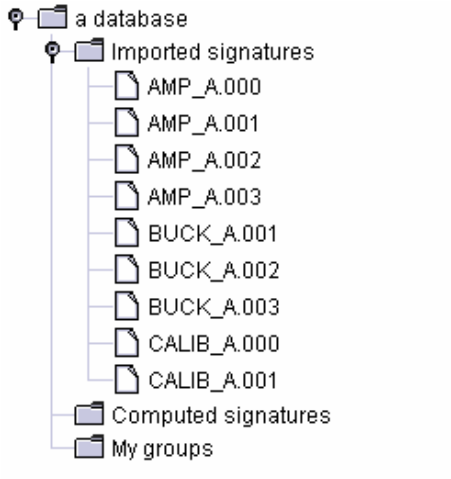


6.1.9.2 Filename

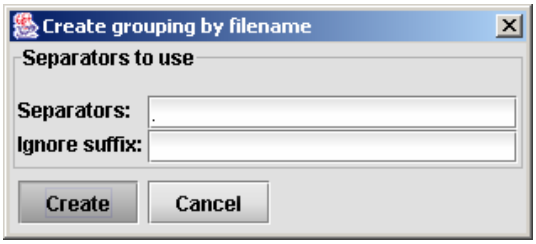
Creates a group for each prefix (set-off by separators assigned by the user) in signature filenames.

- **Separators**. SAMS uses characters like "." to separate groups.
- **Ignore suffix**. SAMS ignores this suffix in separator processing.

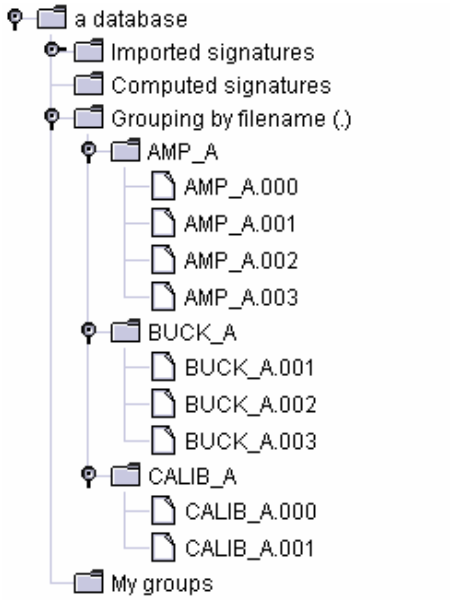
Several signatures are in this example database:



Using '.' as the only separator and leaving the suffix blank:



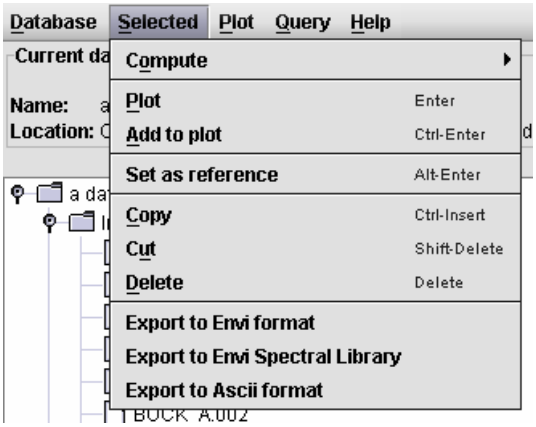
SAMS creates this group structure:



6.1.10 Quit (Ctrl-Q)

Quits program. SAMS asks for confirmation.

6.2 *Selected* menu



6.2.1 Compute

Choose one of these operations to perform on a selection:

- Many-to-one operations. See Section 5.3.
- One-to-one operations. See Section 5.2.
- Reference-based operations. See Section 5.4.

6.2.2 Plot (Enter)

Displays selected signatures in the plot area, allows reassignment of legends.

6.2.3 Add to plot (Ctrl-Enter)

Plots selected signatures in addition to those already displayed.

6.2.4 Set as reference (Alt-Enter)

Sets *focused* signature as the reference signature for reference-based operations. See Section 5.4.

6.2.5 Copy (Ctrl-Insert)

Copies selected signatures to an internal clipboard. To paste references to selected signatures into a group, use **Paste** (Section 6.6.2.1).

6.2.6 Cut (Shift-Delete)

Removes selected signatures from a selection and copies them to an internal clipboard. To paste references to removed signatures into a group, use **Paste** (Section 6.6.2.1).

6.2.7 Delete (Delete)

Deletes selected signatures from the group. SAMS asks for confirmation.

6.2.8 Export options

For all export options, selected signatures, $s_1, s_2, ..., s_n$, must conform to each other as explained in Section 5.3.1. The identification name for signature s_i is $\mathrm{id}(s_i)$ in the following discussion.

6.2.8.1 Export to ASCII format

SAMS exports selected signatures, $s_1, s_2, ..., s_n$, to a CSV (comma-separated-values) file.

`Wavelength,`	$\mathrm{id}(s_1)$,	$\mathrm{id}(s_2)$,	$\cdots$,	$\mathrm{id}(s_n)$
w_1,	$s_1(w_1)$,	$s_2(w_1)$,	$\cdots$,	$s_n(w_1)$
w_2,	$s_1(w_2)$,	$s_2(w_2)$,	$\cdots$,	$s_n(w_2)$
w_m,	$s_1(w_m)$,	$s_2(w_m)$,		$s_n(w_m)$

6.2.8.2 Export to ENVI format

SAMS exports n selected signatures, $s_1, s_2, ..., s_n$, to a multi-band image in ENVI standard format with dimensions:[8]

$$lines = \left\lfloor \sqrt{n} \right\rfloor$$

$$samples = \left\lceil \frac{n}{lines} \right\rceil$$

$$bands = m$$

It follows that the image can store $N = lines \times samples \geq n$ signatures. If $N > n$, then the remaining $N - n$ elements will be zero-filled. So, if $n = 18$, $lines = 4$ and $samples = 5$. Each signature is located in the image as shown:

[8] Where $\lfloor x \rfloor$ is the greatest integer that is not greater than x, and $\lceil x \rceil$ is the smallest integer that is not less than x.

s_1	s_2	s_3	s_4	s_5
s_6	s_7	s_8	s_9	s_{10}
s_{11}	s_{12}	s_{13}	s_{14}	s_{15}
s_{16}	s_{17}	s_{18}	$\varnothing$	$\varnothing$

Where $\varnothing$ denotes a signature with m zero values. SAMS prompts you for a file name to export the selected signatures and writes a corresponding header file, `*.hdr`.

6.2.8.3 Export to ENVI Spectral Library

An ENVI **spectral library** file is an ENVI binary image with the number of samples equal to the number of bands and the number of lines equal to the number of signatures in the selection:

$$lines = n$$

$$samples = m$$

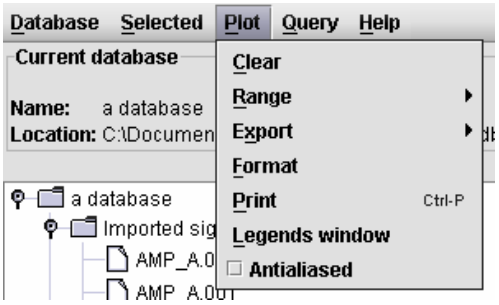
$$bands = 1$$

Signatures are ordered as shown:

$s_1(w_1),$	$s_1(w_2),$	$\cdots,$	$s_1(w_m)$
$s_2(w_1),$	$s_2(w_2),$	$\cdots,$	$s_2(w_m)$
$\ldots$	$\ldots$	$\ldots$	$\ldots$
$s_n(w_1),$	$s_n(w_2),$	$\cdots,$	$s_n(w_m)$

The header displays signature identifications, wavelengths, and **spectral library** for the ENVI file type. SAMS prompts you for a file name and writes a corresponding header file, `*.hdr`.

6.3 *Plot* menu[9]



[9] Plot capabilities based on Ptolemy 2D data plotter package, version 5.1p2: http://ptolemy.eecs.berkeley.edu/java/ptplot/

6.3.1 Clear

Clears contents of plot area.

6.3.2 Range

Opens submenu with options to adjust X and Y ranges. Any range can be specified–see *format* option below.

6.3.2.1 Full range

Rescales plot to fit data.

6.3.2.2 Visible [400:700]

Sets X range to ~400-700 nm.

6.3.2.3 NDVI [500:900]

Sets X range to ~500-900 nm.

6.3.2.4 Chlorophyll [550:680]

Sets X range to ~550-680 nm.

6.3.2.5 Zoom current X-range

Rescales plot vertically to fit data in X range.

6.3.2.6 Zoom current Y-range

Rescales plot horizontally to fit data in Y range.

6.3.3 Export

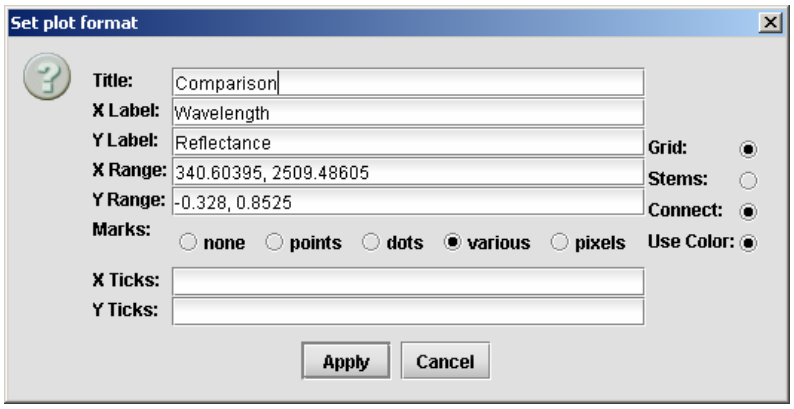
Opens submenu with options to export the plot in different formats. Currently, only EPS is supported.

6.3.3.1 Encapsulated Postscript (EPS) format

Opens dialog box in which to specify a name for the plot file compatible with word processors.

6.3.4 Format

Opens a dialog box to modify plot parameters such as:



- **Title**. Assigns title to plot.
- **X label** and **Y label**. Labels X and Y axes.
- **X range** and **Y range.** Stipulates plotted ranges by separating low values from high with a comma.
- **Marks**. Add marks specified to distinguish spectra.
- **X ticks** and **Y ticks**. Specifies how axes are labeled. SAMS automatically computes them. To change tick marks, enter into the **X Ticks** or **Y Ticks** entry boxes a string of the following form:

  label position, label position, ...

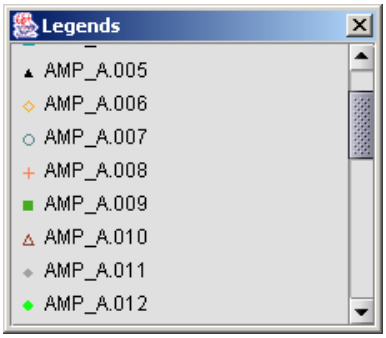
  A *label* must be surrounded by quotation marks if it contains any spaces. A *position* is a number assigning the location of the tick mark along the axis.
- **Grid**. Check to show background grid.
- **Stems**. Check to plot stems.
- **Connect**. Check to connect point values with lines.
- **Use color**. Check to plot spectra with different colors.

6.3.5 Print (Ctrl-P)

Prints plot, opens print dialog box with options to choose paper, orientation, margins, printer.

6.3.6 Legends window

Opens a floating window containing plot legends – a useful tool when many signatures are displayed and there is not enough room for the legends to fit in their normal location.



6.3.7 Anti-aliased

Improves plot appearance.

6.4 *Query* menu

Do not use yet. This menu is in an early stage of development.

6.5 *Help* menu

6.5.1 About SAMS

Shows current version, contact information, and copyright agreement for SAMS.

6.5.2 The BeanShell window

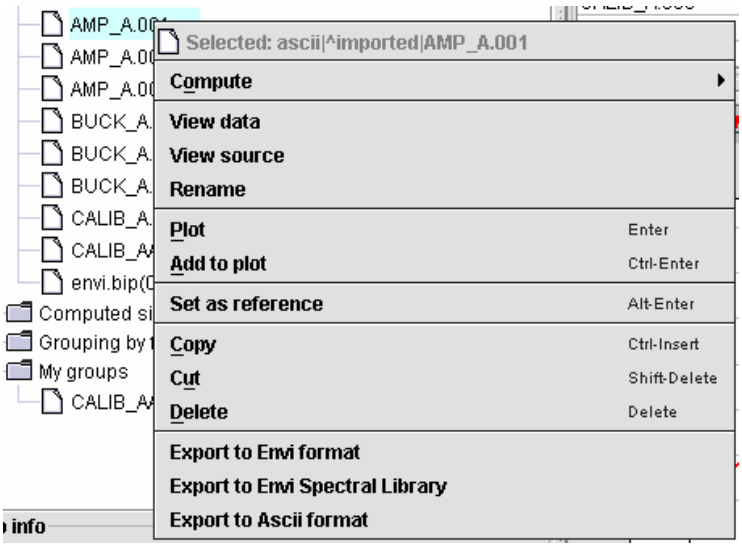
Do not use. Opens a tool for developers to use to test SAMS.

6.6 Pop-up menus

Appear by right-clicking over elements of the selection area like signatures and groups.

6.6.1 Signature popup menu

Contains same options as *Selected* in the menu bar.



Includes the following options, when only one signature is selected.

6.6.1.1 View data

Shows contents of selected signature in SAMS' memory (two columns, wavelength and reflectance).

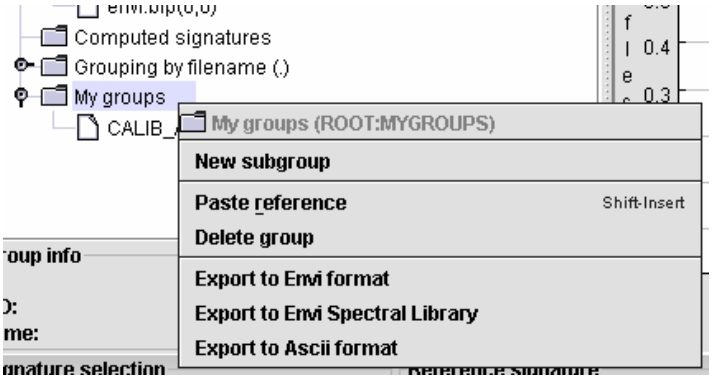
6.6.1.2 View source

Shows contents of source file where selected signature is stored (ASCII sources only). Use option **View data** for binary sources.

6.6.1.3 Rename

Renames selected signature and associated groups.

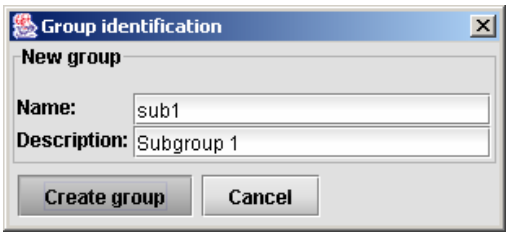
6.6.2 Group pop-up menu



Includes the following options when a group is selected:

6.6.2.1 New subgroup

Applies to **My groups**.



SAMS prompts you for a name and a description.

6.6.2.2 Paste reference

Adds references to signatures to selected group from clipboard. Use **Copy** and **Cut** to put signatures on clipboard (Sections 6.2.5 and 6.2.6).

6.6.2.3 Delete group

Deletes selected group. **Imported signatures**, **Computed signatures**, and **My groups** cannot be deleted.

6.6.2.4 Export options

Applies to members of selected group as explained in Section 6.2.8.

Appendix A Recognized file formats

File formats that SAMS currently recognizes in importing signatures into a database.

ASCII file

SAMS imports this simplest file type using these rules.

- The file is scanned one line at a time.
- Each line is scanned as a sequence of tokens.
- Each token is a floating point value.
- Separators for tokens are simple spaces, commas, and/or tabs.
- A line is recognized if it starts with at least two floating point values. Otherwise, the line is ignored.
- Recognized lines in the same file can contain different numbers of tokens (columns), although the usual case is to have exactly the same number of columns.
- The scanned, consecutive floating point values found in a line are denoted by $v_0, v_1, ..., v_n$.
- The first column in the file, v_0, is interpreted as the abscissa value for all imported signatures.
- For $1 \le i \le n$, the point (v_0, v_i) is assigned to signature i-th, that is, v_0 will be its abscissa and v_i its ordinate.

GER file

GER files are identified as **GER**.

A GER file is an ASCII file that SAMS reads following these rules.

- The first line is expected to be one of the following:

```
///GER SIGNATUR FILE///
///GER ASCII FILE///
```

- Subsequent lines are parsed for three or four numerical values.
- Lines that cannot be parsed to at least three values are ignored.
- The first value is always taken as a wavelength.
- If a fourth value, say w, is parsed successfully, then $w/100$ is taken as the reflectance value.

- Otherwise, the reflectance value will be y/z, where y and z are the second and third values in the line.

Binary ASD file

Binary ASD files are identified as **`ASDb`**.

Reflectance data files generated by an ASD instrument can be read directly by SAMS as long as they are float and little-endian formatted.

ASCII ASD file

ASCII ASD files are identified as **`ASD`**.

SAMS imports ASCII ASD files using the same rules it uses for ASCII files except for the assumption that only one signature comes in the file. In this way the first two tokens (columns) are taken into account.

ENVI Standard file

SAMS can read directly ENVI Standard files in BIP[10] format.

Only-Reflectance

This ASCII file is scanned for at least one column assumed to contain reflectance values. These values are associated with fixed wavelengths: 350, 351, 352, ….

[10] *BIP*, Band Interleaved by Pixel: Reflectance values for each signature are stored together.

Appendix B Available Savitzky-Golay filters

Savitzky-Golay filters in SAMS are named by the convention, $M - n_L - n_R$, where M is the order of the fitting polynomial, n_L is the number of left data points used, and n_R is the number of right data points used.

$M - n_L - n_R$
3-40-40
3-20-20
3-12-12
2-2-2
2-3-1
2-4-0
2-5-5
4-4-4
4-5-5