

QUICK REFERENCE MANUAL

iMineralysis™

Brief description of screen tabs and functionality:
Version 3.6.0

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About iMineralysis™

iMineralysis™ is a software tool that performs multiminerals analysis. It uses a genetic algorithm that allows it to optimize both mineral fractions and properties simultaneously. It tries to be as simple as possible to use and manage while providing that capability effectively.

Multiminerals solutions are typically non-unique. iMineralysis™ algorithm allows it to provide information on the severity of non-uniqueness (**Results: Solution Uniqueness**) and on possible sources of non-uniqueness within the model (**Results: Coefficient Fitness**).

The user interface is essentially a rather long "wizard," walking through the basic steps:

1. Defining the input data,
2. Defining the multiminerals models and geologic intervals,
3. Performing the analysis and viewing the results, and
4. Exporting the results.

Steps, especially 2 and 3, can be iterated as desired, and the whole thing can be saved as a project, but that's it. iMineralysis™ does not have log processing or extensive display features.

An iMineralysis™ project is saved in a project file and the LAS files containing the log data. The project file contains the multiminerals models, geologic intervals, settings, and lists of logs and LAS files - everything except the log data itself. Log data is read from the LAS files when needed, in order to avoid duplicating large amounts of data. More information on iMineralysis™ files can be found in Appendix B.

Quick Start

The iMineralysis™ workflow at its simplest is:

0. Prepare log data BEFORE analyzing with iMineralysis™ (see Appendix A):
 - a. Correct logs (for noise, contractor effects, vintage, etc.)
 - b. Generate calculated logs (pseudo-conductivity CX, volumetric photoelectric factor U, e.g.)
 - c. Generate bad hole log, if needed (to flag washouts, for example)
1. Define the input data:
 - a. Select LAS files: **Input Data: Select LAS Wells**
 - b. Select depth ranges, exclude bad hole: **Input Data: Select Samples**
2. Define multimineral models and geologic intervals:
 - a. Define multimineral models: **Setup Analysis: Search Limits**
 - b. Define geologic intervals: **Setup Analysis: Intervals**
3. Perform analysis and view results:
 - a. Select wells and intervals to analyze, and models to use: **Analyze: Prepare Analysis**
 - b. Review problems and analyze: **Analyze: Start Analysis**. Examine **Quality Metrics** and **Tested Coefficients**.
 - c. View results: **Results: Logs, Coefficients, Analysis Notes, Solution Uniqueness, and Coefficient Fitness**.
4. Export results: **Export: Logs, Coefficients**

Optional steps that may be useful while defining the input data allow:

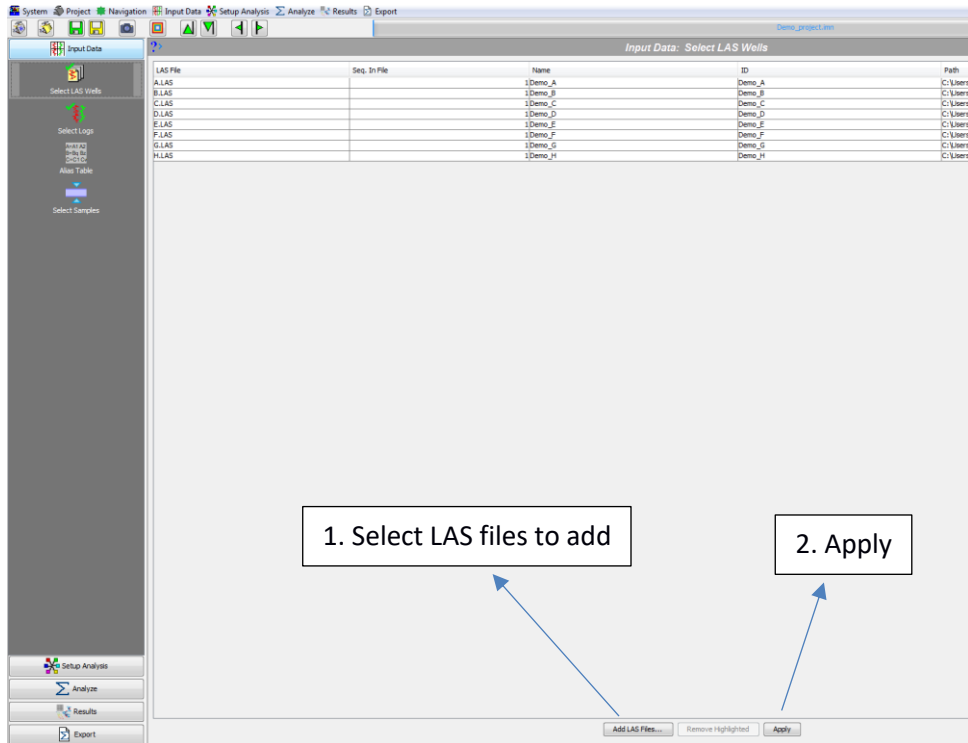
- Selecting unneeded logs to "drop" from the project: **Input Data: Select Logs**, and
- Defining aliases or "common names" for logs: **Input Data: Alias Table**.

Optional steps that are seldom useful while defining multimineral models allow:

- Setting specific tolerances for specific logs in individual wells (**Setup Analysis: Override Log Tolerances**) (Seldom used)
- Setting advanced technical options for the genetic algorithm and linear solver (**Setup Analysis: Advanced Options**) (Almost never used).

When displayed, the *Need-To Hints* option (available on the toolbar or **System: Settings** screen) can guide you through the workflow quickly, and with no required steps missed.

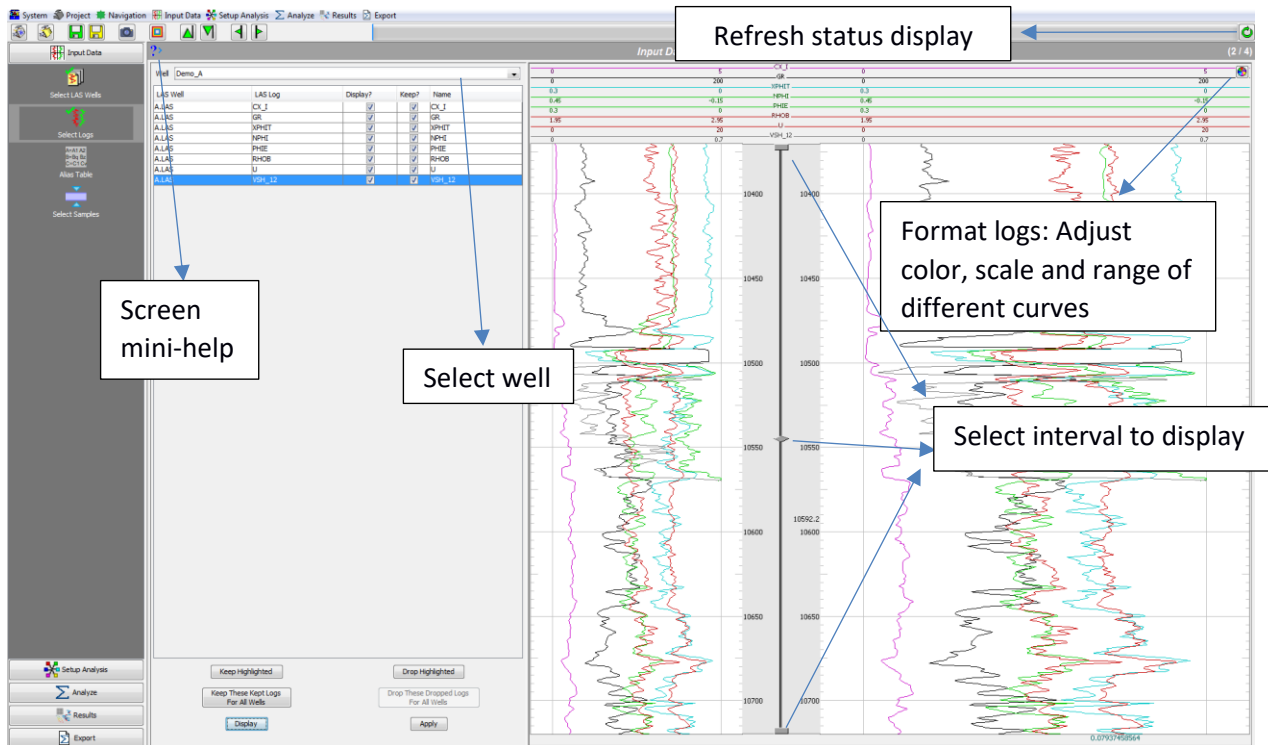
Input Data: Select LAS Wells



Use this screen to select LAS files and wells to analyze. This screen compiles the list of LAS wells to use in the current project. If a single LAS file contains several wells, the wells can be selected or removed individually. If several LAS files contain logs for the same well, the log lists will be merged automatically.

Click **Add LAS Files...** to add wells from LAS files, or select wells in the list and click **Remove Highlighted** to remove them. Click **Apply** when finished.

Input Data: Select Logs (optional)








Use this screen to select logs to keep for analysis and/or display. This should include any bad hole, pay, or facies logs that will be used later in the process. If wells have many logs, keeping only the interesting ones will make log lists shorter and more manageable. If a well has logs with conflicting names from more than one LAS file, they can be assigned unique names or unneeded versions can be dropped.

This step may not be necessary if the input wells do not have a lot of extra logs not needed for the multiminerall analysis.

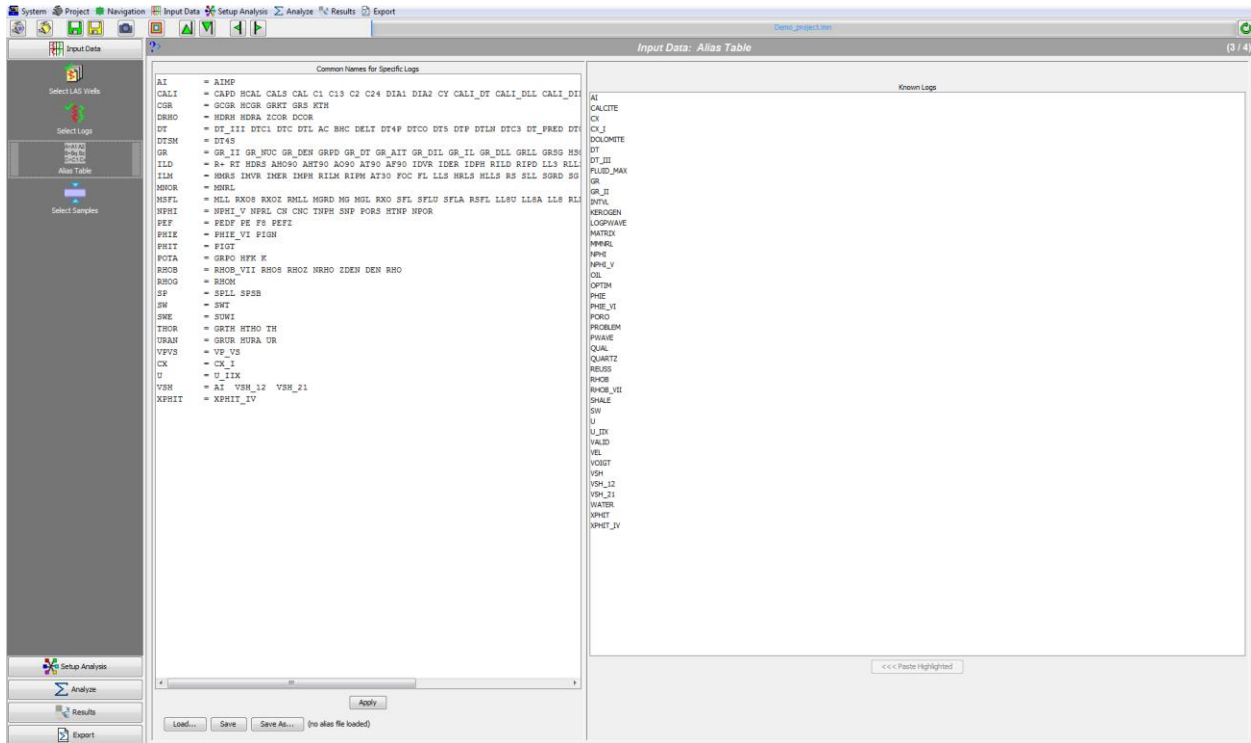
Select a well. Check the box in the **Display?** column in the list to pick logs to preview, then click the **Display** button. Check the box in the **Keep?** column for logs to keep, or clear the box for logs to drop. Edit the **Name** column as needed - each log kept must have a name unique in the well. Click **Keep These Kept Logs For All Wells** or **Drop These Dropped Logs For All Wells** to propagate the current well's keep/drop selections to all wells in the project. Repeat for other wells as needed, and click **Apply** when finished.

To adjust the log display, click the **Format logs**  button, which brings up the log format editor:

Edit Log Formats					
Log	Color	Logarithmic?	Reverse?	Lower Limit	Upper Limit
CX_I		<input type="checkbox"/>	<input type="checkbox"/>	0	0.5
GR		<input type="checkbox"/>	<input type="checkbox"/>	0	200
NPHI		<input type="checkbox"/>	<input checked="" type="checkbox"/>	-0.15	0.45
RHOB		<input type="checkbox"/>	<input type="checkbox"/>	1.95	2.95
U		<input type="checkbox"/>	<input type="checkbox"/>	0	20

Press **Apply** to commit any edits, and close the editor when finished. Note that log formatting defined for this screen will not carry over to other screens. This is because on this screen, each individual log must use its own format, so that it can be distinguished from other logs that may contain the same type of data.

Input Data: Alias Table (optional)



Use this screen to define a common name to refer collectively to logs with the same type of data but different names. If different wells use different names for the same log (for example GR_A and GR_B to denote company A or B), a common name (GR = GR_A_GR_B) can be used to refer to either.

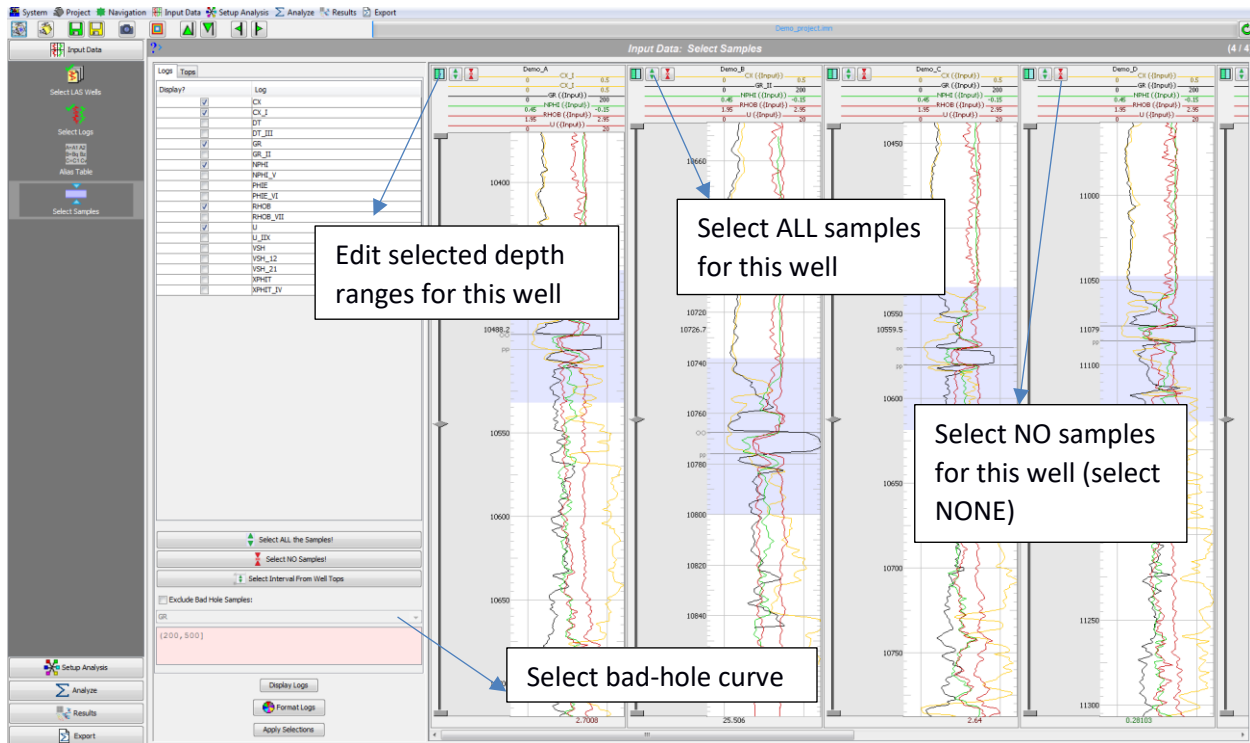
If wells have multiple versions of the same log (for example, raw and one or more processed versions), a common name can be used to refer to any available version. Raw logs are indicated in bold font. A common name also prioritizes the specific logs to which it refers, by the order in which they appear in its definition. Search limits matrices allow only a single log name for each row, and it is good practice to define a common name for each matrix row. Using common names also allows search limits matrices to be exported and imported more easily.

This step may not be necessary if logs in the input wells already have consistent names.

The alias list, **Common Names for Specific Logs**, works like a text editor. For convenience, log names can be inserted from the **Known Logs** list by selecting them and clicking **<<< Paste Highlighted**. Press **Apply** when finished.

You can choose to **Save** the alias list to a file, or to **Load...** an alias list saved from another project.

Input Data: Select Samples



Use this screen to select log samples to be used for analysis. The selections here should include **all** samples to be used; intervals to be analyzed separately will be defined later. Bad hole or unusable samples should be excluded here, either manually or with a bad hole log (if one is available), or both.

Samples may be selected in several ways, including "by eye", by manually entering depth ranges, by tops, and by excluding bad hole; so this screen includes log displays, loading and displaying tops, and identifying bad hole values.

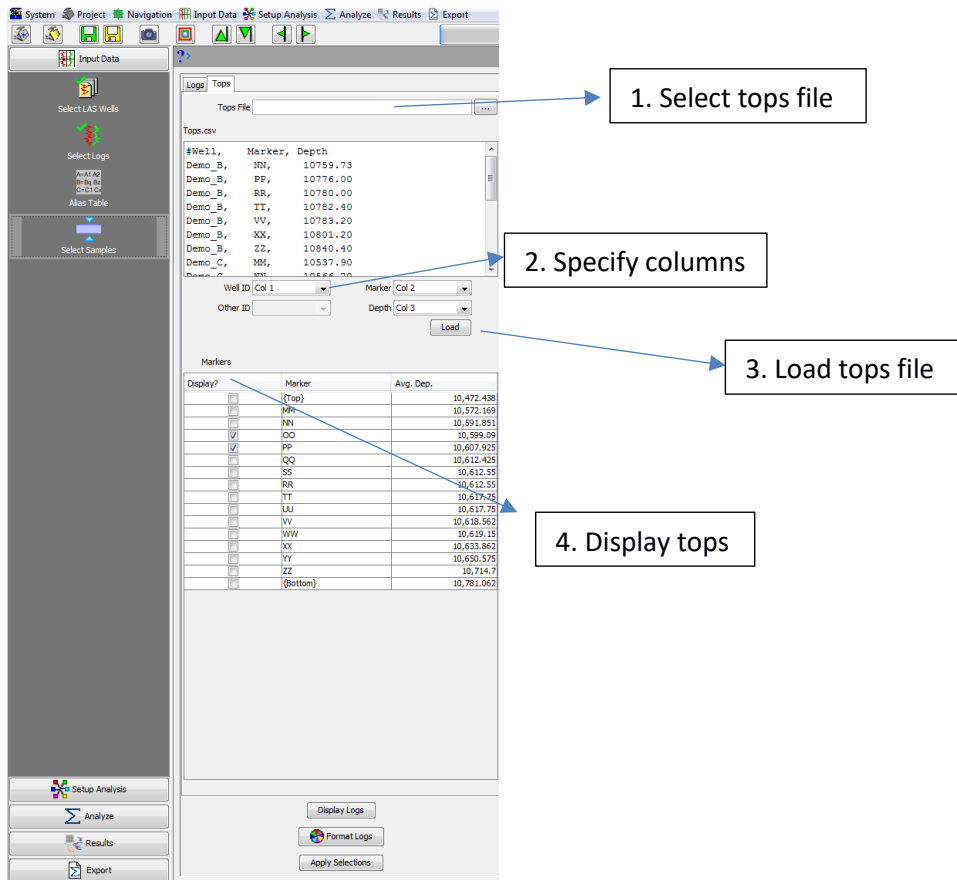
Displaying and Formatting Logs

On the **Logs** tab, check the **Display?** box in the list for logs to display, then click **Display Logs**. Some logs may have a predefined format, others may not. Log formats can be changed if desired by clicking the **Format Logs** button, which brings up the **Log Formats** editor. In the log display, use the range slider to zoom and scroll, or the mouse wheel to scroll, click+wheel to zoom.



Loading and Displaying Tops

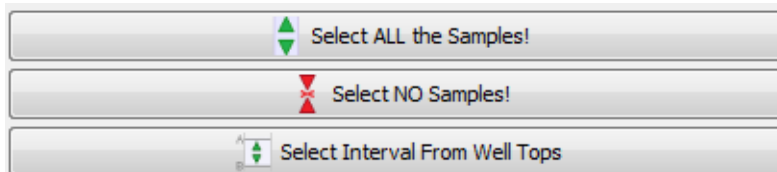
Tops are loaded automatically from LAS files (PETRA* format). Missing tops or updated depths can be loaded on this screen from a comma-separated-values (CSV) file. The CSV file must have Well ID, Tops Name, and Measured Depth columns. On the **Tops** tab, click **...** to select a CSV file. A few lines from the file are displayed. Check and correct the **Well ID**, **Other ID**, **Marker**, and **Depth** columns, and click **Load**.

Select tops to display by checking the **Display?** box in the **Markers** list.



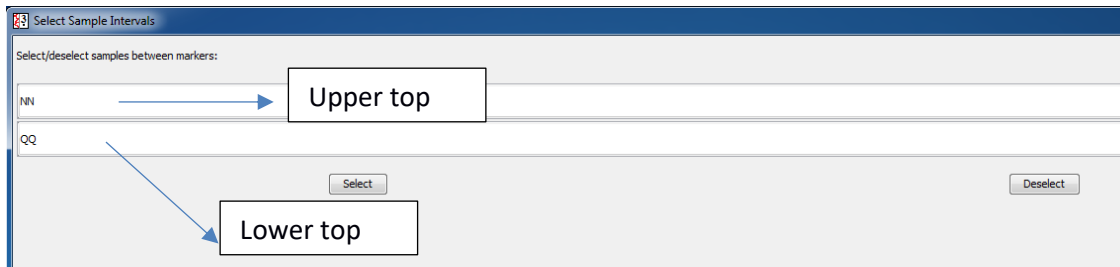
Selecting All Samples or No Samples

To select all or no samples for all wells, on the **Logs** tab, click **Select ALL the Samples!**  or **Select NO Samples!**  buttons. To select all or no samples for a single well, click the **Select All** or **Select None** button on its log display.



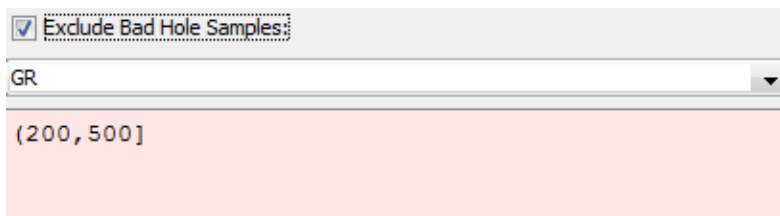
Selecting Samples by Tops

To select or deselect samples between two tops, on the **Logs** tab, click **Select Interval From Well Tops**. This brings up the **Select Sample Intervals** dialog to choose the upper and lower tops and whether to **Select** or **Deselect** samples. Multiple intervals can be selected or deselected, and the selection or deselection will be applied for all wells that have the chosen tops. Close the dialog when finished.




Excluding Depths by Bad Hole

On the **Logs** tab, check the **Exclude Bad Hole Samples:** box, select a log to use to identify bad hole samples, and enter bad hole values in the red text area. Bad hole values can be any combination of single values or intervals. For a 0,1 "flag" log, the bad hole value might be just 1; to exclude samples with log values above 200, the bad hole value would be something like (200, 1000]; or to exclude below 1.95 or above 2.95, the bad hole value could be (-1000, 1.95), (2.95, 1000).

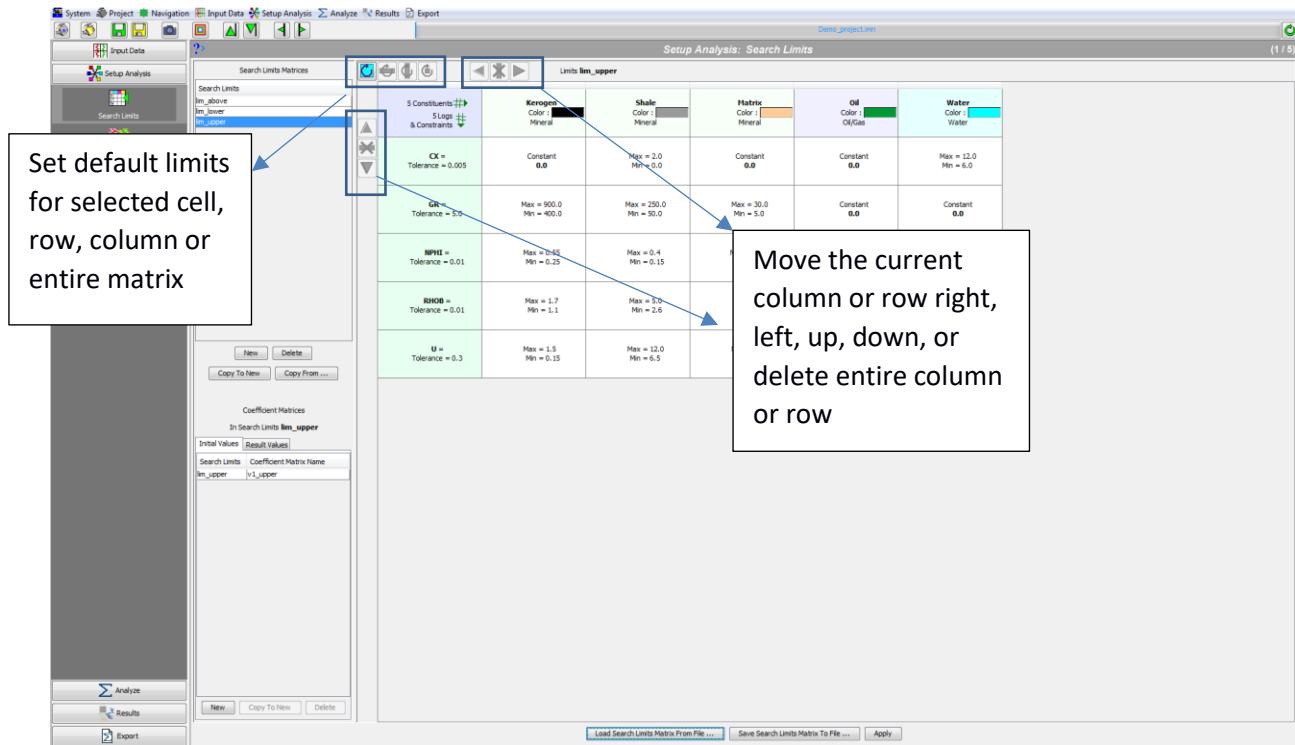


Selecting Samples by Manually Entering Depths


To manually enter selected depth ranges for a well, click the **Selected Depth Ranges** button  on its log display. This brings up the **Edit Selected Depth Ranges** dialog. You can enter multiple ranges to select here; rows are added to the table as needed. Close the dialog when finished.

From	To
10,452.859	10,531.728

Setup Analysis: Search Limits

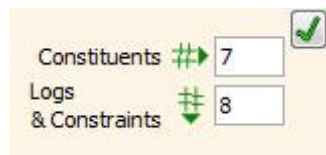


Use this screen to define iMineralysis™ coefficient models, including logs and constraints, and the material constituents present in the rock. An iMineralysis™ coefficient model consists of a Search Limits Matrix (giving ranges of coefficient values to search during analysis) and possibly several Coefficient Matrices: Initial Values to be used in forward modeling or as optional starting points in optimization, and Result Values containing the best values found during an optimization.

This is a very important screen. It is also a large screen, so it may be helpful to click the  toolbar button to hide the navigation bar temporarily.

Defining and Editing a Model

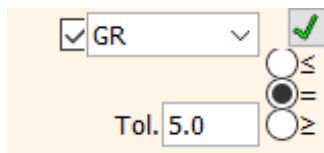
Under the **Search Limits Matrices** list, click **New** and enter a model name, or select an existing model in the list. Modify the name if you wish. The matrix editor on the right now displays a matrix that is ready for editing. For the program to assign the right default values to coefficients related to different logs, log aliases should be properly defined on the **Input Data: Alias Table** screen.



First edit the top-left cell to set the number of rows (logs and constraints) and columns (minerals and fluids).

Note that you do *not* have to define a “Unity” constraint (substance volumes sum to 1) or “Positivity” constraints (each constituent proportion is non-negative) here; they are added automatically.

Next, edit the rows (logs and constraints) and columns (minerals and fluids):



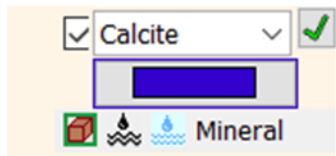
Rows:

Check or clear the log to include or exclude it, respectively.

Select a log, or type a name to define a constraint. Alias logs are underlined.

For a named constraint, it will prompt for a constant value. Logs should usually be equalities; constraints may be any type of relation. Tolerance is in

log units.



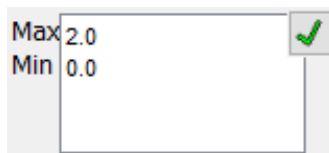
Columns:

Check or clear the constituent to include or exclude it, respectively.

Select a predefined constituent, or type a name to define a custom constituent. Select a distinctive color for the constituent; this color will be used in composition graphs after the analysis is completed. Check whether

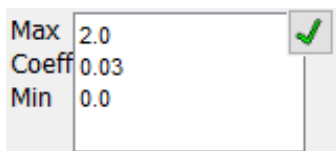
the constituent is a solid, hydrocarbon or water.



Finally, edit individual coefficient cells as needed by specifying **Min** and **Max** for each of them.



Click **Apply** when finished.

Under the **Coefficient Matrices** list, click **New** and, if you wish, enter a name (like “Initial”); then select the name in the list. The matrix editor will show the values introduced for the corresponding Search Limits Matrix and you now need to introduce the initial values of the coefficients for the optimization.



First click the cell once to select it; then, click its  button to edit it. Click its  button to commit any changes when finished. This step is optional.

Click **Apply** when all cells have been filled.

Result Values Coefficient Matrices

To view a Result Values matrix, select its model in the **Search Limits Matrices** list, then under the **Coefficient Matrices** list, select the **Result Values** tab and select the matrix in the list. The search limits and result values are now shown in the matrix editor on the right. Result values cannot be edited or used in forward modeling or optimization, but clicking **Copy To Initial Values** will create a duplicate initial values matrix that can.

Saving and Loading Matrices

Click **Save Search Limits Matrix To File...** to save a Search Limits Matrix and associated Coefficient Matrices to a file, or **Load Search Limits Matrix From File...** to load a previously-saved matrix (either as a separate file or from another iMineralysis™ project). Defining matrices using generic common log names like GR instead of specific log names like I_GR_2 will make it easier to reuse matrices and even collect a library of base matrices that can be used when starting a new project.

The **Export: Coefficients** screen allows Initial or Result Values matrices to be exported for use in other applications.

Please keep in mind the following information when creating the matrices of limits and coefficients:

- Logs are modeled as linear functions of the volume proportions of the material constituents.
- Constraints are equalities or inequalities providing additional information to the linear solver, and will usually have a constant value and constant coefficients.
- Matrices should be overdetermined (more logs than constituents), or a unique solution will not exist.
- A project can have multiple search limits matrices, and each search limits matrix can have multiple coefficient matrices.
- Each analysis run will store the optimized coefficients it finds as another result coefficient matrix in the search limits matrix it used.
- Constraints specifying that constituent volume proportions must be positive and sum to 1 are imposed by default for every analysis, and do not need to be explicitly entered here.
- Tolerances are in log units, must be positive, and control how closely each log should be matched.
- Tolerance values are an important part of the matrix of limits; if you get unexpected results, review the tolerances.
- Be sure each constituent is correctly identified as mineral, water, or oil/gas.

Setup Analysis: Override Log Tolerances (optional)

1. Select well

2. Modify default log tolerances if

Adjust color, scale and range of different curves

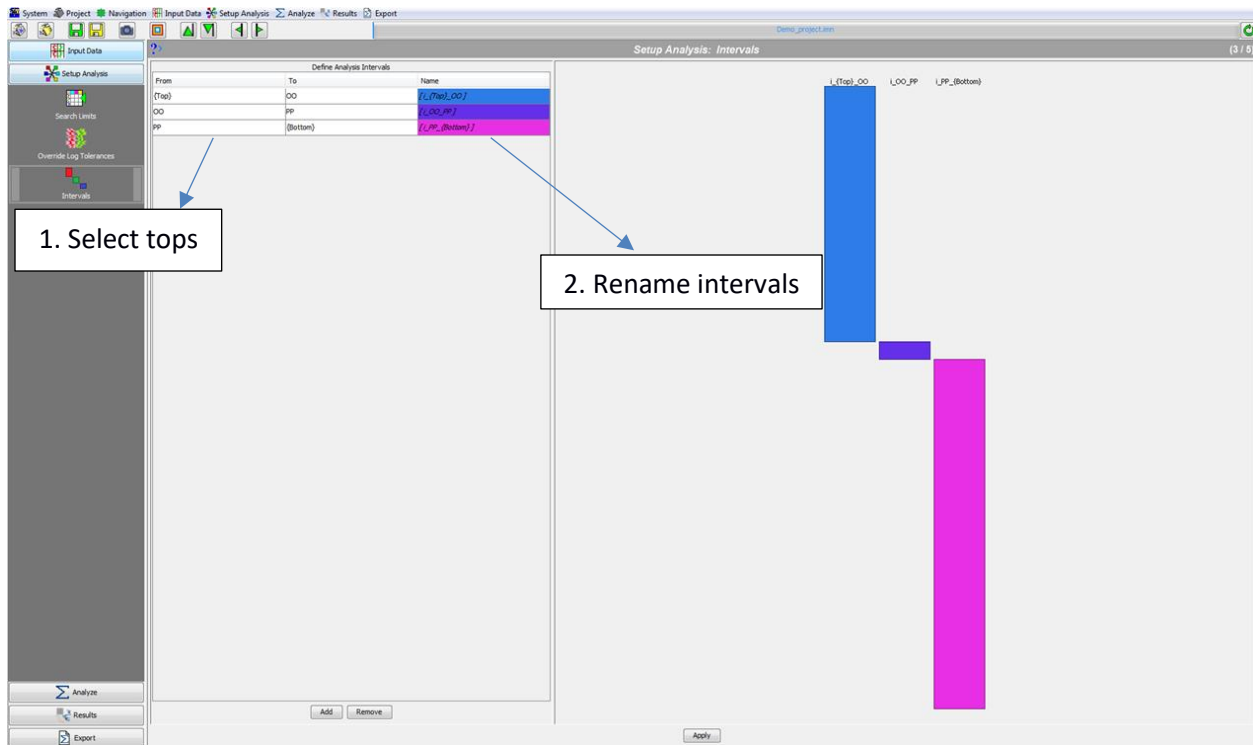
Well	Log Name	Display?	Tolerance
ALIAS	CK_I	<input checked="" type="checkbox"/>	
ALIAS	GR	<input checked="" type="checkbox"/>	
ALIAS	NPHET	<input checked="" type="checkbox"/>	
ALIAS	NPHZ	<input checked="" type="checkbox"/>	
ALIAS	PRZE	<input checked="" type="checkbox"/>	
ALIAS	RHCB	<input checked="" type="checkbox"/>	
ALIAS	VSH_12	<input checked="" type="checkbox"/>	
ALIAS	VSH_12	<input checked="" type="checkbox"/>	

Use this screen to set tolerances for individual logs that may be more or less reliable than the tolerances set in the search limits matrices.

This step is optional.

Select a **Well**, check **Display?** in the list for logs to view, and then click **Display**. Enter log tolerances directly in the list. Click **Apply** when finished with all wells.

Setup Analysis: Intervals



Use this screen to define the intervals to analyze. Separate geologic intervals can be analyzed separately in iMineralysis™. This may be necessary if, for example, a sonic log is only available in a limited interval. In that case, one model with sonic may be used there and another model without it elsewhere. It may also be desirable if, for example, “shallow shale” has markedly different properties than “deep shale”. In that case, the same model may be used for both shallow and deep, but analyzed separately to allow different optimal values to be found.

Under the **Define Analysis Intervals** list, click **Add** to include analysis intervals as desired. Select the tops that limit the interval of interest (**From, To**) and **Name** it. Click **Remove** to deleted analysis intervals if needed.

Click **Apply** when finished.

Setup Analysis: Rock Physics Bounds (Beta)

1. Identify rock physics logs

2. Select: Constrain solutions or only compute bounds?

1. Input Logs
Available logs determine which bounds can be computed.

Bulk: Density Log (RHOB):
RHOB **RHOB**

Compressional Wave (P-Wave) Slowness (Sonic) Log (DT):
DT **DT**

3. Advanced options
By default, optimized coefficients for RHOB and fixed coefficients for DT are used to compute the bounds for all models, and all bounds are used to constrain the solution. To change this, select advanced options.

3.1. Select intervals where coefficients will remain fixed
If checked, values in the table below will be used to compute the bounds. If cleared, values from the optimization will be used.

Interval	Limits Matrix	RHOB	DT
Top_00	lim_above	<input type="checkbox"/>	<input checked="" type="checkbox"/>
00_PP	lim_upper	<input type="checkbox"/>	<input checked="" type="checkbox"/>
PP_Bottom	lim_lower	<input type="checkbox"/>	<input checked="" type="checkbox"/>

If a box cannot be cleared, it means that log is not present in that limits matrix (i.e. it is not modeled), so fixed coefficients must be used.

3.2. Fixed constituent values for non-modeled logs
For logs not in the limits matrix of a coefficient model, fixed coefficient values must be entered here.

Limits Matrix: Limits M...

Limits M...	Log	DT _{Shale} = 104.45	DT _{Dolomite} = 44	DT _{Quartz} = 56	DT _{Oil} = 220	DT _{Water} = 186
lim_lower	DT					
lim_upper	DT					
lim_above	DT					

Apply

2. Apply rock physics bounds?
If checked, rock physics bounds (Voigt, Reuss, and solidity) will be used to constrain the solution. If cleared, bounds will be computed, but will not affect the solution.

Rock physics bounds
These rock physics bounds are computed in iMineralysis, and may be selected to constrain solutions.

Reuss and Voigt Bounds:
For rock constituents c with volume fractions f_c :

$$M = \rho_B \cdot V_P^2 = C_{units} \cdot \rho_B / D_T^2$$

$M \geq [\sum_c f_c / M_c]^{-1}$
 $M \leq \sum_c f_c \cdot M_c$

Solids-Based Bounds:
For solid constituents s with volume fractions f_s :

$$M \leq [\sum_{(solids\ s)} f_s \cdot M_s] / \sum_{(solids\ s)} f_s$$

P-Wave Solids Upper Bound

3. Optional: Specify advanced options

Rock physics bounds Reuss and Voigt are theoretical elastic limits that the multiminer solution must always honor for a given set of mineral fractions and constants. The current implementation of the rock physics bounds in iMineralysis™ only applies to the P-wave elastic modulus, which can be computed from sonic and density logs.

If the multiminer solution does not violate the bounds, it means the solution is plausible. If the bounds are violated, however, it means that there is a problem with the solution that requires further examination. The problem may be related to data errors, wrong elastic parameters, or erroneous multiminer solution due to wrong mineral constants, non-uniqueness, or insufficient data. iMineralysis™ uses a linear approximation (Wylie's equation) to model the sonic log but this approximation is not always valid and may also yield erroneous solutions. Typically, the application of the rock physics bounds is more important as the difference between constants of rock constituents gets smaller. In other words, minerals with similar properties are more likely to result in multiminer solutions that violate the bounds.

Rock physics bounds are used within iMineralysis™ in two ways. The first one is to simply check whether the solution is plausible, without influencing the optimization. The second is by

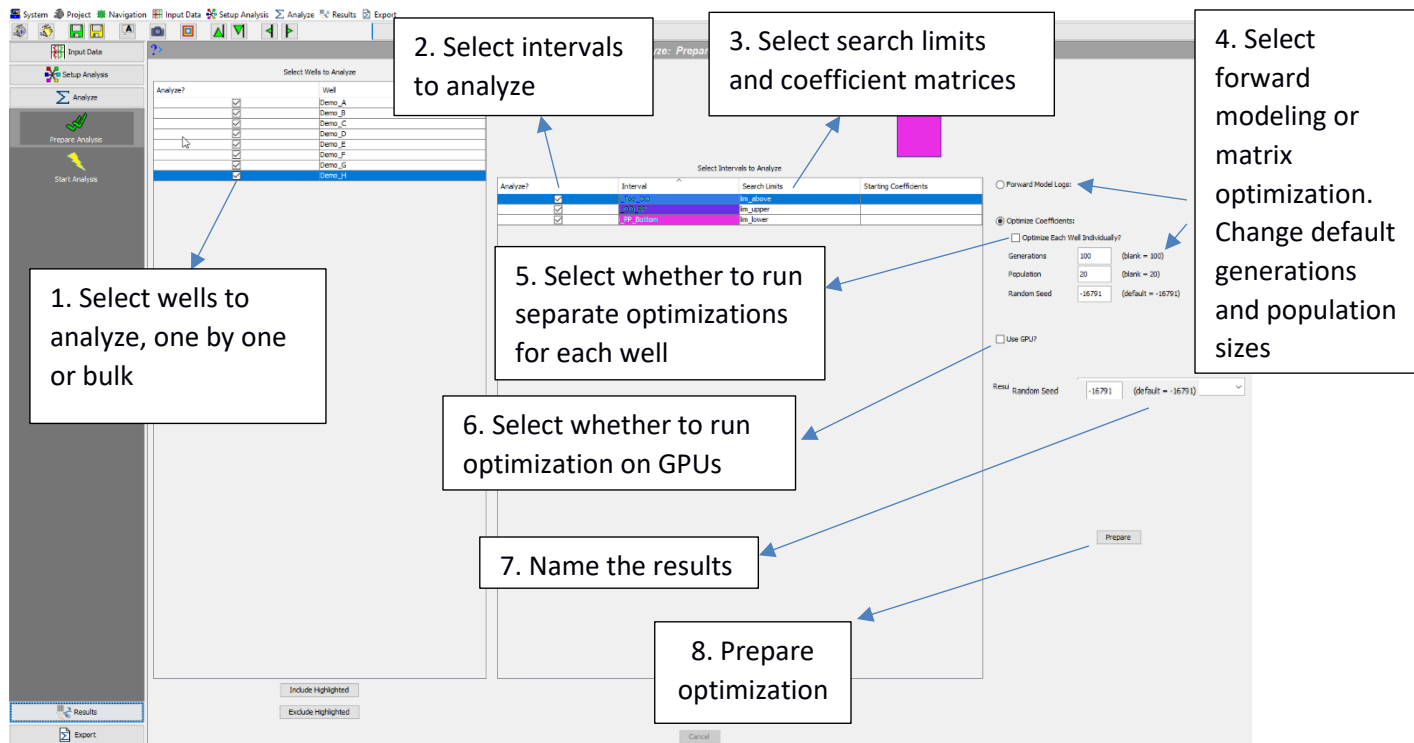
constraining the optimization to force both the linear solver and the genetic search to stay within the bounds as much as possible.

Use this screen to set up computing rock physics bounds, and to optionally apply them to constrain solutions.

Under **1. Input Logs**, select which logs represent measured density and sonic. Select **2. Apply rock physics bounds** to instruct the optimizer to use rock physics to constrain the solution; otherwise, the bounds are computed and displayed, but do not influence the final answer.

When bounds will be applied, **3. Advanced options** can be specified. In the **Rock physics bounds** box, individual bounds can be selected to be applied or not, and the formulas used are shown. Moduli are computed using the input well logs, while bounds are computed from estimated fractions and constituent properties. Constituent properties are either fixed or taken from matrix coefficients from the model: If a needed log is not modeled, or is selected under **3.1 Select intervals where coefficients will remain fixed**, then fixed property values are entered in **3.2 Fixed constituent values for non-modeled logs**.

Analyze: Prepare Analysis



Use this screen to select the wells, intervals, search limits matrices, and coefficient matrices for an analysis run, choose whether to perform optimization or forward modeling, and enter a name for the results. Optimization searches for the matrix of coefficients that fits the data best, and saves a new Result Values matrix. Forward modeling is basically the same as performing optimization using 1 generation and 1 individual starting with the selected Initial Values, except that no Result Values are saved (because they would be identical to the initial values). Initial values are optional; if they are not selected, then the midpoints of the coefficient ranges will be used. For forward modeling only, this is probably not desirable.

The default **Generations** (iterations) and **Population** size used by the genetic optimizer can be overridden here. Larger values may produce better results, but will require longer run times.

If desired, wells can be optimized individually by checking **Optimize Each Well Individually?** This will produce result coefficients optimized for each well, which can be exported and used to identify regional variability in rock composition. Different solutions can be generated from the same model by changing the **Random Number Seed**.

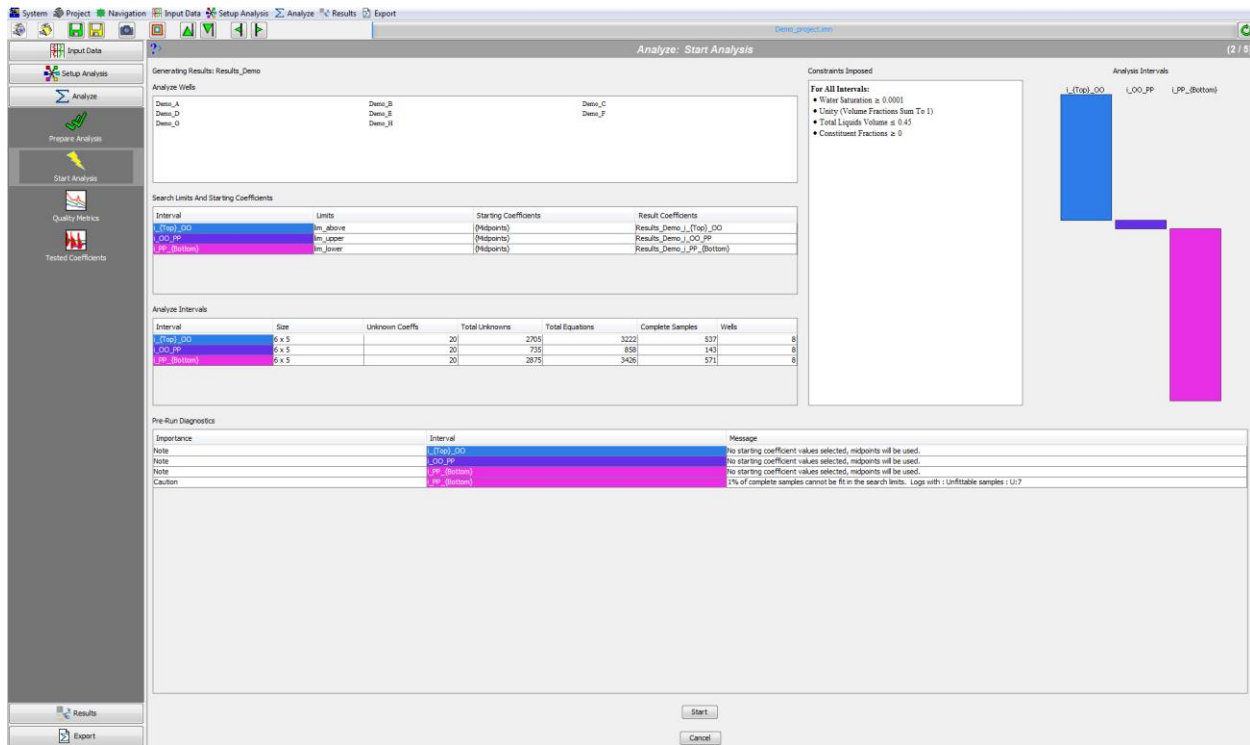
If a compatible NVIDIA® graphics card is detected on the system, optimizations can be significantly accelerated by using its graphical processing units (GPUs). This capability is currently in beta, and is offered now for preview. Activating the option "**Use GPU? (Beta)**" helps accelerate optimizations in most situations, in particular for large intervals (with large numbers of samples) in one or multiple wells. Optimizations for thinner intervals (one or multiple wells) with "few" samples may be more suitable for

conventional CPU processing. We recommend testing each problem separately to assess the improvement of performing computations on the GPUs. This option becomes available when the software detects compatible hardware in the system. Otherwise, the GPU option won't be available.

The same genetic optimizations performed on CPUs or GPUs may yield slightly different results, since they are the result of different floating-point implementations. For GPU processing, optimization is implemented using CUDA®, a parallel computing platform and programming model developed by NVIDIA® for general computing on its own GPUs..

Follow the steps indicated in the figure. Press **Prepare** when ready. The analysis will be prepared and pre-run diagnostics displayed on the **Analyze: Start Analysis** screen.

Analyze: Start Analysis



Use this screen to review the pre-run statistics and diagnostics, and decide whether to continue with the prepared analysis. The information here is populated after pressing **Prepare** in the previous **Analyze: Prepare Analysis** screen. This information allows the user to check whether the analysis has been set up as intended and, if not, go back and make changes. **Constraints Imposed** automatically (such as the Positivity and Unity constraints) are also indicated here.

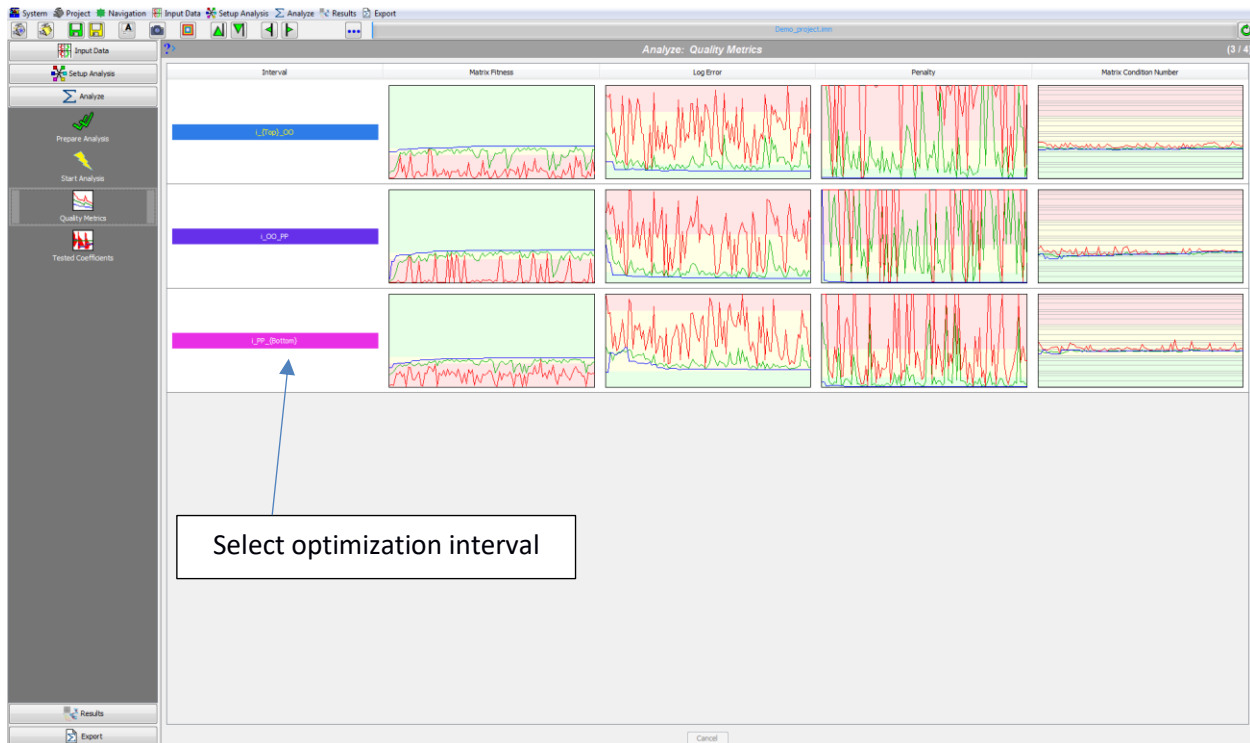
Some potential problems and their impacts on the analysis may be identified in the **Pre-Run Diagnostics** list. Most of these will not prevent the analysis from being run, but may lead to poor results in some cases. In particular, a diagnostic like:

XX% of complete samples cannot be fit in the search limits. Logs with: Unfittable samples:

means that some search limits are too narrow for the indicated logs. More generally, running an analysis that has **Error** diagnostics is likely to produce poor results on the interval where the error was detected.

Press **Start** to initiate the analysis, or **Cancel** to go back and make changes. A running analysis can also be canceled here. While an analysis is prepared or running, changes are disabled on the other screens.

Analyze: Quality Metrics



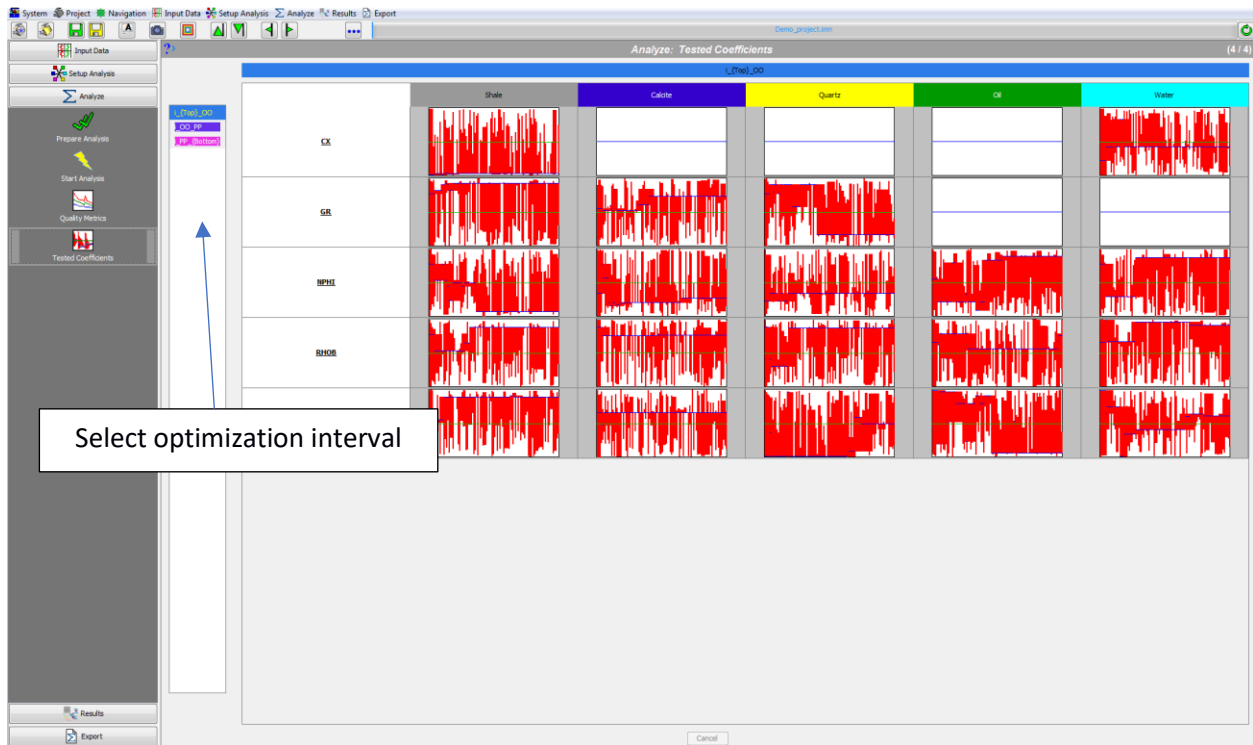
This screen displays various metrics about the running (or most recently run) optimization. It is not shown for forward modeling.

The horizontal axis for all plots is the generation (iteration) number. All plots have three background colors: Green (good), Yellow (intermediate), and Red (poor). Three lines are displayed: Blue (metric value for the best individual for that generation), Green (average metric value for that generation) and Red (the worst metric value for that generation). Ideally, we want Blue lines to be in the Green background zones by the end of the optimization.

The values displayed are:

- **Coefficient Matrix Fitness:** Fitness is the measure the optimizer aims to maximize. It is an arithmetic combination of the **tolerance error** and **violations penalty**, log-scaled to condense low values and separate high ones.
- **Log Error:** Average error in tolerance units between the estimated and observed logs.
- **Penalty:** Average penalty imposed for fraction, liquid, coefficient, and condition number violations.
- **Matrix condition number:** Log10 of the ratio of the largest and smallest nonzero singular values of the model coefficient matrix. Large condition number means that the linear system is unstable, and the modeled logs and fractions are unreliable.

Analyze: Tested Coefficients

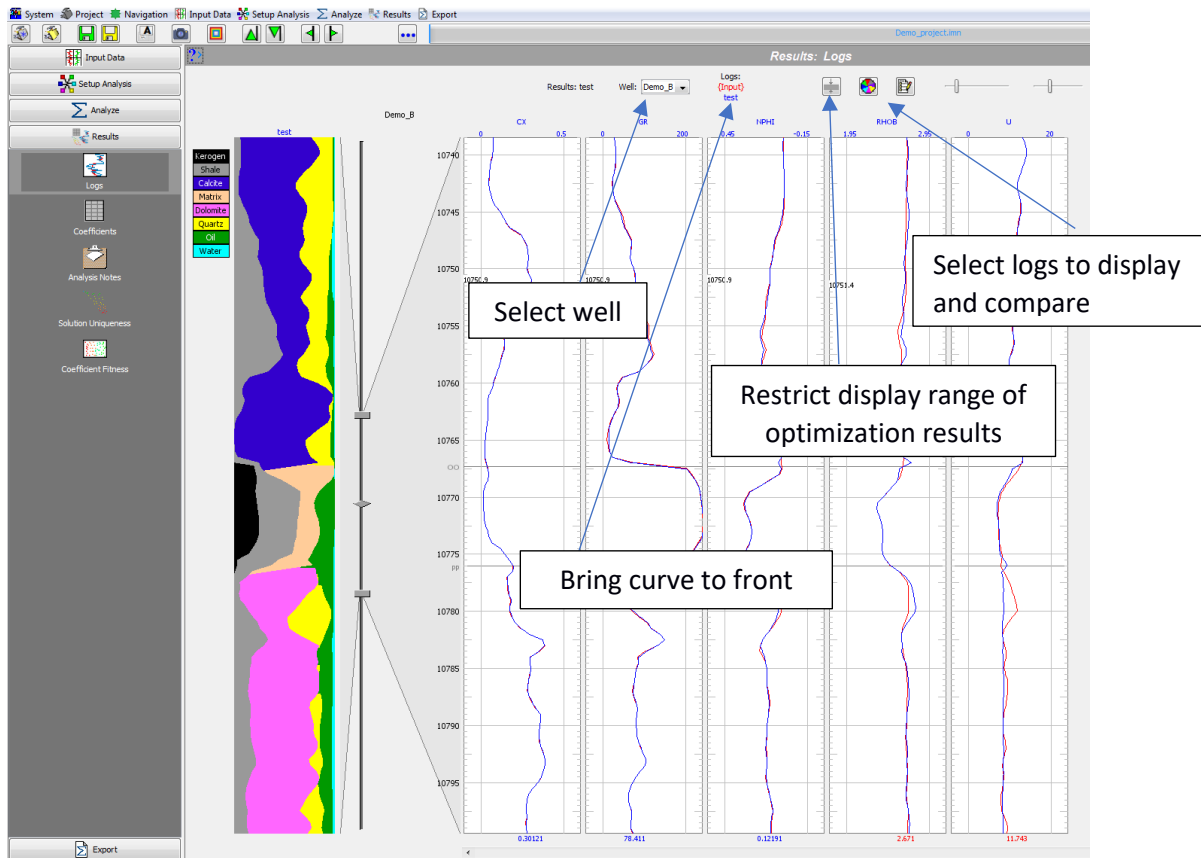



This screen displays the range of coefficient values tested during the running (or most recently run) optimization. It is not shown for forward modeling.

The horizontal axis is the generation number; the vertical axis is the range of allowed values for the coefficient in the search limits matrix. The Green line is the initial value, the Blue line is the best value in each generation, and the Red bar is the tested range.


Select an optimization interval to see the tested values for that interval.

Results: Logs



This screen displays the logs computed by optimization or forward modeling. This is a wide screen, so it may be helpful to click the Hide Navigation Sidebar toolbar button  to hide the navigation bar temporarily.

Select a **Well** to view. Input logs are shown in Red and modeled logs are shown in Blue. Composition for different depths is shown at the left.

Click the Setup Display button  to bring up the results **Display Setup** editor to select which logs and user defined inequalities to display:

Edit Results Display Setup

Display Composition

Compare: ▼

Select Logs to Display Select Inequalities to Display

Display?		Log
<input type="checkbox"/>		CALCITE
<input checked="" type="checkbox"/>		CX
<input type="checkbox"/>		DOLOMITE
<input type="checkbox"/>		DT
<input checked="" type="checkbox"/>		GR
<input type="checkbox"/>		INTVL
<input type="checkbox"/>		KEROGEN
<input type="checkbox"/>		MATRX
<input checked="" type="checkbox"/>		NPHI
<input type="checkbox"/>		OIL
<input checked="" type="checkbox"/>		PORO
<input type="checkbox"/>		PROBLEM
<input type="checkbox"/>		QUARTZ
<input checked="" type="checkbox"/>		RHOB
<input type="checkbox"/>		SHALE
<input checked="" type="checkbox"/>		SW
<input checked="" type="checkbox"/>		U
<input type="checkbox"/>		VALID
<input type="checkbox"/>		WATER

Display the INTVL log to see the interval in which each sample was used, or the VIOL log to see which samples had violation penalties. If prior results are available, select a result to compare with the latest run in the **Compare** box; logs for that result will be shown in Green. Close the editor when finished.

Results: Coefficients

L_Top_OO						L_OO_PP						L_PP_Bottom					
Final: test_I_Top_OO						Final: test_I_OO_PP						Final: test_I_PP_Bottom					
	Shale	Calcite	Quartz	Oil	Water		Kerogen	Shale	Matrix	Oil	Water		Shale	Dolomite	Quartz	Oil	Water
CX	0.0552	0	0	0	9.4254	CX	0	0.01681	0	0	11.264	CX	0.27683	0	0	0	10.982
GR	236.36	16.086	11.66	0	0	GR	874.51	245.68	18.979	0	0	GR	410.48	21.618	13.324	0	0
NPHI	0.25985	-0.00451	-0.03294	0.96862	0.96164	NPHI	0.27125	0.21485	-0.04405	0.79045	0.86293	NPHI	0.33079	0.02285	-0.04353	0.45198	0.86704
RHOB	2.8662	2.7202	2.6698	0.92787	1.1198	RHOB	1.6364	3.2479	2.7851	0.8608	0.92331	RHOB	2.6655	3.1261	2.6096	0.73334	0.86855
U	11.439	15.984	5.9655	0.01446	0.67057	U	0.17523	11.541	13.302	0.01249	0.69434	U	9.8488	9.9628	6.9474	0.26045	1.0044
Starting:						Starting:						Starting:					
	Shale	Calcite	Quartz	Oil	Water		Kerogen	Shale	Matrix	Oil	Water		Shale	Dolomite	Quartz	Oil	Water
CX	1	0	0	0	9.75	CX	0	1	0	0	9	CX	1	0	0	0	9.75
GR	150	12.5	19	0	0	GR	650	150	17.5	0	0	GR	285	35	24	0	0
NPHI	0.325	0	-0.025	0.85	0.85	NPHI	0.4	0.275	-0.01	0.875	0.925	NPHI	0.35	0.025	-0.025	0.7	0.925
RHOB	2.75	2.575	2.64	0.85	0.975	RHOB	1.4	3.8	2.7	0.85	0.975	RHOB	2.745	2.8	2.64	0.85	1.025
U	9.25	15	6	0.125	0.55	U	0.825	9.25	9	0.1	0.55	U	8.25	9.75	5.5	0.15	0.55
Change (% Relative to Allowed Range):						Change (% Relative to Allowed Range):						Change (% Relative to Allowed Range):					
	Shale	Calcite	Quartz	Oil	Water		Kerogen	Shale	Matrix	Oil	Water		Shale	Dolomite	Quartz	Oil	Water
CX	-0.9448 (+7.24%)	0	0	0	-0.22456 (7.2124%)	CX	0	-0.98219 (+9.16%)	0	0	2.2643 (37.738%)	CX	-0.72317 (36.158%)	0	0	0	1.232 (27.378%)
GR	86.36 (43.18%)	3.3896 (23.904%)	-7.338 (33.363%)	0	0	GR	224.51 (44.903%)	95.681 (47.841%)	1.4789 (5.9154%)	0	0	GR	125.48 (46.473%)	-13.382 (44.606%)	-10.676 (33.363%)	0	0
NPHI	-0.06515 (-43.433%)	-0.00451 (-22.55%)	-0.00794 (-15.88%)	0.11862 (9.54%)	0.11164 (37.213%)	NPHI	-0.12876 (-42.917%)	-0.06015 (-24.06%)	-0.03405 (-42.862%)	-0.08455 (-33.82%)	0.06207 (+1.38%)	NPHI	-0.01921 (-19.21%)	-0.00215 (-4.3%)	-0.01853 (-37.06%)	-0.24802 (-41.337%)	-0.05796 (-38.64%)
RHOB	0.11625 (38.75%)	0.14523 (26.405%)	0.02984 (37.3%)	0.07787 (25.957%)	0.14484 (41.383%)	RHOB	0.23638 (39.397%)	-0.55208 (-23.003%)	0.08512 (42.56%)	0.0108 (3.6%)	-0.05169 (-14.769%)	RHOB	-0.0795 (-27.414%)	0.32608 (40.76%)	-0.03038 (-37.975%)	-0.11656 (-38.887%)	-0.15545 (-44.7%)
U	2.1892 (39.804%)	0.984 (16.4%)	-0.03448 (-0.862%)	-0.11054 (-44.216%)	0.12057 (10.961%)	U	-0.64977 (-48.131%)	2.2009 (41.653%)	4.3018 (43.018%)	-0.08751 (-43.755%)	0.14434 (13.122%)	U	1.5988 (45.68%)	0.21281 (3.274%)	1.4474 (48.248%)	0.11045 (36.817%)	0.45443 (41.312%)

This screen displays the final, initial, and change in coefficients for each interval in the latest analysis run. % changes are relative to the range allowed in the search limits matrix.

The **Export: Coefficients** screen allows coefficient values to be exported for use in other applications.

Results: Analysis Notes

Results: Analysis Notes

Results	test
Wells	8
Intervals	3

Interval	I_(Top)_OO	I_OO_PP	I_PP_(Bottom)
Coefficient Matrix Fitness	5.8533	5.9109	5.6441
Average Sample Error (Tolerances)	3.1977	2.5984	6.6429
Average Sample Penalty	0.0018622	0	0.00175131
Matrix Condition Number	82.818	100.36	216.18

Interval	I_(Top)_OO	I_OO_PP	I_PP_(Bottom)
Result Coefficients	test_I_(Top)_OO	test_I_OO_PP	test_I_PP_(Bottom)
Started	Tue Sep 14 16:13:14 MDT 2021	Tue Sep 14 16:13:14 MDT 2021	Tue Sep 14 16:13:14 MDT 2021
Finished	Tue Sep 14 16:13:26 MDT 2021	Tue Sep 14 16:13:23 MDT 2021	Tue Sep 14 16:13:24 MDT 2021
Matrix Size	6 x 5	6 x 5	6 x 5
Search Limits Matrix	lim_above	lim_upper	lim_lower
Coefficient Matrix	(midpoints)	(midpoints)	(midpoints)
GA Generations	100	100	100
GA Population Size	20	20	20
Wells	8	8	8
Unknown Coefficients	20	20	20
Total Unknowns	3242	878	3446
Equations	3222	858	3426
Complete Samples	537	143	571
Unfitable Complete Samples	0	0	7
Unfitable Log Values	(none)	(none)	U: 7
Constraints Imposed	<ul style="list-style-type: none"> • Water Saturation ≥ 0.0001 • Unity (Volume Fractions Sum To 1) • Total Liquids Volume ≤ 0.45 • Constituent Fractions ≥ 0 	<ul style="list-style-type: none"> • Water Saturation ≥ 0.0001 • Unity (Volume Fractions Sum To 1) • Total Liquids Volume ≤ 0.45 • Constituent Fractions ≥ 0 	<ul style="list-style-type: none"> • Water Saturation ≥ 0.0001 • Unity (Volume Fractions Sum To 1) • Total Liquids Volume ≤ 0.45 • Constituent Fractions ≥ 0

Diagnostics

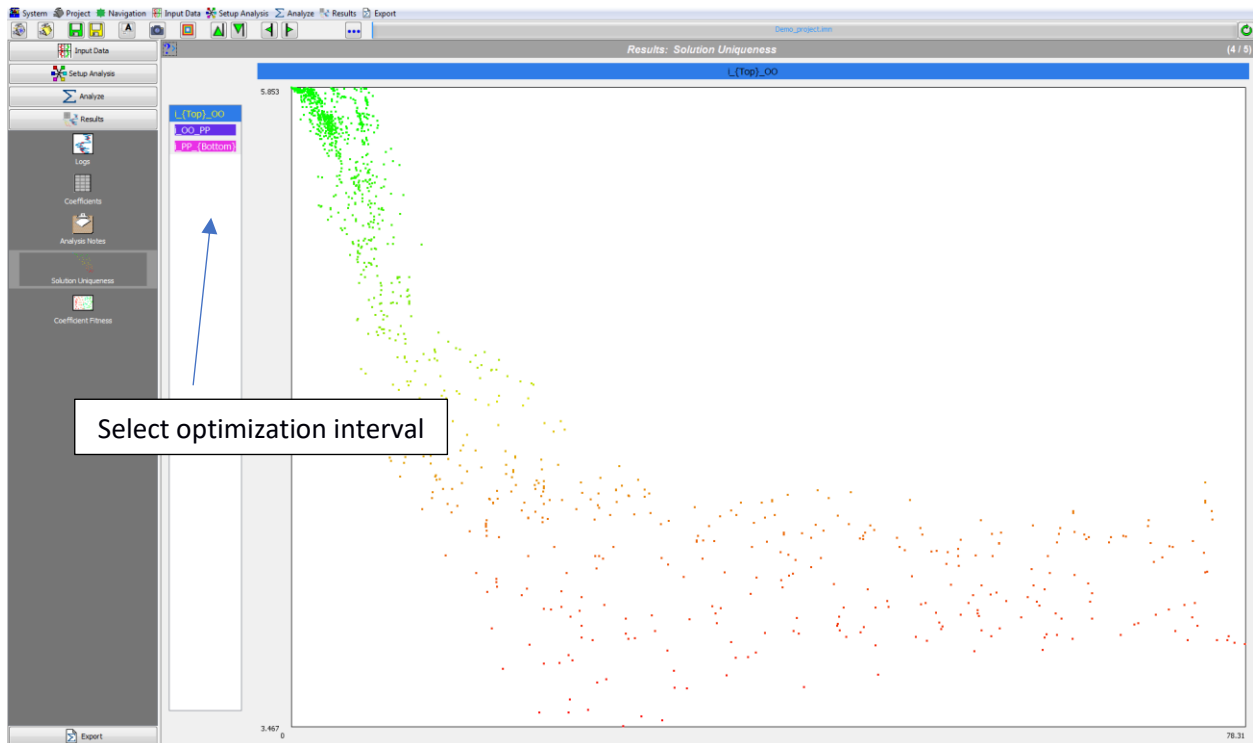
I_(Top)_OO
 Note: No starting coefficient values selected, midpoints will be used.

I_OO_PP
 Note: No starting coefficient values selected, midpoints will be used.

I_PP_(Bottom)
 Caution: 1% of complete samples cannot be fit in the search limits. Logs with : Unfitable samples : U:7
 Note: No starting coefficient values selected, midpoints will be used.

This screen displays information for each interval in the latest analysis run.

Results: Solution Uniqueness

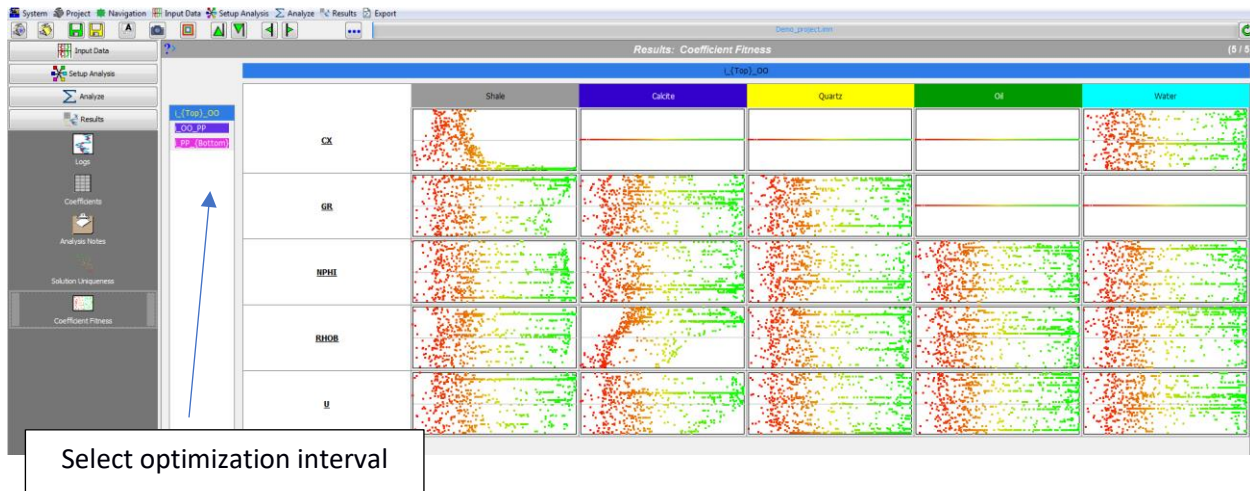


This screen displays a scatterplot of the fitnesses of coefficient matrices considered in the latest optimization run against their (normalized) distances from the final best coefficient matrix (located at zero distance). See the section **Results: Metrics** above for a description of fitness. The vertical axis is the matrix fitness; the horizontal axis is the distance from the final best. Plotted points are color-coded also by fitness, from Red=(poor fit) to Green=(good fit). Ideally, this plot should come to a vertical point in the upper-left corner (the final best); otherwise, there may be non-uniqueness issues with the solution.

Select an optimization interval to see the scatterplot for that interval.

If this screen shows that there is non-uniqueness, the plots on the **Analyze: Coefficient Fitness** screen may provide some information about its source.

Analyze: Coefficient Fitness



This screen displays the fitness of coefficient values tested during the running (or most recently run) optimization. It is not shown for forward modeling.

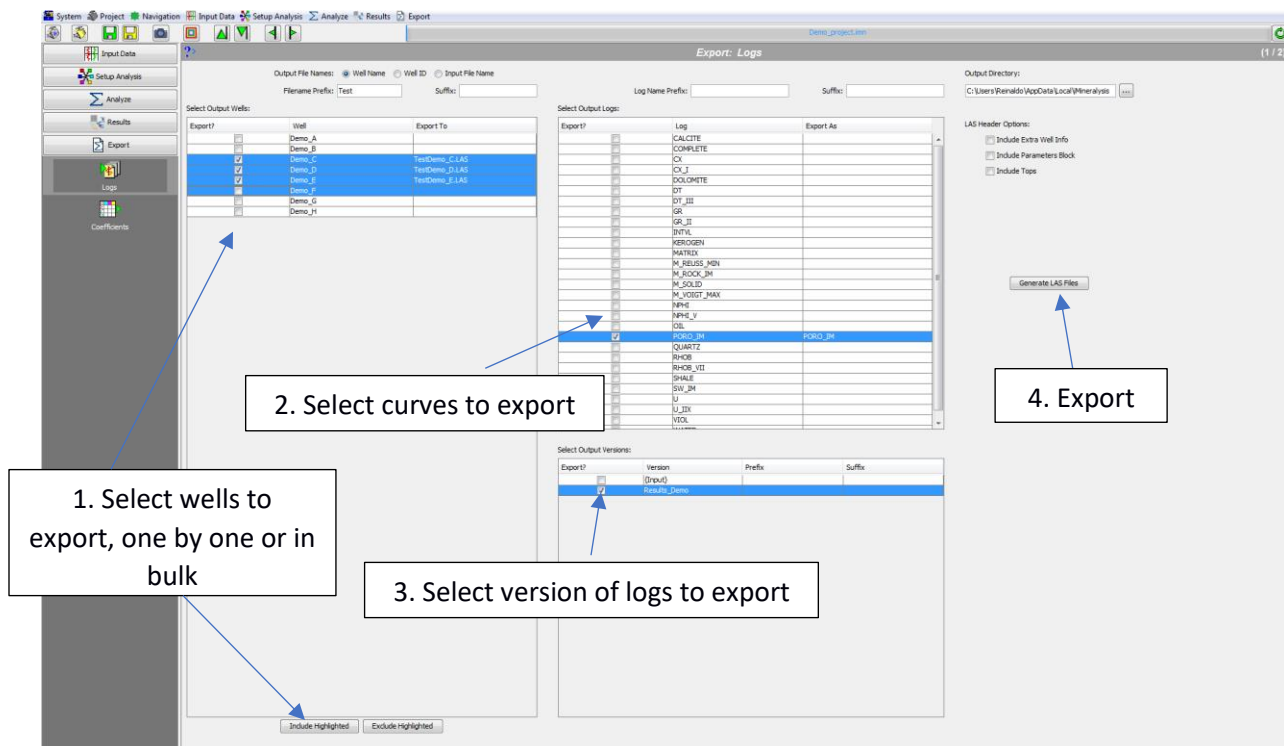
The vertical axis is the tested value within the ranges specified in the search limits matrix; the horizontal axis is the fitness of the coefficient matrix including it. See **Results: Metrics** section below or a brief description of coefficient matrix fitness. Plotted points are color-coded also by fitness, from Red=(poor fit) to Green=(good fit). Ideally, these plots should narrow towards the good end. Otherwise, there may be uniqueness problems with the solution.

Select an optimization interval to see the fitness for the coefficients related to that interval.

This screen may yield diagnostic information about the model:

- If a coefficient plot comes to a sharp point at the good end, and that point is either at the top or bottom of the vertical axis, then the search limits for the coefficient should be reconsidered.
- If the plots on the **Results: Solution Uniqueness** screen show that there are non-uniqueness problems, the plots in this **Analyze: Coefficient Fitness** screen may provide a clue. Consider the logs and constituents for the coefficients whose plots on this screen do not narrow at the good end, especially for the most plentiful constituents. Computationally, these are contributing to the non-uniqueness.

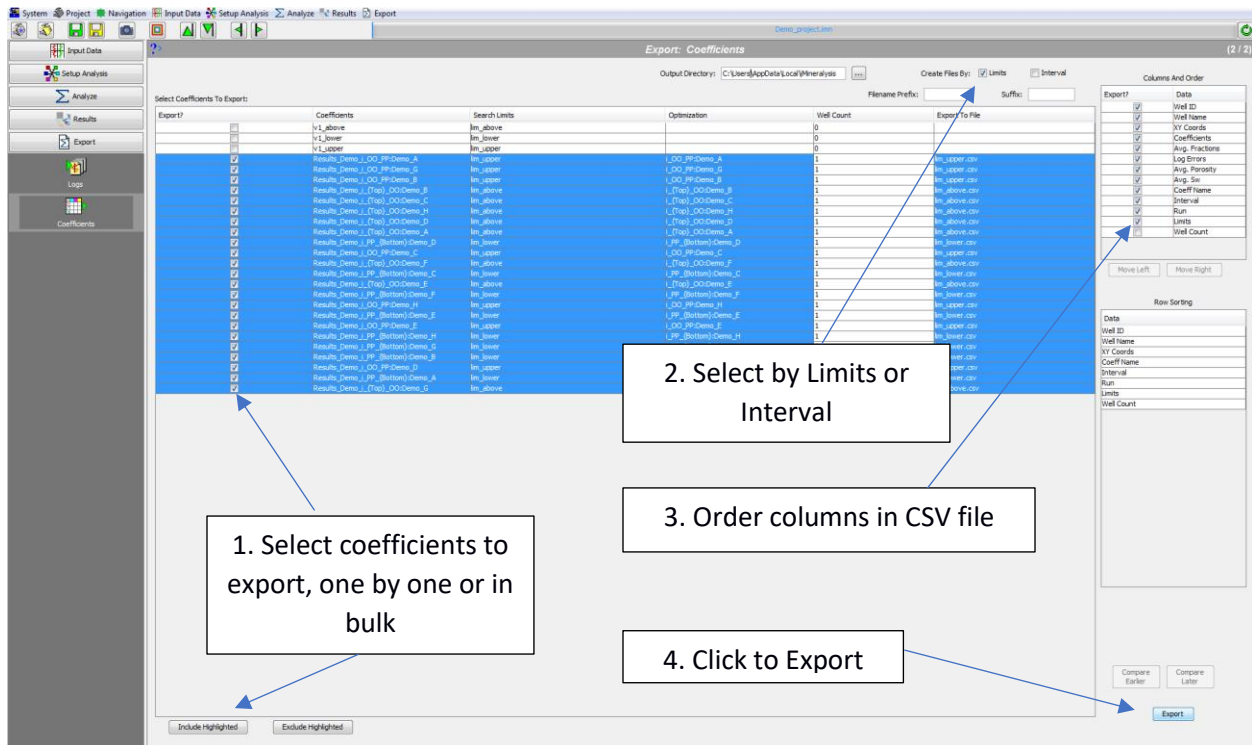
Export: Logs



Use this screen to export well log data to LAS files.

Follow the steps indicated in the figure by selecting the desired wells, logs and versions to export. Logs read from LAS files are the {Input} version; logs generated by optimization or forward modeling are identified by their results name. Exported file and log names can be given distinguishing prefixes and/or suffixes. Tops (in PETRA* format) or additional headers from the LAS input files can optionally be included in the generated LAS files. Press **Generate LAS Files** when ready.

Export: Coefficients



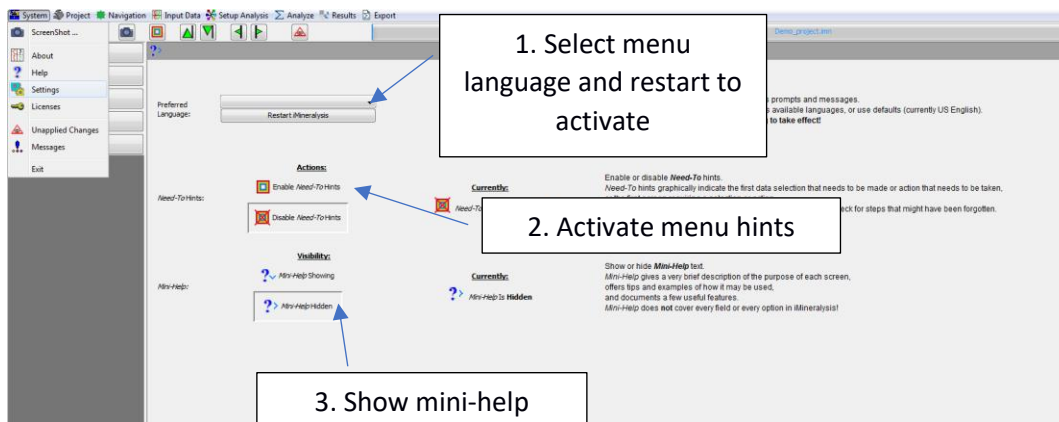
Use this screen to export initial value and results coefficients to comma-separated-values (CSV) files.

Select the directory in which to save files, and the coefficients (rows) and data (columns) to export. Column order and row sorting can be specified optionally, but this should not usually be necessary. By default, exported coefficients are grouped into files by their search limits; they can be grouped also by interval, or into the fewest files possible (by clearing both **Create Files By:** options). Exported file names can be given a distinguishing **Prefix** and/or **Suffix**. Press **Export** when ready.

The output CSV file can be imported into other programs for further analysis and mapping. Note that some cells may be left blank. For example, initial values will not have log errors or average fractions; and result values will not have values for logs or constituents which were excluded when the results were generated.

Name and location				Average mineral volumes					Matrix coefficients								Errors							
Well	X	Y	Interval	Vol_Kerogen	Vol_Shale	Vol_Calcite	Vol_Dolomite	Vol_Quartz	Vol_Oil	Vol_Water	RHOB_Kerogen	RHOB_Shale	RHO_Calcite	RHOB_Dolomite	RHOB_Quartz	RHOB_Oil	RHOB_Water	GR_Kerogen	GR_Shale	GR_Calcite	GR_Dolomite	GR_Quartz	Error_Average	Error_RHOB
1	100	1746	LBS	0.02	0.35	0.44	0.13	0.00	0.01	0.05	1.55	2.80	2.73	2.88	2.66	0.90	1.25	1351	195	13	24	20.9	0.2	0.4
2	398	2096	LBS	0.03	0.39	0.35	0.18	0.00	0.00	0.05	1.54	2.79	2.73	2.89	2.65	0.75	1.23	1351	195	14	24	20.8	0.2	0.4
3	882	2529	LBS	0.07	0.22	0.09	0.26	0.02	0.03	0.01	1.54	2.77	2.70	2.87	2.67	0.84	1.21	1400	187	14	17	19.1	2.1	4.2
4	896	2568	LBS	0.42	0.28	0.07	0.15	0.04	0.03	0.01	1.53	2.76	2.72	2.88	2.65	0.88	1.24	1400	171	9	22	19.7	1.0	2.1
5	896	2109	LBS	0.39	0.12	0.15	0.29	0.06	0.01	0.01	1.54	2.67	2.73	2.88	2.67	0.86	1.22	1400	166	12	23	22.4	1.2	2.6
6	898	2644	LBS	0.35	0.33	0.16	0.04	0.07	0.04	0.01	1.54	2.78	2.72	2.87	2.65	0.81	1.16	1362	94	9	10	20.2	0.9	1.9
7	1359	3177	LBS	0.39	0.22	0.12	0.20	0.02	0.03	0.01	1.54	2.78	2.71	2.88	2.64	0.88	1.21	1400	186	6	24	28.2	1.0	1.8
8	1389	2543	LBS	0.47	0.26	0.15	0.09	0.00	0.02	0.01	1.54	2.75	2.73	2.85	2.67	0.85	1.19	1400	151	13	19	25.9	1.5	3.1
9	1905	3057	LBS	0.36	0.27	0.20	0.07	0.05	0.03	0.02	1.55	2.79	2.72	2.87	2.66	0.74	1.22	1400	194	11	24	19.5	1.0	1.4
10	2579	3989	LBS	0.44	0.14	0.10	0.28	0.00	0.02	0.02	1.54	2.70	2.72	2.87	2.66	0.86	1.24	1400	125	14	18	22.7	1.5	3.2
11	2606	4576	LBS	0.38	0.28	0.20	0.10	0.00	0.02	0.02	1.53	2.80	2.73	2.84	2.66	0.77	1.16	1371	183	13	22	25.9	1.7	3.4
12	3383	5371	LBS	0.54	0.24	0.09	0.12	0.00	0.01	0.01	1.54	2.65	2.73	2.88	2.66	0.76	1.17	1361	108	14	24	28.6	2.1	4.2
13	3685	4734	LBS	0.38	0.32	0.14	0.11	0.02	0.02	0.01	1.53	2.78	2.72	2.85	2.66	0.89	1.19	1371	195	9	14	16.1	1.7	3.6
14	4634	5149	LBS	0.44	0.27	0.13	0.11	0.01	0.03	0.01	1.54	2.78	2.69	2.88	2.66	0.88	1.23	1400	153	14	22	24.0	0.6	1.1
15	5095	6837	LBS	0.44	0.35	0.15	0.02	0.01	0.03	0.01	1.54	2.77	2.70	2.85	2.67	0.82	1.18	1357	89	12	13	28.3	1.0	1.8
16	5259	7225	LBS	0.47	0.18	0.01	0.29	0.00	0.03	0.01	1.52	2.79	2.71	2.88	2.67	0.89	1.17	1371	131	14	19	19.2	1.8	4.0

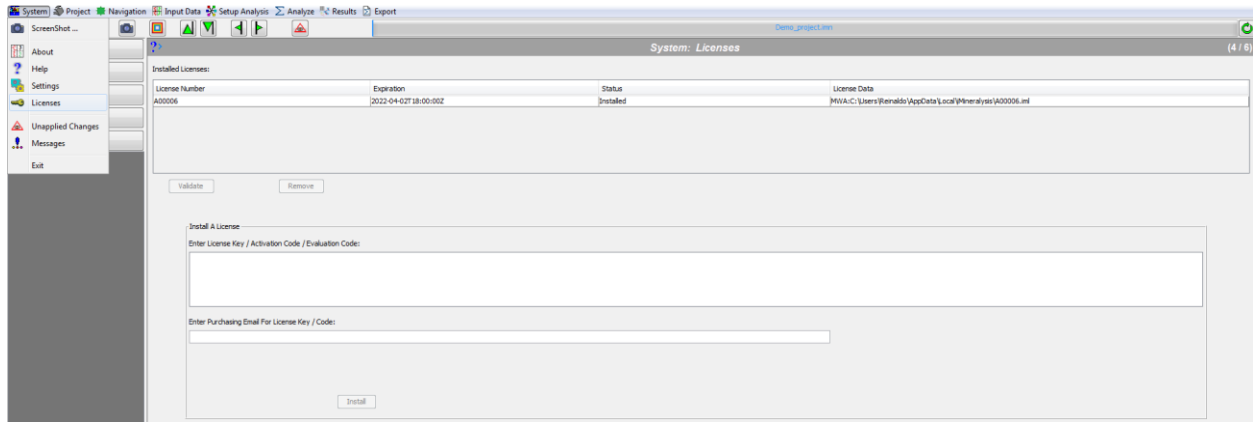
System: Settings



Use this screen to set preferences for the iMineralysis™ program's appearance and behavior.

Select a **Preferred Language**, whether to display **Need-to Hints**, and whether to display **Mini Help**. Changing language requires restarting iMineralysis™; changes to other settings take place immediately.

System: Licenses



Use this screen to install and remove iMineralysis™ licenses.

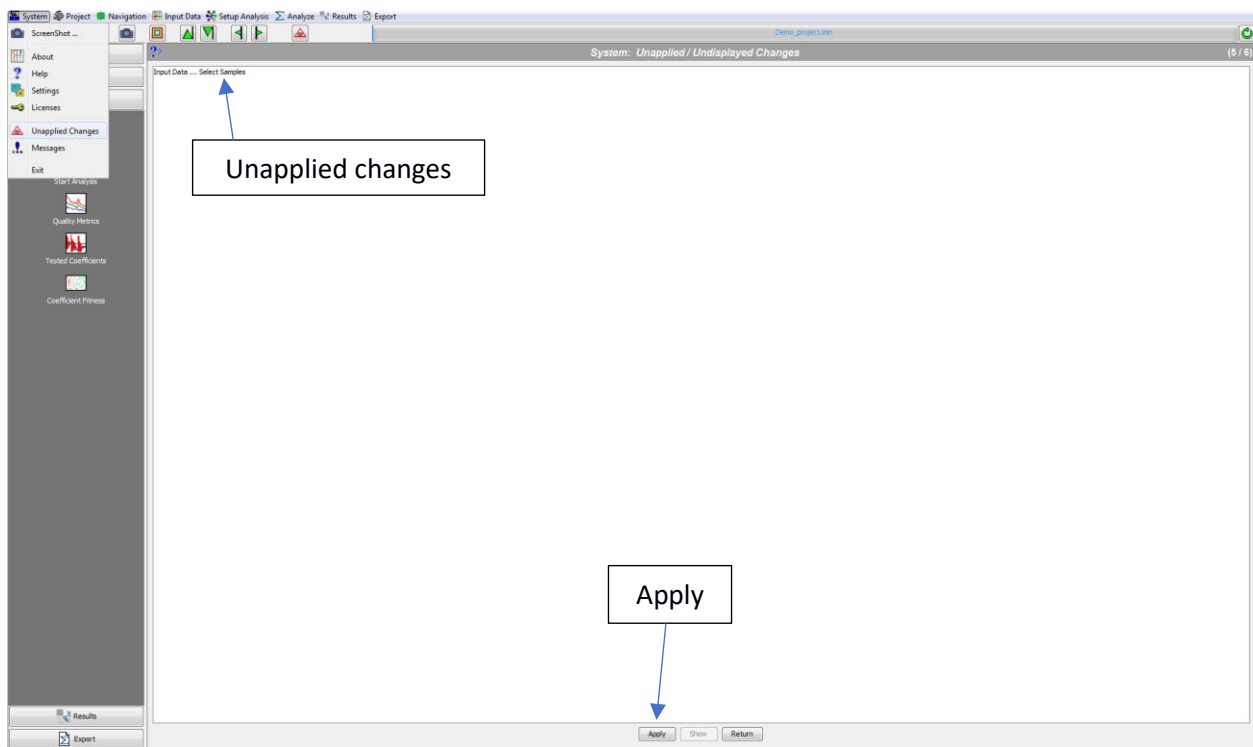
Licenses can be obtained at <https://www.seispetro.com/subscription>. To **Install a License**, both the **License Key** an associated **Purchasing Email** address must be entered; press **Install** when ready. Old licenses do *not* need to be removed before installing new ones.

Evaluation licenses are good for 30 days, and cannot be renewed.

Subscription licenses are good for a year, and can be renewed. When a subscription license is removed from one computer, it can be installed on another, after a certain delay. Subscription licenses can be moved twice per year.

Subscription licenses need to be validated online about once a month. This normally happens automatically and silently. To validate a subscription license manually, select the license in the **Installed Licenses** list and click **Validate**.

System: Unapplied/Undisplayed Changes



This screen lists changes to the input data or analysis setup that have not been applied. Unapplied changes will not be visible to other screens or to analyses prepared before they are applied, and will not be saved with the project.

Press **Apply** to apply all the pending changes, **Show** to go to the screen with the selected change, or **Return** to go back to your previous screen without changing anything.

System: Messages

This screen displays notes and error and warning messages generated by the program.

Hopefully, any message displayed will be self-explanatory and helpful. Press **Clear** to clear the message list or **Return** to go back to your previous screen without changing anything.

Please, **Save** and send any **Internal Error** messages to support@seispetro.com.

References

Here are some resources you can check for help on the use of iMineralysis™:

- For more information on the theory behind iMineralysis™, please refer to the theory [white paper](#) or our SEG 2020 [abstract](#).
- For the latest changes in this version of iMineralysis™, see the Release Notes.
- Other questions? Check out the online iMineralysis™ [Overview](#) and [Tutorials](#) (also on [YouTube](#)). We strongly recommend that you read the [Frequently Asked Questions](#) for more details about the software, data, optimization, subscription, and support.

Appendix A: Data Preparation

Any calculated logs that you want to use inside iMineralysis™ optimization must be generated outside iMineralysis™. For now, iMineralysis™ doesn't provide the option to perform basic operations with logs.

Examples of pre-calculations that you may want to perform before using iMineralysis™ are: pseudo-conductivity Cx to calculate saturations, volumetric photo-electric factor (U), or kerogen volume from Passey method among others.

Calculation of pseudo-conductivity: The simultaneous inversion of all fractions (volumes) of components is based on the assumption that the measured logs are a linear combination of such fractions and the tool responses for each component. However, the resistivity log is not linearly related to the volume of the components of the system. In this case, the resistivity log MUST be linearized by using a "pseudo-conductivity" instead of the original resistivity by assuming a water saturation model based on the modified Archie's equation with $m=n$. Under this assumption, the relation between the original the resistivity R and the pseudo conductivity Cx is given by

$$Cx = \sqrt[n]{\frac{1}{R}} .$$

This equation should be used to transform both the log data and the tabulated values for resistivity. If there is uncertainty on the proper values of $m=n$ in the interval of interest, it is recommended that the user generates various pseudo conductivity logs for different values of $m=n$ and import all into iMineralysis™ when setting up the project to test which one yields better results.

Calculation of volumetric photoelectric factor: The litho-density tool measures the Photoelectric Factor (PE). Although the PE log doesn't relate linearly with the volume of the components of the system, the photoelectric factor U estimated as $U=PE*RHOB$ does.

Data preconditioning: iMineralysis™ performs the optimization using all the input data in the interval of interest. If part of the data is not good quality (washouts, for instance) a separate log containing a bad-hole flag is required. Erroneous log values (tails, spikes, etc.) must be removed prior to loading into iMineralysis™. Log variability due to different contractors, vintages, processing parameters, etc., should be corrected prior to loading into iMineralysis™. This will ensure that results from the optimization represent real changes in the subsurface rather than other types of noise. It is also recommended that well names and log names are consistent across the data.

Appendix B: iMineralysis™ File Descriptions

This Appendix describes the different files and directories used for iMineralysis™.

Note: *user_home* is the user's home directory; on Microsoft® Windows® 10 this is typically `C:\Users\accountname`.

Installed Files

Desktop:

(Usually in *user_home\Desktop*)

iMineralysis 3.5 Application shortcut to start iMineralysis™

- This shortcut launches the iMineralysis™ GUI using the appropriate Java Runtime Environment. If it is deleted, lost, or broken, there is a duplicate shortcut in the application folder.

Application folder:

(Defaults to *user_home\AppData\Local\iMineralysis*)

<code>._jre</code>	Dedicated (not shared) Java Runtime Environment for the iMineralysis™ GUI, if installed
<code>.uninst.all.exe</code>	Uninstaller
<code>dna32.dll</code>	softWORKZ* license library (32-bit)
<code>dna64.dll</code>	softWORKZ* license library (64-bit)
<code>EULA_iMineralysis_en.pdf</code>	End User License Agreement (English)
<code>EULA_iMineralysis_es.pdf</code>	End User License Agreement (Spanish)
<code>iMin_icon.ico</code>	iMineralysis™ icon
<code>imin3_hashes.txt</code>	Digital signatures for iMineralysis™ application
<code>iMineralysis 3.5</code>	Application shortcut to start iMineralysis™
<code>iMineralysis3.exe</code>	iMineralysis™ analysis engine
<code>iMineralysis3.jar</code>	iMineralysis™ GUI
<code>libiomp5md.dll</code>	Redistributable OpenMP parallel processing library from Intel*
<code>Release_Notes.txt</code>	Changes, new features, and bug fixes

- The GUI, analysis engine, JRE (if installed), libraries and signatures are all required, and must not be deleted or modified.
- The other files are optional and can be deleted or moved. If any of these files are deleted or corrupted, they can be recovered by running the installer and selecting the **Application** component.

Documentation folder:

(Defaults to *user_home\Documents\iMineralysis*)

<code>iMin3_QuickRef.pdf</code>	Quick Start and brief screen reference
<code>iMin3_Theory.pdf</code>	Very brief description of the theory behind iMineralysis™

- These files are optional and can be deleted or moved. To restore them, run the installer and select

the **Documentation** component.

Data folder:

(Defaults to `user_home\iMineralysis\Data`)

.\Models:

All_default.imm
Carbonates_default.imm
Mudstones_default.imm
Sand_shale_default.imm
Sand_shale_porosity_default.imm

.\Sample_Project:

A.LAS - H.las	Log data files of the sample project
Sample_Project.imn	iMineralysis™ project file of the sample project
Tops.csv	Marker depths for the sample project

- These files are optional and can be edited, deleted, or moved. To restore the original versions (for example, after experimenting with the sample project), run the installer and select the **Default Models** or **Sample Project** components, respectively.

Licensing and Settings Files

(Usually in `user_home\AppData\Local\iMineralysis`)

Licensing:

imin3_licenses.txt	Installed license list
iMineralysis3.cdm	softWORKZ* license file
iMineralysis3.fsa_*	softWORKZ* evaluation license backup copies
*.iml	License extensions

Settings:

imin3_settings.ini	Application settings (screen size, table columns, etc)
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- A license is required to run iMineralysis™.
- Licenses can be obtained at <https://www.seispetro.com/subscriptions>.
- Standard licenses are automatically validated online periodically by our licensing partner softWORKZ*.
- The program warns you and provides the ability to manually validate your license if automatic validation fails.

Project files

(Can be located anywhere)

projectname.imn	iMineralysis™ project file
*.las	Project log data files
projectname.history.txt	Project history file

- An iMineralysis™ project consists of well lists, well ID and logging information, log lists, multiminerals models, analysis intervals, various other lists and settings, and well log data.

- "Everything else" is stored in the iMineralysis™ project file, but the log data itself is left in and read from the LAS files that are "added to" the project on the **Input Data: Select LAS Wells** screen.
- "Read from" but not "Saved to": iMineralysis™ never modifies the LAS files added to a project. This allows users the option to either make a dedicated copy of the LAS files for an iMineralysis™ project, or share them with another application (thereby keeping the iMineralysis™ data in sync with the other application, and saving a little disk space).
- The LAS files are thus part of the project, but they do not have to be in the same place as the iMineralysis™ project file, or even be all in the same directory: the iMineralysis™ project file includes the full path of each LAS file.
- When loading a project, if any LAS files are missing, they are searched for (briefly); if any can't be found, then the user is given the option to specify a new location. If any are found to have changed, the user is given the option of reparsing them for updated logging info and log lists.
- Note that if any LAS files are relocated or reparsed, then the project (i.e. the iMineralysis™ project file) should be saved, or the updates will be forgotten the next time the project is opened.
- When transferring a project, **both the iMineralysis™ project file and the added LAS files** must be included.
- As noted below, iMineralysis™ can also import or load information from a few other types of files (e.g. tops files). This non-log-data information is saved in the iMineralysis™ project file, and the files are not part of, and do not need to be copied with, the project. They can be deleted or changed, and the iMineralysis™ project will be completely oblivious to the fact.
- For each project, iMineralysis™ maintains a history file that includes information on all the analyses run in the project. The history file is in the same directory as the iMineralysis™ project file. This is a human-readable (albeit technical) text file, which can help technical support solve problems. It is not required or part of the project, and can be deleted at any time.

Import / Export files

(can be located anywhere)

Alias Tables:	*.ima	Import / Export
	*.txt	
Tops:	*.csv	Import only
Model:	*.imm	Import / Export
Coefficients:	*.csv	Export only
LAS Files:	*.las	Add-to-Project / Export

- **Alias Tables:** These should be text files. Lines starting with a # character are ignored; other lines should specify common log names:
`common_name = specific_name_1 specific_name_2 ...`
- **Tops:** Tops files should be comma-separated-values. Each line should contain well ID, marker name, and marker depth columns.
- **Model:** Multimineral models are imported/exported in an iMineralysis™-specific format.
- **Coefficients:** Coefficients are exported in comma-separated-value format. See section **Export: Coefficients** above for details.
- **LAS Files Exported:** Can contain input and computed well log data. They are not part of or remembered by the project.
- **LAS Files Added-to-Project:** As described above, an LAS file that is added to a project remains part of the project. The well ID and logging information is saved in the iMineralysis™ project file, but the well log data data itself is left in the LAS file and read as needed.

- **Imported files:** Data imported from (non-LAS) source files is saved in the iMineralysis™ project file. The source file is not part of or remembered by the project. (It follows that if the source file changes, iMineralysis™ will not notice, and will not ask the user whether to reload the data.)
- **Exported files:** Are not part of or remembered by the project.

Temp files

(Usually in `user_home\AppData\Local\Temp`)

`m3_*.*`

Temporary files

- While the program is running, iMineralysis™ caches various things in various temporary files. All start with `m3_`; should be deleted when program closes; can be deleted if desired when program is closed.