

Crystal Miner Release Note v2.3.0

for the Naica[™] System



All modifications made to Crystal Miner software from version 1.2.0 to version 2.3.0 are listed in the Table below.

Modification types include:

- New feature addition, highlighted in blue when significant
- Improvement, highlighted in blue when significant
- Configuration change, highlighted in gray when significant
- Bug correction, highlighted in orange when significant
- Modification in the exported data, written in red

Soft.	Modification				
version	ID	Туре	Description		
2.3.0	N/A	Feature	This feature has been added: Addition of the possibility to pool (resp. unpool) chambers in Crystal Miner, by going to "SETUP > Edit Experiment", then selecting the chambers and clicking on the button "Pool" (resp. "Unpool"). The pooling results are automatically updated accordingly (see below the new "pooling" feature in Crystal Miner version 2.2.1). By considering each set of pooled chambers as one larger chamber, this pooling strategy allows to increase the analyzed volume and thus gain detection sensitivity and quantification precision.		
	N/A	Bug	This bug has been corrected: The management of chamber pooling is sometimes not robust.		



Soft.		Modification				
version	ID	Туре	Description			
	N/A	Improv.	 This improvement has been made: The usability of moving and editing of polygon zones has been greatly improved in the 2D dot plot graphs of "ANALYZE DATA > Plots & Populations" and of "ANALYZE DATA > Explore Crystals": Left-click on an edge of the polygon to select the polygon (for example in order to remove it) Left-click on an edge of the polygon then drag & drop to translate the polygon Left-click on a vertex of the polygon to modify the position of this vertex Left-click in a vertex of the polygon to remove this vertex Left-click on a vertex of the polygon to remove this vertex Left-click on a vertex of the polygon to remove this vertex 			
	#1240	Improv.	This improvement has been made: The saturated objects which are located outside of the chamber are not counted as saturated objects anymore.			
	#1468	Improv.	This improvement has been made: The population separability formula has been modified in order to make it more invariant with respect to extremely low concentrations (few number of positive droplets) and extremely high concentrations (few number of negative droplets). This modification consists in replacing the weights of the clusters' standard deviations with the Bessel correction weight. For the three default populations ("Blue", "Green" and "Red" detection channels) in "Lines" thresholding mode, the separability formula is the following: $\frac{\mu_{POS} - \mu_{NEG}}{\sqrt{\frac{p}{p-1}} \sigma_{POS} + \sqrt{\frac{q}{q-1}} \sigma_{Neg}}$ where <i>p</i> (resp. <i>q</i>) is the number of positive (resp. negative) droplets for the channel of interest, μ_{POS} (resp. μ_{NEG}) is the mean of positive (resp. negative) droplet fluorescence values in the channel of interest, and σ_{POS} (resp. σ_{NEG}) is the standard deviation of positive (resp. negative) droplet fluorescence values in the channel of interest.			



Soft.		Modification			
version	ID	Туре	Description		
	#1472	Improv.	This improvement has been made:		
			All occurrences of the word "FlowJo" have been replaced with the		
			word "Droplet-Level Data" in the EXPORT menu and in the name of		
			the exported folder containing droplet-level data.		
	#1508	Improv.	This improvement has been made:		
			Addition of the possibility to copy-paste the result table shown in		
			"VIEW RESULTS > Result Table" by selecting the chamber rows and		
			using Ctrl+C / Ctrl+V (for example to copy their results in an Excel		
			document).		
2.2.1	#1402	Improv.	This improvement has been made:		
			The zoom-in/zoom-out capacity is not constrained anymore for all the		
			graphs displayed in Crystal Miner.		
	#1415	Feature	This feature has been added:		
			In the "Chamber_Details" sheet of the exported .xlsx file, a new		
			column "Droplet Diameter (microns)" has been added after the last		
			column "Chip Type". This new column indicates for each chamber the		
			estimated average droplet diameter "m_drop_diameter" in microns (as		
			defined in the .yaml image analysis configuration file).		



Soft.		Modification				
version	ID	Туре	Description			
	N/A	Feature	This feature has been added: The pooling results associated with a set of chambers previously pooled in Crystal Reader are automatically computed in "VIEW RESULTS", by considering each set of pooled chambers as one large chamber, and under the assumption that pure replicates have been loaded in the pooled chambers (e.g. the same sample has been loaded). The pooling formula for the estimation of each concentration is simply based on the sum of the positive droplets and on the sum of the negative droplets among the pooled chambers. In "VIEW RESULTS > Result Table", one line is added for the result of the pooled "parent chamber" and the result lines of the non-pooled "children chambers" are kept below. These new lines are exported in the same order in the "Results" sheet of the exported .xlsx file. To ensure traceability, a new column "PoolingID" has been added just after the "ChamberContext" column in the "Chamber_Details" sheet and in the "Results" sheet of the exported .xlsx file. This "PoolingID" indicates for each chamber its unique pooling ID (previously displayed in Crystal Reader) and this value is empty if the chamber is not pooled. For the "parent chamber", the value in column "ChamberID" is empty and the value in column "ChamberName" is equal to the value in column "SampleName".			
			By definition, all chambers pooled together share the same "sample name", "chamber context" and, for each detection channel, the same "sample type", "reference concentration" and "dilution factor".			
	N/A	Improv.	This improvement has been made: Addition of the possibility to process future chip models with different chamber's quantity and/or geometry and/or positioning, as well as different image analysis parameters (e.g. the Opal chip with status "in development" which can be selected in Crystal Reader).			
	#1349	Bug	This bug has been corrected: In "ANAYZE DATA > Plots & Populations > 2D dot plot", the polygons drawn in "Polygons" thresholding mode are not shown if the axes of the 2D dot plot graphs are inverted afterwards.			



Soft.			Modification
version	ID	Туре	Description
	#1387	Improv.	This improvement has been made:
			The FlowJo files (droplet-level data files) include additional files that
			are created for each population. These new files contain the subset of
			droplets belonging to the population (file with a filename including
			"XXX_POS") and the subset of droplets defined as negative for the
			population (file with a filename including "XXX_NEG"), where "XXX"
			refers to the population name.
	N/A	Bug	This bug has been corrected:
			The edition of a specific negative population in "ANALYZE DATA >
			Plots & Populations > Population Editor" is sometimes not robust.
	#1374	Improv.	This improvement has been made:
			In "VIEW RESULTS > Advanced Graphs > Concentration Graphs",
			the concentration graphs only display the data of the selected
			chambers.
	#1360	Feature	This feature has been added:
			Upon data export completion, the output folder is automatically
			opened in a pop-up window.



Soft.	Modification					
version	ID	Туре	Description			
Soft. version	ID #1369	Type Improv.	Modification Description This improvement has been made: The separability scores are now: • defined per population (by default there are 3 populations: above the "Blue" line threshold, above the "Green" line threshold, above the "Red" line threshold); • based on 1D points if the type of thresholding mode is "Lines" with the 3 default populations ("Blue", "Green", "Red") • based on 2D points if the type of thresholding mode is "Lines" with custom populations defined in 2 detection channels • based on 3D points if the type of thresholding mode is "Lines" with custom populations defined in 3 detection channels • based on 2D points if the type of thresholding mode is "Lines" with custom populations defined in 3 detection channels • based on 2D points if the type of thresholding mode is "Polygons" (defined in 2 detection channels) • computed according to a generic formula where the fluorescence mean is the cluster center (in 1D, 2D or 3D) and where the fluorescence standard deviation is the standard deviation of the intra-cluster distances to this cluster center; • computed according to a weighted formula such that the			
			 deviation of the intra-cluster distances to this cluster center; computed according to a weighted formula such that the intra-cluster standard deviation is weighted by twice the proportion of points belonging to the cluster (among the "positive cluster" points that belong to the population and the "negative cluster" points that are defined as negative for the 			
			population). In the exported files, a new column "XXX_dimensions" is added just before the "XXX_separability" column for each population, where "XXX" is the population name, and "dimensions" states for the list of detection channels (ordered from "1" to "3") that were needed to define the population.			
			exported in the mean columns ("XXX_mu_pos" and "XXX_mu_neg") are vectors instead of number (with as many elements as listed in the dimension column).			



Soft.	Modification			
version	ID	Туре	Description	
2.1.0	#1340	Feature	This new feature has been added: For RNA analysis experiments using the XLT mix, a specific image analysis configuration file named "AnalysisConfiguration_GenericTemplate_mix-XLT.yaml" (.yaml format) has been added to the software distribution. It is stored in the following folder: "C:\Program Files\Stilla\CrystalMiner\config". In this configuration file, the parameter "m_drop_diameter" is set to 101.53 microns. This value corresponds to the estimated average diameter of the droplets in the V4 version of the Sapphire chips when using the XLT mix.	
	N/A	Config.	This configuration has been changed: The "What's New in V2?" item has been removed from the Home page as it was related to the software update from v1.x.x to v2.x.x	
	#1327	Feature	 This feature has been added: In 2D dot plot panel of "ANALYZE DATA > Plots & Populations" and in "Polygon" thresholding mode: The created polygons are automatically colored with the color of their population if the polygon is associated with only one population; A read-only population list including current population names and colors is displayed instead of the Rosace widget. 	
	N/A	Bug	This bug has been corrected: Some UTF-8 characters cause the logs to crash.	
	#1290	Bug	This bug has been corrected: Entering min or max values for a dot plot sometimes causes them to be swapped.	
	#1324	Improv.	This improvement has been made: There is now a tooltip appearing on the channel selection buttons to display the fluorophore name and the target name associated with each detection channel.	
	#1323	Bug	This bug has been corrected: Entering min and max values for a dot plot axis is sometimes not robust.	
	#1278	Bug	This bug has been corrected: In the "FILE > Home" panel, clicking on the link to a "recent file" to open it makes the application to crash if this file has been moved or deleted.	



Soft.		Modification			
version	ID	Туре	Description		
	#1525	Improv.	This improvement has been made:		
			Addition of a unique droplet ID "index" in the last column of the		
			exported FlowJo files (droplet-level data files).		
2.0.0	N/A	Config.	Display of a What's New panel presenting the new features of the		
			software version v2.0.0		
	N/A	Feature	This new feature has been added:		
	(too		Addition of a "Home" page and new menu organization:		
	many		QUALITY CONTROL		
	IDs)		SETUP > Edit Experiment Compensate Spillover		
			ANALYZE DATA > Plots & Populations Explore Crystals		
			VIEW RESULTS > Result Table Advanced Graphs		
			• EXPORT		
	N/A	Feature	This new feature has been added:		
	(too		Possibility to adjust fluorescence thresholds at the chamber level		
	many		ANALYZE DATA > Plots & Populations > 1D/2D dot plot		
	IDs)		• (1) Thresholding Mode > Definition Scope > Individual		
			per chamber		
			• (2) In dot plot graph: Left-click + Drag & drop		
			• (3) Apply		
	N/A	Feature	This new feature has been added:		
	(too		Possibility to defined polygon zones in 2D fluorescence graphs		
	many		ANALYZE DATA > Plots & Populations > 2D dot plot		
	IDs)		• (1) Thresholding Mode > Type > Polygons		
			• (2) In dot plot graph: Ctrl + Right-clicks		
	N/A	Feature	This new feature has been added:		
	(too		Possibility to build droplets populations from zones		
	many		ANALYZE DATA > Plots & Populations > Population Editor		
	IDs)		• (1) Zones List: select zone(s) in 2D dot plot or Rosace		
			 (2) Populations > Add Population 		
	N/A	Feature	This new feature has been added:		
	(too		Possibility to define specific negative populations (e.g. for drop-off		
	many		cases)		
	IDs)		ANALYZE DATA > Plots & Populations > Population Editor >		
			"Populations > EDIT > Edit Negatives		
	N/A	Feature	This new feature has been added:		
	(too		Possibility to visualize each droplet population in 3D		
	many		ANALYZE DATA > Plots & Populations > Population Editor >		
	IDs)		Zones > 3D Dotplot		



Soft.	Modification			
version	ID	Туре	Description	
	N/A	Feature	This new feature has been added:	
	(too		Possibility to reveal each droplet population in the crystal images	
	many		ANALYZE DATA > Explore Crystals > Select a population	
	IDs)			



N/A	Feature	These new features have been added:
(too		Export of all new information related to Zoning & Population Data in
many		two new tab sheets and .csv files:
IDs)		"Zone Details" includes for each fluorescence zone:
IDs)		 "Zone Details" includes for each fluorescence zone: Chip ID and chamber position, sample name and chamber context Zone ID (note that in "Line" thresholding mode there are always 8 fluorescence zones, while in "Polygon" thresholding mode there is one zone per user-defined polygon) Zone type (quadrant in "Line" mode, polygon in "Polygon" mode) The x and y channels used to define the zone, and the z channel (where "Chan1" stands for "Blue", "Chan 2" for Green and "Chan 3" for "Red"). List of x-y coordinates of the 2D points defining the zone (note that in "Line" thresholding mode there are always 5 points defining a square) Coordinates of the z boundaries of the zone (note that in "Polygon" thresholding mode the z-values for the boundaries are always 0-65535 RFU) "Population Details" includes for each population: Population color (RGB values) List of the ID(s) of the zone(s) specifically defined as "negatives" for the population
		"QC Indicators":
		• Chip ID and chamber position, sample name and chamber context
		 Value of the global quality flag for the experiment Value of the quality flag "Image Sharpness, and its exact score value
		 Value of the quality flag "Number of Analyzable Droplets" and its exact number value
		 Value of the quality flag "Number of Saturated Objects", and its exact number value
		"Advanced QC Indicators":
		 Chip ID and chamber position, sample name and chamber context
		 Automated threshold values for each channel In "Line" thresholding mode article
		 manual threshold values for each channel



Soft.		Modification			
version	ID	Туре	Description		
			 separability, µpos, µ neg, std-dev pos, std- dev neg values for each channel 		
	N/A	Improv.	This improvement has been made:		
	(too		The global robustness of the software has been improved.		
	many				
	IDs)				
	N/A	Improv.	This improvement has been made:		
	(too		The runtime performance of software functionalities has been		
	many		improved.		
	IDs)				
	N/A	Improv.	This improvement has been made:		
	(too		The global usability of the software has been improved.		
	many				
	IDs)				
	N/A	Improv.	This improvement has been made:		
	(too		For better traceability: display of the filename of the currently applied		
	many		spillover compensation (in "SETUP > Compensate Spillover >		
	IDs)		Spillover Compensation")		
		Improv.	This improvement has been made:		
			Clarification of the use of the dilution factor in the estimated		
			concentrations (always applied except if the droplet population covers		
			at least 2 fluorescence zones with distinct dilutions values, in which		
			case "N/A" is displayed for the applied dilution in Result Table)		
1.6.0	#1017	Config.	This configuration has been changed:		
			The parameter "m_drop_diameter" is now set to 103.82 microns in the		
			.yami configuration file. This value corresponds to the estimated		
			average diameter of the droplets in the V4 version of the Sapphire		
1.5.0	#817	Bug	I his bug has been corrected:		
			The EDIT EXPERIMENT > Custom Populations, the triple positive		
			region of a custom population defined in "Color" mode is automatically		
			set to activated when opening a .ncr file (and the associated results		
			are updated accordingly), even if the user has deactivated this when		
			creating the .ncr me.		



Soft.		Modification			
version	ID	Туре	Description		
1.4.10	#807	Feature	This new feature has been added: A new field "Chamber Comment" has been added in the table of the EDIT EXPERIMENT menu, allowing to trace, from the Crystal Reader application, a unique context associated with each chamber (for example in case of chamber rescan). This also allows to import several times the data of the same chamber, under the condition that distinct chamber comments have been previously entered by the user in the Crystal Reader application. The "Chamber Comment" field of each chamber is empty by default and is automatically exported in the		
			"Chamber_Details" category.		
	#803	Feature	This new feature has been added: If the user manually excludes droplets from a chamber, then the QC flag of the chamber and the QC flag of the whole experiment are overlapped with oblique stripes in the left panel, to indicate droplet exclusion. The number of manually removed droplets per chamber is always automatically exported in the "Chamber_Details" category.		
	#812	Bug	This bug has been corrected: The application crashes when the user computes a new spillover compensation matrix and then clicks on the "image capture" icon before applying the compensation.		
	#806	Bug	This bug has been corrected: The application crashes when the experiment is empty and when the user clicks Up and Down in the chamber sorting widget of the "EDIT EXPERIMENT" menu.		



Soft.	Modification		
version	ID	Туре	Description
1.4.8	#773	Feature	 This new feature has been added: Two new functionalities have been added in the toolbar located on the top right side of the application: The "question mark" icon does not display the static help anymore (go to FILE > HELP for the quick static help), but gives access to a dynamic help functionality that is displayed once the user left-clicks on a given widget (this replaces some previous mouse-over help windows which could be distracting). The additional "image capture" icon on the left allows the user to interactively save the image of a given widget by simply left-clicking on it, according to a predefined format chosen in the drop-down menu. Three formats are proposed when applicable: (a) "Save Image" records the image in .png format; (b) "Save Vector Image" to copy to clipboard.
	#715	Improv.	This improvement has been made: The content of the Help menu has been updated.
	#780	Improv.	This improvement has been made: The .csv export mode is deactivated by default in the EXPORT menu, as the .xlsx export mode is sufficient.
	#781	Improv.	This improvement has been made: The value of the QC indicator "image sharpness" has been normalized with respect to the number of generated droplets (the same improvement has been made in the Crystal Reader application).
1.4.5	#779	Improv.	This improvement has been made: In 1D dot plot, 2D dot plot, and Compensation graphs, the point size should be automatically adjusted by default according to the zoom value: the larger the zoom value, the larger the point size.
	#771	Bug	This bug has been corrected: The export functionalities crashes when the .xlsx file is already opened in Excel at the same time.
1.4.4	#768	Improv.	This improvement has been made: Add lateral margins to the concentration graphs in order to better visualize the first and last concentration points.
	#766	Improv.	This improvement has been made: Update the license content of some open source components (C++ REST SDK, CMake, QuaZip).



Soft.	Modification		
version	ID	Туре	Description
	#757	Improv.	This improvement has been made: Improved computation of the translation for spillover compensation without "NNN" control and without all probes or primers for "PNN", "NPN" or "NNP" controls. If there is no "NNN" and if probes or primers are missing for the "PNN", "NPN" or "NNP" controls (such that the background fluorescence is lower in some control chambers), then the currently computed translation norm is underestimated because it is based on the average of all the points belonging to all the negative clusters of all control chambers. The new method only includes for each coordinate of the translation (i.e; Blue, Green or Red coordinate), the average of the points belonging to the union of the negative cluster of the control chambers which include the positive control for this coordinate.
	#756	Config.	This configuration has been changed: The parameter "m_fluo_percentile" is added in the .yaml configuration file with the default value "0.5" (it was already use by the image analysis algorithm but not easily accessible for modification purposes). This parameter indicates the percentile value to be used for the computation of the droplet fluorescence from a disk image inside the droplet object.
	#755	Improv.	This improvement has been made: Update the legal notice information by adding the XLNT library.
	#748	Bug	This bug has been corrected: In the compensation widget, the chambers listed in the "compute" popup are not in the current order.
	#742	Improv.	This improvement has been made: In the "Settings" widget of "Concentration Graphs" and "Uncertainty Curves", the height of the "Population fields" should be slightly increased to make the field more readable.
	#718	Improv.	This improvement has been made: For consistency purposes, the channel name in the y-axis legend of the concentration graphs is removed (as it is the case in the other graphs).



Soft.	Modification		
version	ID	Туре	Description
	#669	Feature	This new feature has been added: The column "Chip Position" is added in 3rd position in the "EDIT EXPERIMENT" table. It corresponds to the order in which the chips of the experiments have been scanned from left to right in each chip holder (it is incremented from one chip holder to another). This "Chip Position" index becomes the default sort index of the chambers in the experiment.
1.4.3	#746	Bug	This bug has been corrected: If the user does not click on "OK" at the end of the export process, after having modified the name of the export folder, then the software crashes.
	#743	Bug	This bug has been corrected: If the user modifies the chamber order (e.g. via a sort function in the "VIEW RESULTS" menu), then selects all the chambers in the 1D dot plots of "ANALYSE DATA" and then immediately removes some chambers in the "EDIT EXPERIMENT" menu, the software may crash.
	#741	Improv.	This improvement has been made: In all the warning popup windows appearing in case of experiment import with different context or parameter values, the word "original" has been replaced by the word "current" to clarify the message.
	#738	Bug	This bug has been corrected: The order of the chamber names displayed in the x-axis legend of the concentration graphs is not updated after a the modification of the chamber ordering (note that the concentration points were correctly updated).
	#621	Improv.	This improvement has been made: The demonstration data have been changed, in order to include 8 chambers showing duplicates of 4-point dilution test in Blue and Red channels with constant control in Green channel, as well as 4 chambers showing "NNN", "PNN" and "NPN" controls.
1.4.2	#737	Config.	This configuration has been changed: The calculation of the automated chamber boundary registration and for the QC image sharpness value has been slightly modified by not using anymore the a-priori location, size and shape of the chamber pillars. This modification has no significant impact on the software performance.



	Soft.	Modification		
	version	ID	Туре	Description
		#736	Improv. /Config.	This improvement / configuration change has been made: The neural network has been modified in order to improve the droplet recognition performance by decreasing the number of false positives (e.g. false droplets recognized in the oil). The new neural network is named "StillaNeuralNet_2017_03_14" in the .yaml configuration file (parameter "m_identification_neural_network").
1.4.1	#733	Bug	This bug has been corrected: If the sample name of a chamber contains a "-" character, then if the user re-analyses the chambers in the QC menu, the software crashes.	
		#732	Bug	This bug has been corrected: When the user edits the name of a custom population, this name is not updated in the drop-down menus allowing to select the displayed populations in the graphs of the "VIEW RESULTS" menu. This bug correction handles the name update once the user presses Enter or clicks on another field or menu.
	#681	Feature	This new feature has been added: To improve traceability, the number of manually removed droplets in each chamber is systematically added in the last column of the exported "QC Details" data (by default no droplets are removed so the value is equal to 0).	
		#658	Feature	This new feature has been added: When multiple experiment files (.ncx or .ncr files) are opened in multiple Crystal Miner applications, only one Crystal Miner icon appears in the Windows task bar and each Crystal Miner application appearing at mouse-over includes the name of its own experiment file.
1.4.0	1.4.0	#717	Config.	This configuration has been changed: The optional criteria "m_drop_area_min" and "m_drop_area_max" (in number of pixels belonging to the droplets) are added in the .yaml configuration to accept or reject droplet geometry based on the area of the imaged droplet section (this criteria are not activated by default).
		#628	Bug	This bug has been corrected: When a concentration is very high (e.g. with only 6 negative droplets over 28000), the uncertainty curve displayed in "VIEW" results is wrong at the neighborhood of the concentration point.



Soft.	Modification		
version	ID	Туре	Description
	#712	Bug	This bug has been corrected: If the user loads a corrupted .ncm file (fluorescence spillover compensation file) in the "Compensation" menu of "ANALYSE DATA", then the software crashes. The bug correction includes the display of an explicit error message.
	#710	Bug	This bug has been corrected: When the user opens a .ncx file which includes a normalized .ncm file (fluorescence spillover compensation file) previously loaded via the Crystal Reader application, the software crashes.
	#709	Improv.	This improvement has been made: In the column names of the exported result data and in the filenames of the exported results graphs, the channel ID is replaced by the channel color (Blue, Green, Red) or by the custom population name, when applicable. This improves traceability.
	#694	Improv.	This improvement has been made: If the user tries to load a .ncr file which is too recent and not compatible with the current Crystal Miner version, an explicit error message is displayed.
	#684	Feature	This new feature has been added: The user has the possibility to select a given custom population to be visualized in each graph of the "VIEW RESULTS" menu (via a drop- down menu in the "Concentration Graphs" and in the "Uncertainty Curves").
	#683	Improv.	This improvement has been made: When the user makes a mouse-over on the title line of the "Result Table" in the "VIEW RESULT" menu, the name of the population is displayed, which is useful for the custom populations.



Soft.	Modification		
version	ID	Туре	Description
	#203	Feature	This new feature has been added: Addition of the possibility to define custom droplet population in "EDIT EXPERIMENT> Custom Populations" (add a population with "+", give it a name and a color, and choose the method "Color" or "Polygon"). The "Color" method allows to define a droplet population by union or co-occurrence of targets (left-click to select channel union or intersection in the Rosace widget). The "Polygon" method allows to define a droplet population by including it in a polygon which is manually drawn in a 2D fluorescence graph (using Ctrl & right-clicks as in "EXPLORE CRYSTAL" menu). For each user-defined population, the concentration and the confidence interval are automatically calculated for each chamber, by considering the ratio between the number of droplets included in the selection (Rosace or Polygon) and the total number of droplets in the chamber. All custom results will be automatically exported together with the exported data . Note that the Blue, Green and Red channel populations cannot be edited.
	#690	Feature	This new feature has been added: Addition of a .xlsx format in the "EXPORT" menu, allowing export a single.xlsx file (compatible with Excel) which includes the content of each exported .csv file in a specific tab. Besides, the .xlsx format is always activated, while the .csv format is activated by default but can be deactivated.
1.3.2	#753	Config.	This configuration has been changed: Modified thresholds for the QC flag "image sharpness" in the .yaml configuration file: yellow flag should be displayed if focus value is < 0.04; green flag should be displayed if focus value is > 0.06 (this better fits image quality constraints).
	#651	Feature	This new feature has been added: Addition of the following values in the exported QC indicators, for each chamber and in each channel: separability $(\mu_{pos} - \mu_{neg})/(\sigma_{pos} + \sigma_{neg})$ between the positive & negative droplet fluorescence values; mean μ_{pos} and standard deviation σ_{pos} of the positive droplet fluorescence values; mean μ_{neg} and standard deviation σ_{neg} of the negative droplet fluorescence values.
	#645	Improv.	This improvement has been made: All the prerequisites are now included in the installation setup, which makes Crystal Miner installation or upgrade standalone.



Soft.	Modification		
version	ID	Туре	Description
	#556	Improv.	This improvement has been made: The user has the possibility to directly compensate the fluorescence spillover of Duplex experiments (by selecting chambers in only 2 positive control columns) without having to set coefficient values to 0 after the automated computation.
	#657	Bug	This bug has been corrected: When the user re-analyses the chambers in the QC menu and then manually modifies chamber ordering in the "EDIT EXPERIMENT" menu, the software crashes.
	#656	Improv.	This improvement has been made: The content of the "Help" menu is updated according to the last modifications.
	#650	Improv.	This improvement has been made: To save time, the chambers for which the sample types specified as NNN, PNN, NPN or NNP by the user (in Crystal Reader or Crystal Miner applications) are selected by default in the popup window used for the automated computation of the fluorescence spillover (where the sample types are displayed for each chamber).
	#647	Feature	This new feature has been added: Addition of a "Population opacity" cursor in the Color Mode widget of the "EXPLORE CRYSTAL" menu, allowing to make the currently selected droplet population more or less transparent in the chamber image.
	#646	Bug	This bug has been corrected: When the user manually modifies fluorescence thresholds, then compensates fluorescence spillover and confirms automated re- calculation of fluorescence thresholds, the colors of the dot plots are not updated according to the new threshold values.
1.3.0	#649	Improv. /Config.	This improvement / configuration change has been made: The droplet recognition algorithm based on neural network runs faster thanks to the input batch mode strategy (so a new neural network is used in the .yaml configuration file). If the user re-analyses an image with an obsolete .yaml configuration file, then a warning message is displayed (there is no back-compatibility). The new neural network is named " StillaNeuralNet_2016_11_24" in the .yaml configuration file (parameter "m_identification_neural_network").



Soft.	Modification		
version	ID	Туре	Description
	#635	Feature	This new feature has been added: Add the possibility to directly copy images or graphs in the clipboard, by simply right-clicking on the capture icon.
	#633	Config.	This configuration has been changed: The parameter value for the maximal size of the droplet diameter in the .yaml configuration file ("m_drop_size_max") has been increased from 16 pixels to 18 pixels (where resolution is 6.7 microns / pixel), which better represents the variability of the appearance of droplet size in the fluorescence images.
	#632	Config.	This configuration has been changed: Modified thresholds for the QC flag "image sharpness" in the .yaml configuration file: yellow flag should be displayed if focus value is < 0.07; green flag should be displayed if focus value is > 0.085 (this better fits image quality constraints).
	#631	Improv.	This improvement has been made: Incrementation of the channel ID "i" used at the end of the default filename for the image or graph snapshots (1: Blue; 2: Green; 3: Red).
	#630	Bug	This bug has been corrected: Software crashes after modifying the lowest y-axis limit in 1D dot plot (via double-click on the y-axis).
1.2.3	#623	Bug	This bug has been corrected: In the "EDIT EXPERIMENT" menu, the manual modification of the chamber order in the left panel doesn't work properly.
	#622	Bug	This bug has been corrected: Crash in the "EXPLORE CRYSTAL" menu when the user starts creating a polygon in the chamber image and then clicks outside of the chamber display.
	#619	Config.	This configuration has been changed: Add a parameter "m_min_post_analysis_density" in the .yaml configuration file to enable the post-analysis rejection of droplets which are too close to each other (by default this parameter value is "0.2").
1.2.2	#615	Improv.	This improvement has been made: The temporary fluorescence threshold values (i.e. manually moved or edited before being applied) should always be synchronized with all the dot plots and histograms displayed in the "ANALYZE DATA" menu. The threshold reset function should also be consistently synchronized.



Soft.	Modification		
version	ID	Туре	Description
	#614	Improv.	This improvement has been made: The default name when saving chamber image snapshots via the capture icon should end with "_channel{i}" where "i" is the channel ID (0: Blue; 1: Green; 2: Red).
	#613	Feature	This new feature has been added: Add the x-y coordinates of the analyzed droplets in the exported FlowJo files in 2 additional columns (for raw data and compensated data).
	#610	Config.	This configuration has been changed: Modify the droplet diameter from 96 microns to 94.5 microns in the .yaml configuration file, which is closer to the ground-truth and ensures more accurate concentration results.
	#600	Feature	This new feature has been added: From the image re-analysis popup in QC menu, add the possibility to visualize the content of the current .yaml configuration file in a popup window that is displayed on mouse-over above the filename.
	#382	Bug	This bug has been corrected: The software does not open experiment when user double-clicks on a .ncx or .ncr file having unicode characters in its path.
	#599	Improv. /Config.	This improvement / configuration change has been made: Set the neural network configuration as the default image analysis method in the .yaml file (using the tag "m_identification_neural_network" with the network name "StillaNeuralNet_2016_10_07", and using the tag "m_identification_neural_network_threshold" with the threshold value "0.5"). This improves droplet recognition performance.
	#598	Feature	This new feature has been added: Add the possibility in 1D dot plot to modify the droplet ordering method by double clicking on the x-axis (shuffled by default, or spatial).
	#597	Bug	This bug has been corrected: When the user draws a concave polygon in a chamber image and then right-clicks on a droplet near the polygon boundary, the excluded droplet is wrong.
1.2.0	-	-	-