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nSpec Version 0.22.1.0

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Major Features: Custom Reporting & Exporting, High Resolution Mosaics

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Overview

Introducing nSpec v0.22.1.0! This release is packed with some powerful new functionality that we're excited to see running in the field, including:

- **High Resolution Stitched Mosaic Generation**
- **Custom Reporter** - a dynamic new tool for embedding data wrangling scripts into production recipes
- **Custom Exporter** - a highly configurable tool for generating analysis result exports with the exact data you need
- **Live View Enhancements** - pausing, informational banner with live intensity, FPS readings, and more
- **Option to Skip Pre-alignment** - For optimally fast wafer handling


In combination, these new tools allow nSpec to support almost any application demand, no matter how niche, with a little assistance from our Applications Engineering team.


Upgrading to v0.22.1.0

Required Library Update!

To upgrade from previous versions, a few things need to be checked:

1. Run all upgrading steps for versions **v0.21.0.0**, **v0.21.1.0**, and **v0.22.0.0** - we recommend running all installers for major builds of nSpec between the previous version and the target version.
2. Run the **nanotronics-libraries-installer-v22_1-20220321** installer to update 3rd party libraries related to the new software build. Contact technical service if you are missing this installer.
3. **nJson** format has been updated compared to v0.22.0.0, resulting in a breaking change for customers using the Dislocation Analyzer if configured for that version

 **Important for any customers using the Dislocation Analyzer:** The structure of the Dislocation Analyzer **nJson** file changed between versions v0.22.0.0 and v0.22.1.0

 **Conversion Instructions:** To convert the old format to the new format, move all root-level fields except for "parameters" into an object that is assigned to the new field "Dislocation"

Old nJson format:

```
{
  "parameters": [
    ...
  ],
  "classifications": ...,
  "otherClass": ...,
  "chainClass": ...,
  ...
}
```

New nJson Format:

```
{
  "parameters": [
    ...
  ],
  "Dislocation": {
    "classifications": ...,
    "otherClass": ...,
    "chainClass": ...,
    ...
  }
}
```

Major Enhancements

Custom Reporter

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Overview

This is an exciting new feature for this version that makes it possible to build highly customizable and consolidated reports using one *or more* previously run analysis results. This can be used in a myriad of ways to meet specific customer needs. Importantly, this has been implemented in a manner that is entirely generic, so this will work for all defect-type analysis results across nSpec.

Here are a few use case examples:

- **Combine Device Inspection & AI Analysis reports** so that you can remove nuisance defects one either analysis, while also creating a report that has defect class information and pixel-accurate area.
- **Combine multi-type Device Inspection analysis into a single report** for easier defect review.

- **Combine AI and Basic Selection Analyses Results for pixel-accurate Area reporting**


The possibilities with this new post-analysis are truly endless. We on the product team foresee a long roadmap that will build on this post-analysis approach to bring powerful and intuitive defect reporting to end-users.


How Does it Work?

The **Custom Reporter** generates a new analysis entry in the image database, generated via an embedded SQL query. This Query must generate data that can be saved into Defects table in the scan database. Therefore in order to generate fully supported reports within nSpec, the query must output a set of defects where each defect has *all* the following columns of information:

- X
- Y
- W
- H
- Area
- Eccentricity
- Orientation
- ImageID
- AnalysisID
- Intensity
- XinDevice
- YinDevice
- Score
- IntensityDeviation
- DeviceID
- Contour (can be an empty string)
- ClassName (optional)

The column `ClassName` is optional and can be used to output defect classes within the SQL script. If `ClassName` is written, nView will allow users to view the Class Report when reviewing results.

 The custom reporter is a tool to **access** the database, **NOT** to **modify** the database. Neither do Applications/Tech Services Engineers nor customers have the right to modify the database. This means that no query should attempt to create or delete data.

 The **Custom Reporter** and **Custom Exporter** were built with the intention that an internal Nanotronics Applications Engineer or Technical Service Engineer would assist customers by configuring an nJson file for custom applications. Then users are able to point at these nJson files within the parameters for the Custom Reporter, by populating the **Import** or **Report Setting** field:

GUI parameters

Analysis Parameters

Analysis: Custom Reporter

Group: Default

Description: Custom Reporter

Pos	Name	Type	Low	PV	High	Default	Picklist	Desc
01	Base Analysis IDs Mode	PickList		Relative		Relative	Absolute, Relative	the way next param (analysis ID) is treated
02	Base Analysis IDs	String						Coma Separated Analysis IDs
04	Report Setting	PickFile		\\4622105182\ProgramData\ConfigFiles\Analysis\Custom Reporter\Setting\Sample.nJson		\\462210518...	nJson	Reporer Setting File Path

Param Name	Options	Description
Base Analysis IDs Mode	Absolute, Relative	<div> <i>i</i> See Post-Analysis Referencing section (Link) </div>
Base Analysis IDs		<div> <i>i</i> See Post-Analysis Referencing section (Link) </div>
Import Setting		Select a nJson file of the import setting.

Referencing Prior Analyses

For guidance on how to set up post-analysis referencing, visit the appendix page for [Post-Analysis Referencing \[EXTERNAL\]](#)

Configuring the nJson File

The nJson file must be written and configured by Nanotronics Technical Service or Applications Engineers. To request a new custom reporting application that may require assistance, please contact support@nanotronics.co to request support.

For nJson formatting guidance, visit [nJson Format: Custom Reporter](#)

Custom Exporter

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Overview


The Custom Exporter allows users to build highly customizable exports that report on all the desired defect information collected during prior analysis. Like the custom reporter and Dislocation Analyzer, the Custom Exporter also requires an nJson file loaded with relevant SQL scripts.

Core Features

CSV column headers are now completely configurable - no matter what nSpec calls a defect attribute, we have the ability to rename them to align with the customer vernacular. For example, within nSpec databases we might refer to defect width as “W”, but in this export we can rename that to “width” or “defectWidth”, or anything else that is required for smooth integration with the customer application.

Embedding math and custom calculations

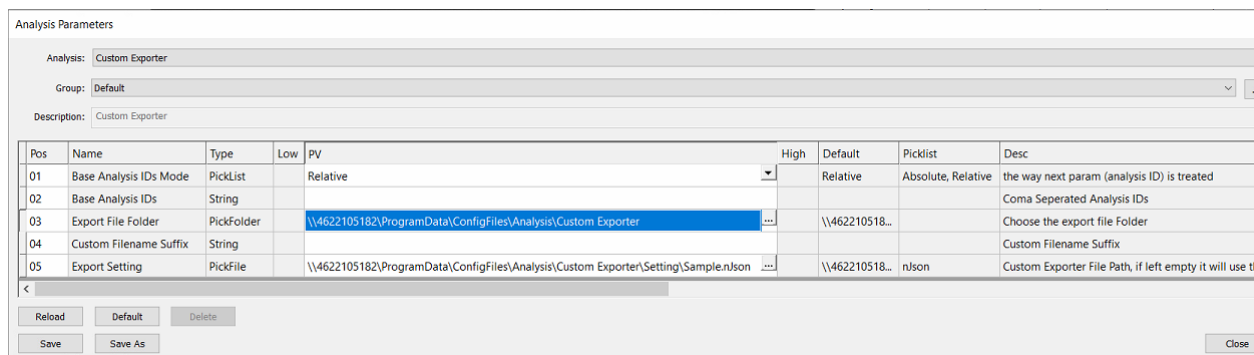
In addition to simply exporting columns directly, the custom exporter will allow us to perform any operation that is legal within SQL code. This gives us enormous flexibility for reporting exactly what customers need.

 For more information on embedded calculations via the custom exporter, please contact the applications team


Supported Exports



Export File	Expected Release
CSV	v0.22.1.0
JSON	v0.22.1.1
XML	v0.22.1.1
KLARF (Device Inspection Scans)	v0.22.1.1
KLARF (All Scans)	TBD

GUI parameters



Pos	Name	Type	Low	PV	High	Default	Picklist	Desc
01	Base Analysis IDs Mode	PickList		Relative		Relative	Absolute, Relative	the way next param (analysis ID) is treated
02	Base Analysis IDs	String						Coma Separated Analysis IDs
03	Export File Folder	PickFolder		\\4622105182\\ProgramData\\ConfigFiles\\Analysis\\Custom Exporter		\\462210518...		Choose the export file Folder
04	Custom Filename Suffix	String						Custom Filename Suffix
05	Export Setting	PickFile		\\4622105182\\ProgramData\\ConfigFiles\\Analysis\\Custom Exporter\\Setting\\Sample.nJson		\\462210518...	nJson	Custom Exporter File Path, if left empty it will use t

Param Name	Options	
Base Analysis IDs Mode	Absolute, Relative	

		See Post-Analysis Referencing section (Link)
Base Analysis IDs		 See Post-Analysis Referencing section (Link)
Export File Folder		Select a folder to save the export file
Custom Filename Suffix	Optional	If non-empty, this suffix will be directly added to filename. If using nSpec v0.23.1.0 or earlier, the suffix will be added following an underscore.
Report Setting		Select a nJson file of the Report setting  If you have a new request for a new functionality, please request support from support@nanotronics.co

Referencing Prior Analyses

For guidance on how to set up post-analysis referencing, visit the appendix page for [Post-Analysis Referencing \[EXTERNAL\]](#)

Configuring the nJson File

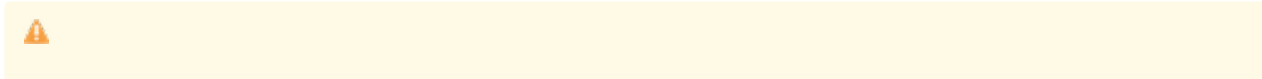
The nJson file must be written and configured by Nanotronics Technical Service or Applications Engineers. To request a new custom reporting application that may require assistance, please contact support@nanotronics.co to request support.

For nJson formatting guidance, visit [nJson Format: Custom Exporter](#)

High Resolution Mosaics

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Overview



The High Resolution Mosaic Generator is disabled by default. If you would like to use this feature and it is not currently enabled, reach out to support@nanotronics.co for assistance to activate

Currently, the scan mosaic generated by nSpec after a scan is a low resolution copy of what appears on the Stage View after a scan. The High Resolution Mosaic Generator (HRMG) allows users to generate flawless, perfectly stitched, and up to *full resolution* mosaics matching the input scan pixel resolution. This is valuable in a number of use cases, and we are excited to launch this feature for general use.

The most common use cases are:

1. **Saving a single high quality continuous image** of wafer samples for manual defect inspection
2. **Removing gaps between image tiles** caused by optical aberration
3. Generating image sets for the new **Virtual Device Inspection (VDI) workflow**

More on the VDI workflow next, but first we'll cover important details pertaining to the High Resolution Mosaic Generator itself.

Basic Usage

In general, the mosaic generator is highly flexible and accepts an overlapped nSpec scan, then outputs a mosaic or image sets depending on the runtime configuration. The most basic output would generate a full-resolution mosaic of a wafer scan *without* any image registration. In this scenario, the algorithm simply positions the input image tiles adjacent to each other. More useful is to input an **overlapped scan**, which will cause the Mosaic Generator to perform stitching registration calculations between all of the image tiles. This means there will be no discontinuities across the output high resolution image (under nominal input conditions).

Here is the matrix describing supported input scan types:

Scan Type	Requires Device Layout	Output	Supported?
Wafer	-	High-res Image	✓
Aligned Wafer	-	High-res Image	✓
Aligned Wafer	Yes	Device Scan* (VDI Workflow)	✓
Device	Yes	High-res Image	✓
User-Defined	-	High-Res Image	✗

Notice that if the input wafer is aligned, and a device layout is provided as an input in the High Resolution Mosaic Generator parameters, the output is not a single mosaic image but rather a *Device Type Scan*. This is called the **Virtual Device Inspection** workflow, and merits it's own documentation section.

Parameters

Analysis Parameters

Analysis: High Resolution Mosaic Generation

Group: Default

Description: High resolution Mosaic Generation Params

ID	Name	Type	Low	PV	High	Defa...	Picklist	Desc
01	Final Calibration Factor	Double	0	0	1	0		Used to brighten or darken images in response to light source power fluctuations. Must be positive. Value of 1.0 has no affect
02	Compression Factor 1	Double	4.940...	1	1	1		Quality (1.0 is max quality) of the first set of mosaics to be output.
03	Compression Factor 2	Double	0	0	1	0		Quality (1.0 is max quality) of the second set of mosaics to be output. If set to 0 (zero), only one set of mosaics will be generated.
04	Blending Option	PickList		Pixel Fill			Pixel...	How Blending of Overlapping tiles should be calculated
05	Desired Output Width	Long	0	0	21474...	0		(Pixels) Desired output width of each mosaic. Zero means it will be calculated automatically.
06	Desired Output Height	Long	0	0	21474...	0		(Pixels) Desired output height of each mosaic. Zero means it will be calculated automatically.
07	Timeout	Long	0	300	21474...	300		(Seconds) Timeout. This is for the whole batch of mosaics, not per-mosaic.
08	Desired Output Left edge	Long	0	0	21474...	0		(Pixels) Desired left edge of each mosaic. Zero means it will be calculated automatically.
09	Desired Output Top edge	Long	0	0	21474...	0		(Pixels) Desired top edge of each mosaic. Zero means it will be calculated automatically.
10	Tile Correction Options	PickList		None		None	None...	The set of corrections (Flatfield, darkfield, darkcurrent) that will be applied to each tile.
11	Flatfield Correction Image Path	PickFile		C:\...		C:\...	png.tif...	Path to the flatfield correction matrix. Only used if the tile correction option is set to correct for flatfield.
12	Darkfield Correction Image Path	PickFile		C:\...		C:\...	png.tif...	Path to the darkfield correction matrix. Only used if the tile correction option is set to correct for darkfield.
13	Darkcurrent Correction Image Path	PickFile		C:\...		C:\...	png.tif...	Path to the darkcurrent correction matrix. Only used if the tile correction option is set to correct for darkcurrent.
14	Pre-stitching downsample factor	Double	0	1	1	1		Amount each tile will be downsampled by before stitching
15	Device Inspection CSV input path	PickFile		C:\...		C:\...	csv	If supplied, multiple devices from this CSV file will be output
16	Desired Device Inspection Tile Width	Long	0	0	21474...	0		(Pixels) Desired output width of each tile in Device inspection scan.
17	Desired Device Inspection Tile Height	Long	0	0	21474...	0		(Pixels) Desired output height of each tile in Device inspection scan.
18	Tile overlap Fraction X	Double	0	0	1	0		(Percent) Desired X-direction overlap of each tile in Device inspection scan.
19	Tile Overlap Fraction Y	Double	0	0	1	0		(Percent) Desired Y-direction overlap of each tile in Device inspection scan.
20	Export JSON	PickList		TRUE		TRUE	TRUE, F...	Set to TRUE to export analysis results to JSON file. Set to FALSE to disable.

Buttons: Reload, Default, Delete, Save, Save As, Close

There are many parameters for this analysis, but for the most part these can be left as default values! Just in case you need to fiddle with these, here are the descriptions with some practical notes for each field:

Parameter	Description	Note
Final Calibration Factor	Used to brighten or darken images in response to light source power fluctuations. Must be positive. Value of 1.0 has no affect	*Recommend ignoring unless instructed by Technical Service team. This interacts with other features not yet rolled out for all customers
Compression Factor 1	Quality (1.0 is max quality) of the first set of mosaics to be output.	<div> Important! High Resolution Mosaics can only save to disk if small enough to comply with Windows and TIF image format constraints. Compression must be small enough to generate an image < 4GB </div> <p>If the mosaic is larger than this, the Mosaic Generator will silently fail and reports as complete in the exception log even though no mosaic is output</p>
Compression Factor 2	Quality (1.0 is max quality) of the second set of mosaics to be output. If set to 0 (zero), only one set of mosaics will be generated.	

Blending Option	How Blending of Overlapping tiles should be calculated (Pixel Fill, Gradient Mask)	For smoother blends, Gradient Mask is recommended
Desired Output Width	(Pixels) Desired output width of each mosaic. Zero means it will be calculated automatically.	Setting this will override compression factors
Desired Output Height	(Pixels) Desired output height of each mosaic. Zero means it will be calculated automatically.	Setting this will override compression factors
Timeout	(Seconds) Timeout. This is for the whole batch of mosaics, not per-mosaic.	
Desired Output Left edge	(Pixels) Desired left edge of each mosaic. Zero means it will be calculated automatically.	Recommend 0
Desired Output Top edge	(Pixels) Desired top edge of each mosaic. Zero means it will be calculated automatically.	Recommend 0
Tile Correction Options	The set of corrections (Flatfield, darkfield, darkcurrent) that will be applied to each tile.	Recommend setting to None and using global system flatfield correction (FFC)
Flatfield Correction Image Path	Path to the flatfield correction matrix. Only used if the tile correction option is set to correct for flatfield.	See above
Darkfield Correction Image Path	Path to the darkfield correction matrix. Only used if the tile correction option is set to correct for darkfield.	See above
Darkcurrent Correction Image Path	Path to the darkcurrent correction matrix. Only used if the tile correction option is set to correct for darkcurrent.	See above
Pre-stitching downsample factor	Amount each tile will be downsampled by before stitching	Recommend stitching at full resolution (1.0)
Device Inspection CSV input path	If supplied, multiple devices from this CSV file will be output	*See Virtual Device Inspection workflow for details on this format

Desired Device Inspection Tile Width	(Pixels) Desired output width of each tile in Device inspection scan.	Recommend outputting image tiles that match the input tile width (ex: 4096px by 4096px for systems with a Bonito Camera with standard configuration)
Desired Device Inspection Tile Height	(Pixels) Desired output height of each tile in Device inspection scan.	See above
Tile overlap Fraction X	(Percent) Desired X-direction overlap of each tile in Device inspection scan.	Recommend setting to 0
Tile Overlap Fraction Y	(Percent) Desired Y-direction overlap of each tile in Device inspection scan.	Recommend setting to 0
Export JSON	Set to TRUE to export analysis results to JSON file. Set to FALSE to disable.	

Most important is the note on the compression factor, so I will repeat this a second time

i Important! High Resolution Mosaics can only save to disk if small enough to comply with Windows and TIF image format constraints. Compression must be small enough to generate an image < **4GB**

If the mosaic is larger than this, the Mosaic Generator will silently fail and reports as complete in the exception log even though no mosaic is output

Important Notes

This analyzer sets a foundation for many upcoming features on nSpec's roadmap. As such, this first rollout is necessarily preliminary - while there is much user value already supported in version v0.22.1.0, there is a lot that is yet to come. New workflows involving this analyzer will be rolled out over the next 1-2 years. These include features like macro defect analysis using AI, measuring defect dimensions when they span multiple fields of view, compensating for rotations in the position of diced devices, and more.

That said some interactions are known to not yet be supported but are coming soon:

⚠ Important! This analyzer is not fully compatible with SECS/GEM interfaces. Support is planned for version **v0.22.2.0**

For now, we hope you enjoy flawlessly stitch high resolution imaging and find value for this application within your inspection process. If you have ideas for ways to leverage this capability, please contact support@nanotronics.co with your thoughts!

New Features

Highlights

NSPEC-5501: Pixel Intensity for Field of View in Live View


At the bottom left of the Live View, an informational ribbon now includes some information about the Live View such as **Refresh Rate**, and **Average Intensity**. Average Intensity is reported as a percentage from 0-100%, where 0 represents a fully dark image, and 100% represents a totally white or bright image.

To report on average image intensity of a specific *Region of Interest* within the live view, use **Ctrl-Left Click** to drag and define a Region of Interest. While this selection is active, only this region of interest will be sampled and reported for intensity.

This feature could be helpful for tuning optimal Image Settings for different recipes, to verify that specific ROIs within a device are not over-saturated.


NSPEC-6039: Pausing Live View

Even best efforts to ensure a vibration-free environment for inspection cannot completely eradicate ambient vibrations. These vibrations can be especially visible when working with very high magnification objectives (ex: 20x, 50x, 100x). We have added an ability to pause the live view, which makes it so much easier to perform **Critical Dimension Measurements** without having to deal with shaking images.

When paused, an orange-red border appears on Live View and a “Pause” icon  appears in the upper left corner of the display.

There are two ways to pause the live view:

1. On the keyboard, click the **Pause** or **Pause/Break** button
2. Right click the Live View window to open the context menu, and select “*Pause Live View*”.

 While paused, clicking the Live View display will no longer move the stage to the clicked position.

NSPEC-6057: Option to Skip Prealigner During Wafer Loading

There are some use cases where pre-alignment is not a necessary step in the wafer loading process. This feature provides an option to completely skip the pre-alignment station when loading wafers. This option can reduce total cassette scan-time by about 40 seconds.

To set this up, open the Autoloader Calibration dialog. For the alignment algorithm, select “None” - that’s it!

NSPEC-5624: Remove Translations from the Codebase

Translations were added to nSpec in a way that wasn’t able to scale as new features were developed. An audit of our translations throughout nSpec revealed they were in a sad state and were full of inaccurate or missing translations. Translations will be reintroduced someday again soon in a way that actually help non English language speakers get the most out of nSpec.

New Features Changelog

T	Key	Release Notes Summary
	NSPEC-3220	Remove Golden Tile Scanning (GTS) Program Options (Deprecated Feature)
	NSPEC-3814	Reorganize all Autoloader-related Program Options into the "Autoloader" Section
	NSPEC-5501	Display Average Pixel Intensity for Field of View (FOV) Selection in Live View

- NSPEC-5537 Display Live View Frame Rate (FPS)
- NSPEC-5624 Remove Translations From the Codebase
- NSPEC-5927 Improve Handling of Larger Defect Count in nView
- NSPEC-6039 Add Ability to Pause Live View
- NSPEC-6054 New Custom Reporter (Post-Analysis)
- NSPEC-6057 Add Option to Skip the Prealigner During Wafer Loading
- NSPEC-6070 New Custom Exporter (Post-Analysis)
- NSPEC-6217 Update Camera Buffer Default to 600

11 issues

Bug Fixes


Highlights

NSPEC-5911: nView resizing button doesn't expand to fit entire multi-tile Field of View










Previously, at the lower right corner of nView's image tile window, if you clicked on the `Zoom to Fit` button the field of view would not fully expand as advertised. Now it will! The zoom to fit feature will zoom out even below the level that you can select manually through the slider. This is great because it means you will always be able to zoom out to see the desired field of view. This fix sounds minor, but has a pretty big impact on quality of life when reviewing image sets and analysis results inside of nView.

NSPEC-5577: Select Analysis Dialog is slow for DBs containing many defects

When working with analysis results containing defect counts in the millions, we have observed that nSpec's dialogs can take a long time to load. This has now been fixed (or at least dramatically improved) with this version. The dialog most affected by this performance issue was the "Select Analysis" dialog, which can be opened from the main view by the menu options *Analysis View Analysis Results...*

-  On first selection of a legacy folder or image database, the initial load will take some extra time (sometimes as much as ~30 seconds). This happens because this fix requires some calculations to be made within the database. After this first pause, opening that folder location through the *Select Analysis Dialog* will be much improved.

Changelog

T	Key	Release Notes Summary	Affected Releases
	NSPEC-5279	Long exposures sometimes cause "Waited too long for camera image" error	0.21.0.0, 0.20.1.3, 0.21.1.0, 0.22.0.0
	NSPEC-5577	Select Analysis Dialog is slow for DBs containing many defects	0.21.1.0, 0.22.0.0
	NSPEC-5689	Stage & camera angle not reset before running Scans that perform Bare Wafer Alignment	0.21.1.0, 0.22.0.0
	NSPEC-5911	nView resizing button doesn't expand to fit entire multi-tile Field of View	0.21.1.0
	NSPEC-6038	nScan Crashes if user exits out of Imaging Settings During Scan	0.22.0.0
	NSPEC-6155	Cannot manually schedule Multi-type or Group Analyses	0.22.0.0
	NSPEC-6157	Scan Folder Naming Incorrect when a Period is included in the Sample ID	0.22.0.0
	NSPEC-6199	Autoloader Aligner sometimes can't find starting position (sensor U S2)	0.22.0.0
	NSPEC-6266	Autofocus mask not used during scan	0.21.0.0, 0.21.1.0, 0.22.0.0

[9 issues](#)

Appendices

Post-Analysis Referencing

There are a few nSpec Analyses that reference other, previously run analyses. As of version v0.23.0.0 this includes **Custom Reporter**, **Custom Exporter**, and **Defect Classifier** post-analyses.

The fields pertaining to prior referencing include:

Base Analysis IDs Mode	Absolute, Relative	The user selects the nature of analysis ID(s) to be specified in the following field. Relative = most recently run, while absolute = the numeric integer reference of a prior run analysis
Base Analysis IDs		Comma separated set of IDs. If <i>Mode</i> is Absolute, it is a set of integers (example: "1,2"). If <i>mode</i> is Relative, it is a set of source analysis names. For example, Device Inspection, Gen IV

Analysis means that first view (DI from the nJson) will be the Defects of the last analysis of type **Device Inspection**, while the second source analysis (GenIV from the nJson) will be populated with the Defects from the most recently run **Gen IV Analysis**.

Relative Reference Notes

When using Relative mode, you also have the option to reference any previously run analysis, by adding a numeric indicator at the end of the analysis name. Let's say an image database ran 3 analyses:

1. Gen IV AI Analysis (parameter set 1)
2. Gen IV AI Analysis (parameter set 2)
3. Device Inspection

To point at #2 and #3, you would input the following for the **Base Analysis IDs** field:

```
"DeviceInspection, Gen IV Analysis"
```

To point at #1 and #3, you would input the following for the **Base Analysis IDs** field:

```
"DeviceInspection, Gen IV Analysis.2"
```

The .2 at the end of Gen IV Analysis informs nSpec to reference the second most recently run Gen VI Analysis. In this way, you have complete flexibility to point at any previously run analysis using both absolute or relative modes.

i If you wish to reference the most recent analysis, there is no need to add the ".1" after the analysis internal name reference. This means that "DeviceInspection" is the same as "DeviceInspection.1"

Analysis Reference List

The user-facing name of an analysis is not necessarily identical to the ID that should be used to reference that analysis.

Analysis Name (user facing)	Analysis Reference ID (IntName)
AI Analysis	AIAnalysis
Basic Selection (Contrast, Morphological Range)	nrad_rangeselect
Basic Selection (Intensity, Exclusive)	nrad_intensityselectexclusive
Basic Selection (Intensity, Inclusive)	nrad_intensityselectinclusive
Crack Detection V2	CrackDetectionV2
Custom Exporter	Custom Exporter
Custom Reporter	Custom Reporter
Device Inspection	DeviceInspection

Die Yield	nrad_dieyield
Dislocation Defect Analyzer	Dislocation
Gen IV AI Analysis	Gen IV Analysis
High Resolution Mosaic Generation	High Resolution Mosaic Generation Analysis
Surface Scattering Analysis	Surface Scattering Analysis
Utility: Launch Executable	LaunchScript

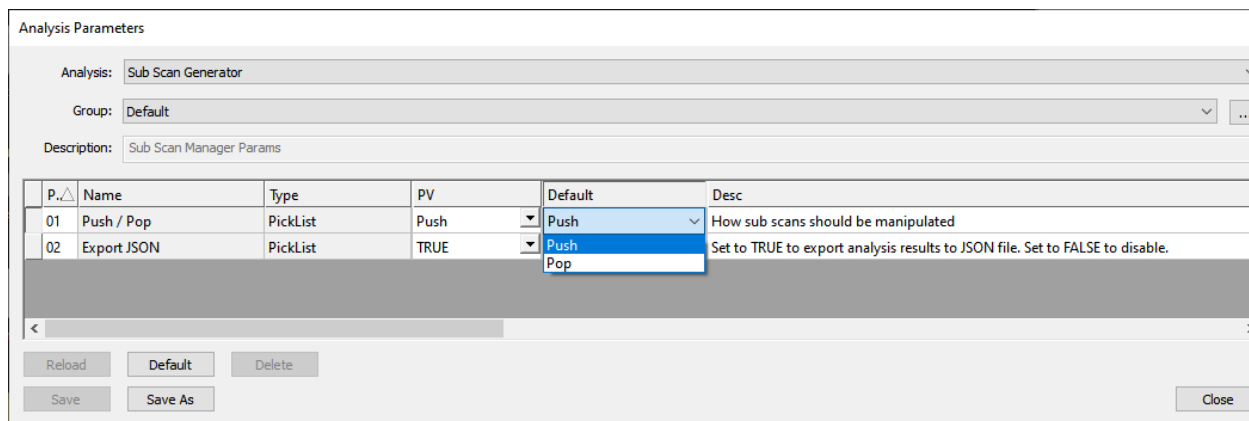
When to use Absolute, and when to use Relative

When testing a new script, it might be useful to use absolute mode. However, in the majority of cases, we believe that relative mode is most likely to be the optimal mode, especially when running in production. Consider a case where you scan a wafer and perform a Group Analysis on this scan. The first time, using absolute references to point at the 1st and 2nd analyses may work fine. But what happens if you run that group analysis a second time? Now, the post-analysis is still performed on the first and second analyses ever performed, rather than the ones most recently performed as part of that new analysis group.

i When running in production, we recommend always using **relative mode**

Sub Scan Generator

The *Sub Scan Generator* is a nSpec analyzer that manages target scans for queued analyses. It has one (useful) parameter - `Push / Pop`, which can be set to either `Push` or `Pop`.



P.	Name	Type	PV	Default	Desc
01	Push / Pop	PickList	Push	Push	How sub scans should be manipulated
02	Export JSON	PickList	TRUE	Push	Set to TRUE to export analysis results to JSON file. Set to FALSE to disable.

This analyzer is meant to be strategically placed within an analysis group of other analyzers. This analyzer has a special relation with the [Virtual Device Inspection Workflow](#)

For the following sections, the following terms will be used:

- *Pushed/Virtual Scan*: Scan created when sub scan generator is run in **push** mode
- *Source Scan*: Scan that was the target of the sub scan generator
- *Target Scan*: Scan that is the target on non-sub scan generator analyses

Push Mode

When the *Sub Scan Generator's* `Push / Pop` parameter is set to `Push`, the generator is in *push* mode.

In *push* mode, the behavior of the *sub scan generator* is as follows:

- When run as a standalone analysis (not in an analysis group):
 1. A new virtual scan ID is created in the scan's database
 2. A new virtual scan folder will be created in the scan's folder
 3. The new virtual scan's ID will be the biggest scan's ID + 1
 4. The scan property `Pushed ScanID` will be written into the `ScanProperties` table for the source and virtual scans. The scan property's value will be the virtual scan's ID
- When run in an analysis group
 1. Everything that happens when the sub scan generator is run as a standalone analysis happens here
 2. The *target scan* is the newly created *virtual scan*

Pop Mode

When the *Sub Scan Generator's* `Push / Pop` parameter is set to `Pop`, the generator is in *push* mode.

In *pop* mode, the behavior of the *sub scan generator* is as follows:

- Nothing happens when run as a standalone analysis (not in analysis group):
- When run in an analysis group
 - The *target scan* is the *source scan*, no matter what a previous sub scan generator did in *push* mode