nanotronics

nSpec v0.24.2.0 External Release Notes

nSpec Version 0.24.2.0

Release Date: Nov 13, 2024

Documentation Updated: Nov 13, 2024

Major Features: nView Device Viewer, Custom Export File Formats

Overview

nSpec v0.24.2.0. contains some exciting new updates, features, bug fixes, and also important deprecations.

This update includes the ability to write custom formatters for **Custom Exporter** analyses using newly developed **nfmt** (nano-format). Additionally, **nView** now has a **Device Viewer**, allowing users to look at entire device scans instead of partial tile scans in nView.

Customers with Bonito cameras will see changes to job exposure times due to a measured error between the manufacturer's reported and actual exposure times, however this will **not** affect scan times.

Additionally, this version deprecates the use of 0-based indexing for bare wafer and custom scan image tiles, scanned using continuous scanning mode. Previously, bare wafer and custom scans running in continuous scanning mode used 0-based indexing, whereas bare wafer and custom scans running in stop and go mode would use 1-based indexing. This change will ensure that all scans regardless of scan mode will follow the same indexing convention. See **v0.24.2.0 Deprecations** for more details.

Deprecations

There are a number of deprecations in nSpec v0.24.2.0 to be aware of when upgrading the software.

NSPEC-7195: Deprecate Multi-type Device Inspection for workflows with multiple device sizes and pitches

Previously, multi-type device inspections could be performed for customers with multi-type device samples, in which the devices had different pitches and sizes. Now, users can **only** perform multi-type device inspections for multi-type device samples that have the same size and pitch. We will implement a workflow to replace the deprecated workflow in the future.

See Multi-Type Device Inspection Workflow for information on the new workflow, also included in the **Appendix** section.

NSPEC-7252: Fix incorrect exposure times for nSpec systems with Bonito cameras

For nSpec systems with Bonito cameras, exposure times will increase for all scans. This is due to a difference found between the manufacturer's stated exposure times and actual measured exposure times.

All jobs will be automatically adjusted to run at the same speeds as before, so although exposure times will increase on paper by 34 µs for all scans with Bonito cameras, scan times should stay the same.

Part of this automatic adjustment is setting and increasing the value of job property `cs-allowable-pixels-motion-blur`, which allows users to set the number of allowable pixels of motion blur. For certain contexts, it is acceptable to have more than 1 pixel of motion blur. Setting this property can be used to increase or decrease the stage speed by setting an allowable limit of motion blur.

`cs-allowable-pixels-motion-blur` can be set to any value in the range `[0.1, 1000.0]`. Setting this value less than 1 will decrease stage speed, while setting it to greater than 1 will increase the stage speed. For example, given a scan that is running at 50 mm/s, setting this job property to `4.0` would allow the scan to proceed at `200 mm/s` on a stage that supports those speeds. Conversely for a scan running at `200 mm/s`, setting this value to `0.25` reduce scan speeds to `50 mm/s`.

NSPEC-8374: Deprecate 0-based indexing for bare wafer and custom scan image tiles via Continuous Scanning Mode

Previously, when running bare wafer and custom scans in continuous scanning mode, the first scanned image tile would start at 000. Now, the first image tile index will start at 001. This change was made to match the behavior of both wafer and custom scans running in stop and go mode **and** device scans, which already use 1-based indexing.

Now all scans will follow the same 1-based indexing convention for naming image tiles across bare wafer, custom, and patterned wafer device scans.

Existing analyses relying on the previous image indexing for bare wafer and custom scans may need to be reconfigured. This will not impact device scans.

For users that wish to continue using the legacy image index, new program option **Use Legacy Scan Images Index** under **Scanning** program options can be enabled to restore legacy behavior. Legacy behavior means that bare wafer and custom scans performed with continuous scanning use 0-based indexing, and bare wafer and custom scans performed with stop and go scanning use 1-based indexing for image tiles.

Additionally, when the **Use Legacy Scan Images Index** option is disabled, all bare wafer scans follow a horizontal scan path. Previously, when running a stop and go scan with the **Path Optimization** program option enabled under **Scanning** options, the system would scan in a vertical pattern. The new behavior ensures parity between both scanning modes.

The following table summarizes the indexing scheme and scan paths for bare wafer scans, with the following parameter combinations:

- **Scan Mode**: Continuous Scanning or Stop and Go
- **Program Option: Path Optimization**: Enabled or disabled

- **Program Option: Legacy Scan Images Index**: Enabled or disabled

Scan Type	Scan Mode	Program Option: Path Optimization	Program Option: Legacy Scan Images Index	Scan Path	Indexing Scheme
Bare wafer	Continuous Scanning	Enabled	Enabled	Horizontal	0
Bare wafer	Stop and Go	Enabled	Enabled	Vertical	1
Bare wafer	Continuous Scanning	Disabled	Enabled	Horizontal	0
Bare wafer	Stop and Go	Disabled	Enabled	Horizontal	1
Bare wafer	Continuous Scanning	Enabled	Disabled	Horizontal	1
Bare wafer	Stop and Go	Enabled	Disabled	Horizontal	1
Bare wafer	Continuous Scanning	Disabled	Disabled	Horizontal	1
Bare wafer	Stop and Go	Disabled	Disabled	Horizontal	1

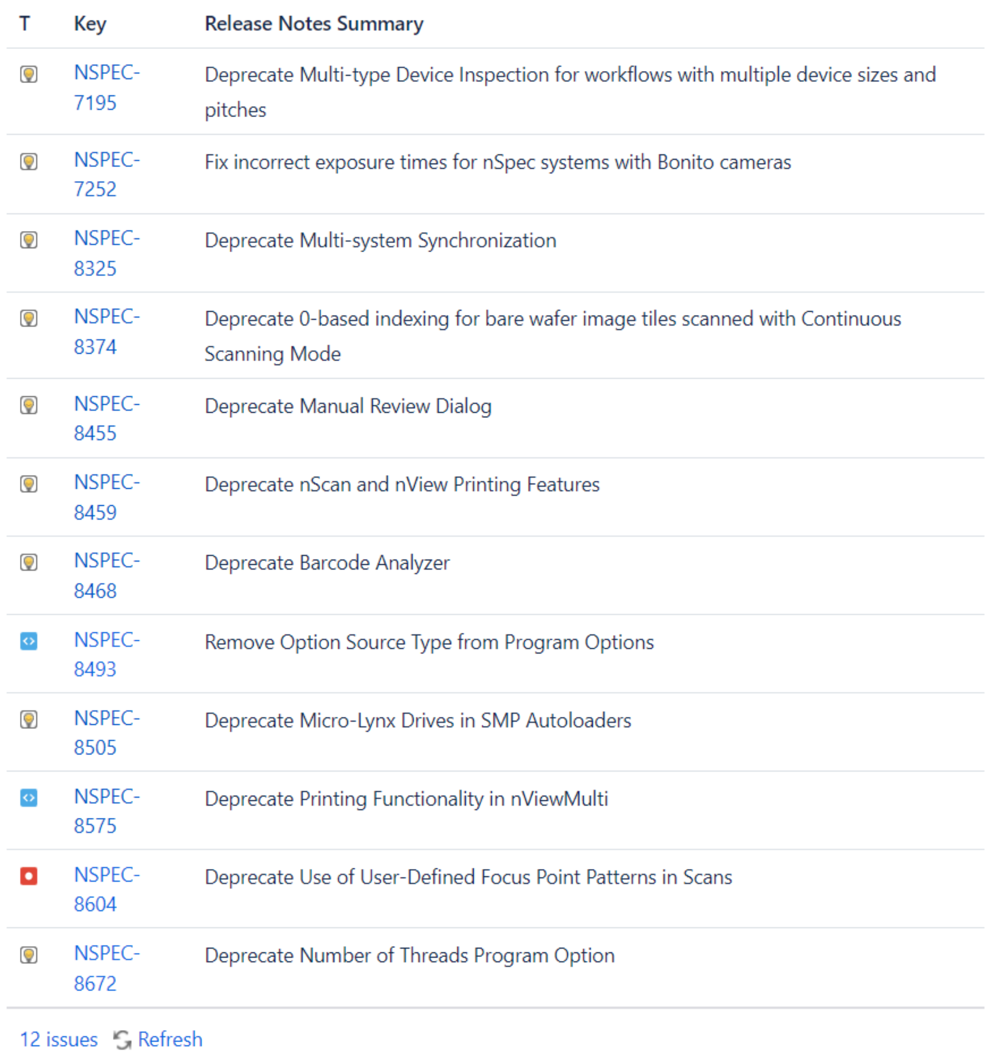
Scan Type	Scan Mode	Program Option: Path Optimization	Program Option: Legacy Scan Images Index	Scan Path	Indexing Scheme
Custom	Continuous Scanning	Enabled	Enabled	Horizontal	0
Custom	Stop and Go	Enabled	Enabled	Random	1
Custom	Continuous Scanning	Disabled	Enabled	Horizontal	0
Custom	Stop and Go	Disabled	Enabled	Horizontal	1
Custom	Continuous Scanning	Enabled	Disabled	Horizontal	1
Custom	Stop and Go	Enabled	Disabled	Random	1
Custom	Continuous Scanning	Disabled	Disabled	Horizontal	1
Custom	Stop and Go	Disabled	Disabled	Horizontal	1

Deprecation Changelog

T	Key	Release Notes Summary
	NSPEC-7195	Deprecate Multi-type Device Inspection for workflows with multiple device sizes and pitches

	NSPEC-7252	Fix incorrect exposure times for nSpec systems with Bonito cameras
	NSPEC-8325	Deprecate Multi-system Synchronization
	NSPEC-8374	Deprecate 0-based indexing for bare wafer and custom scan image tiles via Continuous Scanning Mode
	NSPEC-8455	Deprecate Manual Review Dialog
	NSPEC-8459	Deprecate nScan and nView Printing Features
	NSPEC-8468	Deprecate Barcode Analyzer
	NSPEC-8493	Remove Option Source Type from Program Options
	NSPEC-8505	Deprecate Micro-Lynx Drives in SMP Autoloaders
	NSPEC-8575	Deprecate Printing Functionality in nViewMulti
	NSPEC-8604	Deprecate Use of User-Defined Focus Point Patterns in Scans
	NSPEC-8672	Deprecate Number of Threads Program Option

12 issues



T	Key	Release Notes Summary
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🟥	NSPEC-8604	Deprecate Use of User-Defined Focus Point Patterns in Scans
💡	NSPEC-8672	Deprecate Number of Threads Program Option

12 issues Refresh

Major Enhancements

Device Yield Report - Device View

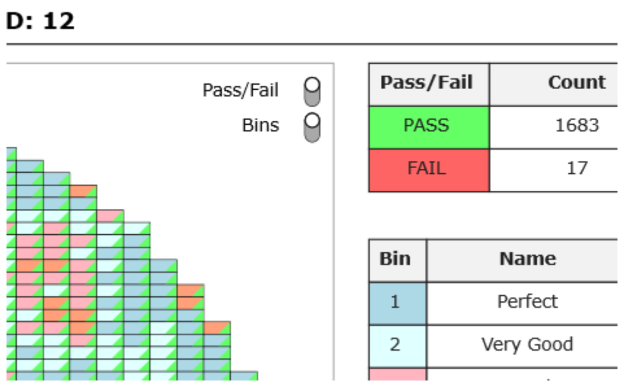
Device Yield Reports now include **Device View**. Previously, when inspecting devices, users could only view scanned images on a per-tile basis. Now, users can view entire devices at a time when viewing device yield reports in **nView**.

Overview

After successfully running Device Yield analysis on a defect-type scan, the analysis results can be viewed in nView. The Device Yield report can be viewed by accessing **nView > View > Device Yield Report** or `Ctrl+ 7`.

Device Yield Report Views

The Device Yield report has multiple different views that can be seen by toggling **Pass/Fail** and **Bins**, in addition to hovering over individual pass/fail or bin table rows.



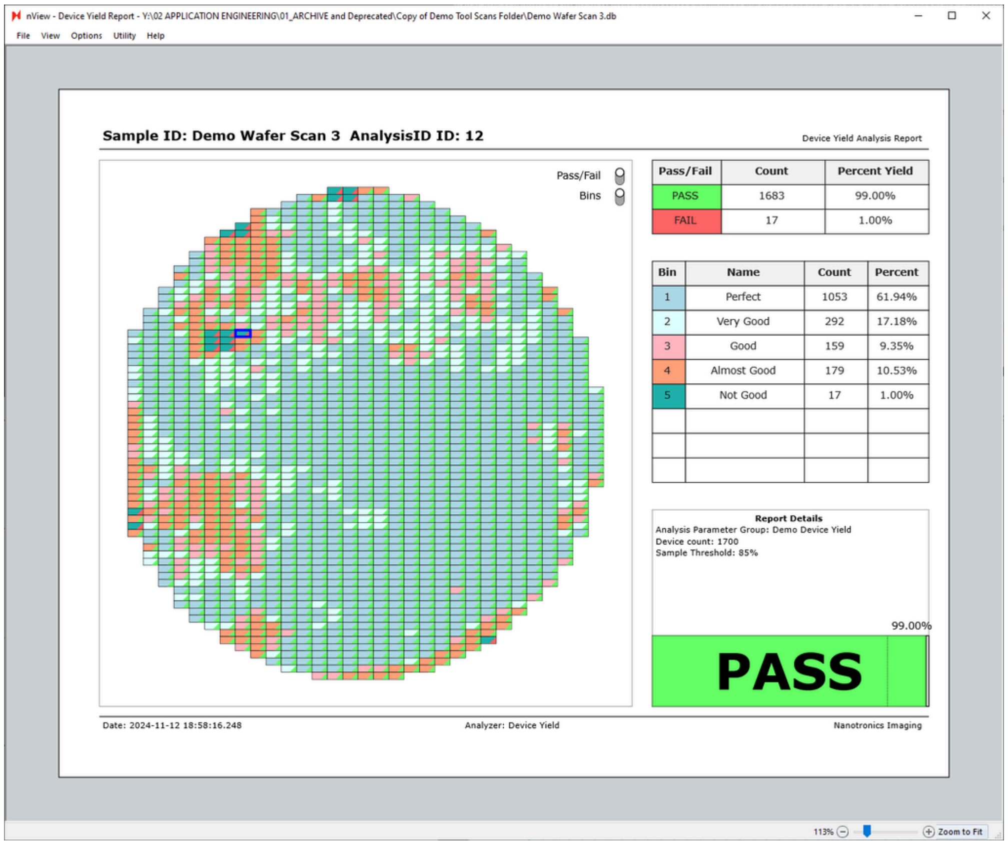
D: 12

Pass/Fail	Count
PASS	1683
FAIL	17

Bin	Name
1	Perfect
2	Very Good

In the next image, both the **Pass/Fail** and **Bins** views are turned on.

Each square represents a device, with the color in the top left corner of each device representing the bin associated with the device, and the color in the bottom right corner representing the pass/fail status of the device.


nView - Device Yield Report - Y:\02 APPLICATION ENGINEERING\01_ARCHIVE and Deprecated\Copy of Demo Tool Scans Folder\Demo Wafer Scan 3.db
File View Options Utility Help
Pass/Fail
Bins
113%
Zoom to Fit

Sample ID: Demo Wafer Scan 3 AnalysisID ID: 12

Device Yield Analysis Report

Pass/Fail	Count	Percent Yield
PASS	1683	99.00%
FAIL	17	1.00%

Bin	Name	Count	Percent
1	Perfect	1053	61.94%
2	Very Good	292	17.18%
3	Good	159	9.35%
4	Almost Good	179	10.53%
5	Not Good	17	1.00%

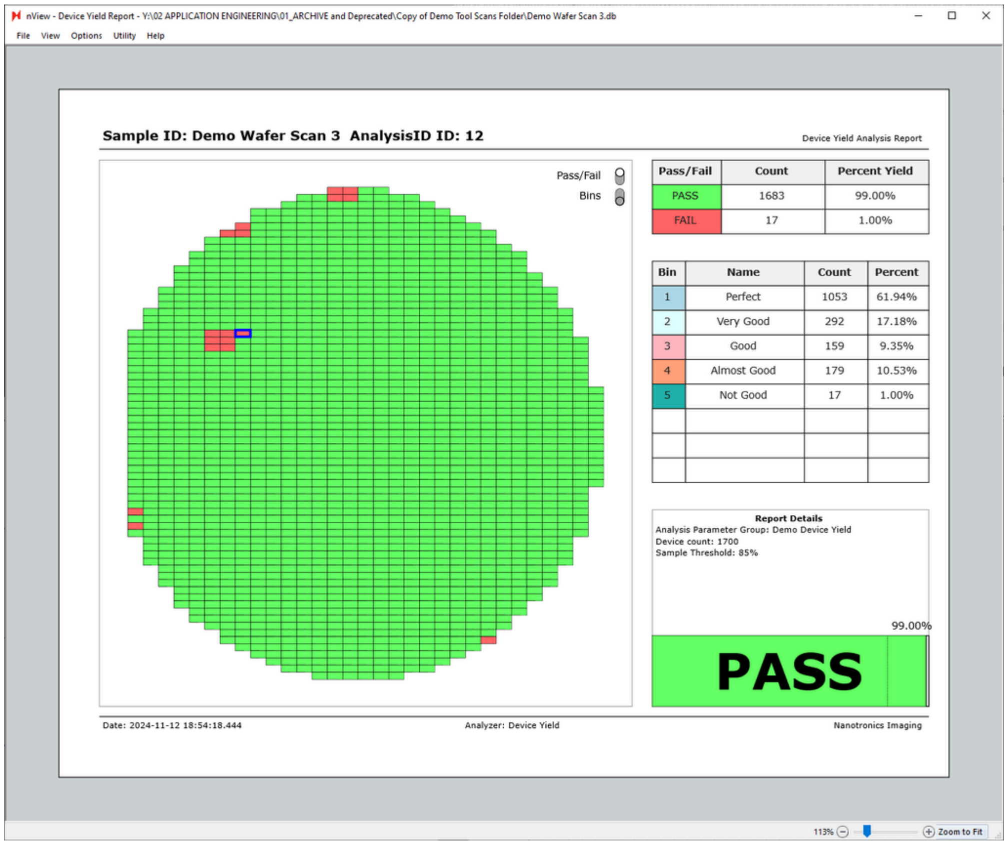
Report Details
Analysis Parameter Group: Demo Device Yield
Device count: 1700
Sample Threshold: 85%

99.00%

PASS

Date: 2024-11-12 18:58:16.248 Analyzer: Device Yield Nanotronics Imaging

Bins can be toggled off to only show the pass/fail status of each device.


nView - Device Yield Report - Y:\02 APPLICATION ENGINEERING\01_ARCHIVE and Deprecated\Copy of Demo Tool Scans Folder\Demo Wafer Scan 3.db
File
View
Options
Utility
Help
Pass/Fail
Bins
113%
Zoom to Fit

Sample ID: Demo Wafer Scan 3 AnalysisID ID: 12

Device Yield Analysis Report

Pass/Fail	Count	Percent Yield
PASS	1683	99.00%
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Bin	Name	Count	Percent
1	Perfect	1053	61.94%
2	Very Good	292	17.18%
3	Good	159	9.35%
4	Almost Good	179	10.53%
5	Not Good	17	1.00%

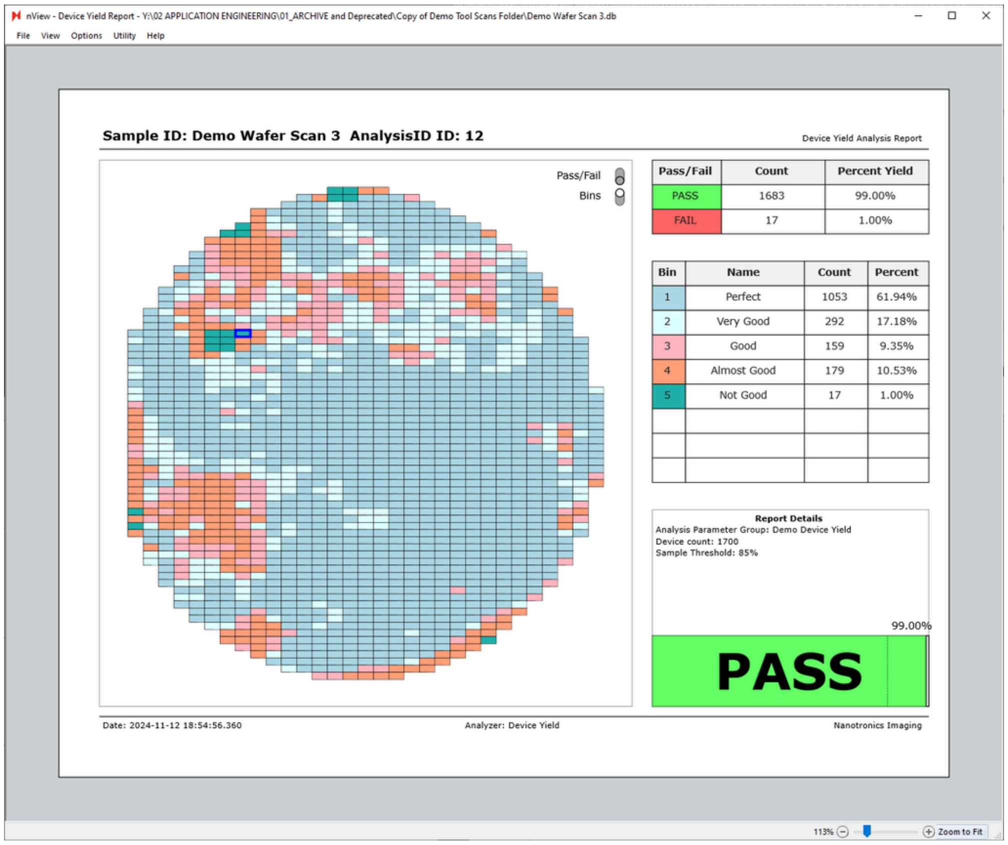
Report Details
Analysis Parameter Group: Demo Device Yield
Device count: 1700
Sample Threshold: 85%

99.00%

PASS

Date: 2024-11-12 18:54:18.444 Analyzer: Device Yield Nanotronics Imaging

Similarly, **Pass/Fail** can be toggled off to show the device bins only.


nView - Device Yield Report - Y:\02 APPLICATION ENGINEERING\01_ARCHIVE and Deprecated\Copy of Demo Tool Scans Folder\Demo Wafer Scan 3.db
File View Options Utility Help
Pass/Fail
Bins
113%
Zoom to Fit

Sample ID: Demo Wafer Scan 3 AnalysisID ID: 12

Device Yield Analysis Report

Pass/Fail	Count	Percent Yield
PASS	1683	99.00%
FAIL	17	1.00%

Bin	Name	Count	Percent
1	Perfect	1053	61.94%
2	Very Good	292	17.18%
3	Good	159	9.35%
4	Almost Good	179	10.53%
5	Not Good	17	1.00%

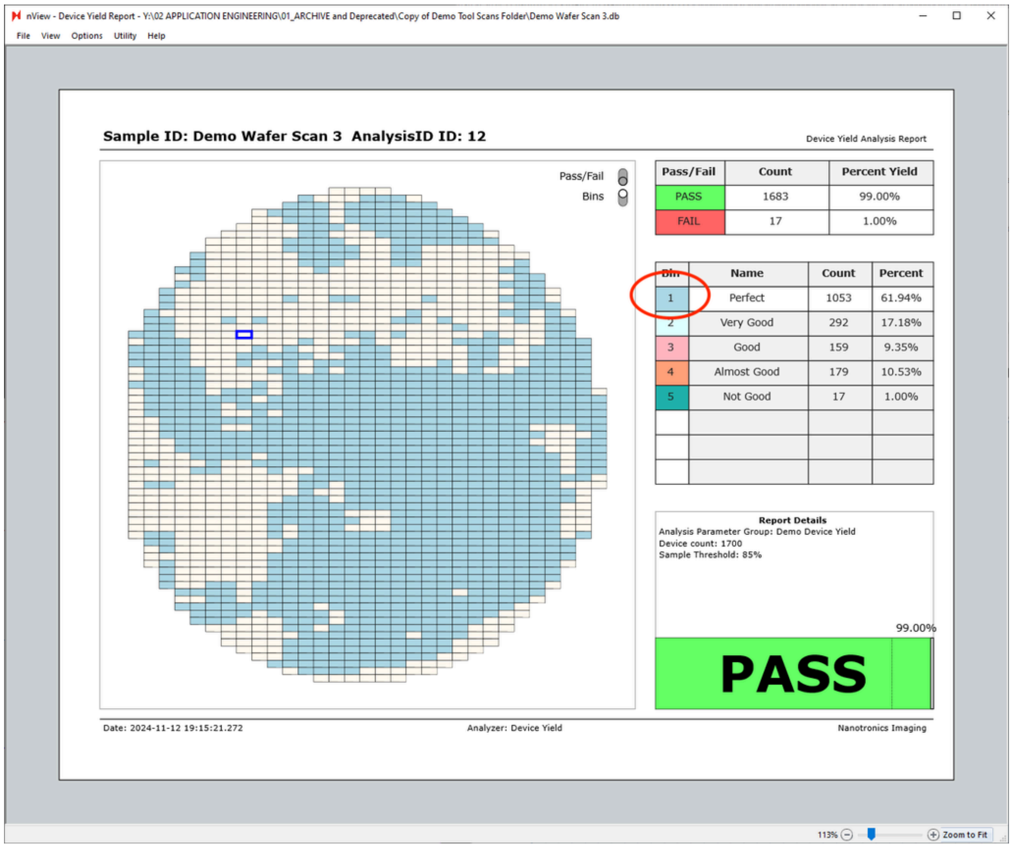
Report Details
Analysis Parameter Group: Demo Device Yield
Device count: 1700
Sample Threshold: 85%

99.00%

PASS

Date: 2024-11-12 18:54:56.360 Analyzer: Device Yield Nanotronics Imaging

Additionally, hovering over any of the table rows on the right side of the report will highlight the given row's bin. The view below is with the bins view only enabled, with cursor hovered over the "Bin 1 - Perfect" row.


nView - Device Yield Report - Y:\02 APPLICATION ENGINEERING\01_ARCHIVE and Deprecated\Copy of Demo Tool Scans Folder\Demo Wafer Scan 3.db

Sample ID: Demo Wafer Scan 3 AnalysisID ID: 12

Device Yield Analysis Report

Pass/Fail	Count	Percent Yield
PASS	1683	99.00%
FAIL	17	1.00%

Bin	Name	Count	Percent
1	Perfect	1053	61.94%
2	Very Good	292	17.18%
3	Good	159	9.35%
4	Almost Good	179	10.53%
5	Not Good	17	1.00%

Report Details
Analysis Parameter Group: Demo Device Yield
Device count: 1700
Sample Threshold: 85%

99.00%

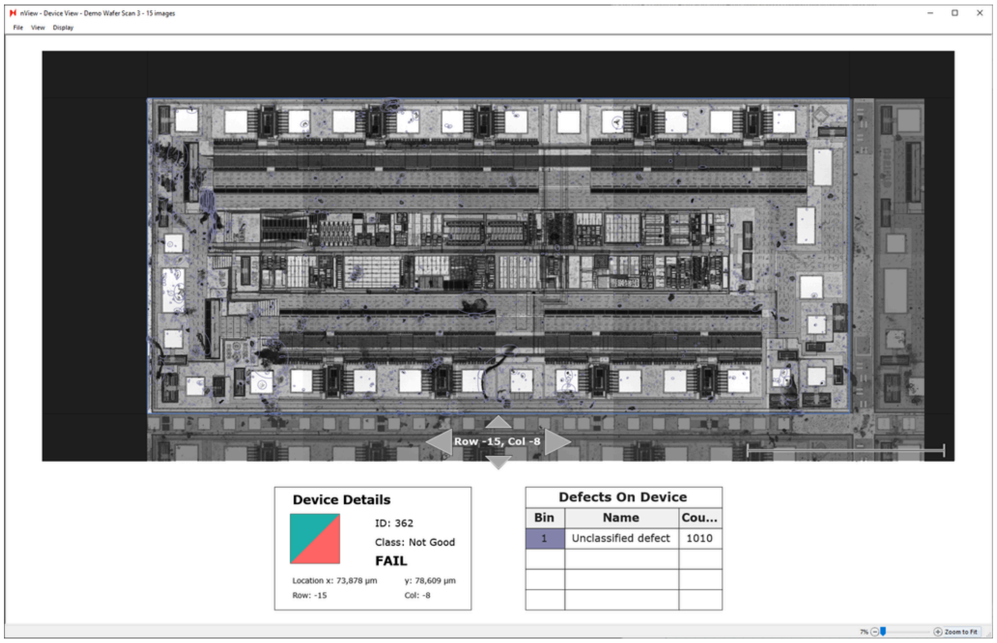
PASS

Date: 2024-11-12 19:15:21.272   Analyzer: Device Yield   Nanotronics Imaging

Individual Device View

Individual devices can also be inspected more closely by double-clicking any of the device tiles in the device yield report. Double-clicking a device tile will open a new window of the device view.

Using the up, left, down, right arrows allows you to navigate to view neighboring devices.



Device Details

ID: 362
Class: Not Good
FAIL
Location x: 73,878 µm y: 78,609 µm
Row: -15 Col: -8

Defects On Device

Bin	Name	Cou...
1	Unclassified defect	1010

Exporting Device Yield Report

Device yield reports can be manually saved and exported directly at **nView** > **File** > **Save As…**

Additionally, they can be exported automatically by placing a **Report Summary Image Export** after a device yield analysis in an analysis group.

Custom String Template Export File Formatting

Users can create custom export file formatting in **Custom Exporter** using string templates.

Overview

Users can create custom formatted export files in **Custom Exporter** using user-defined **nfmt** (Nano format) files.

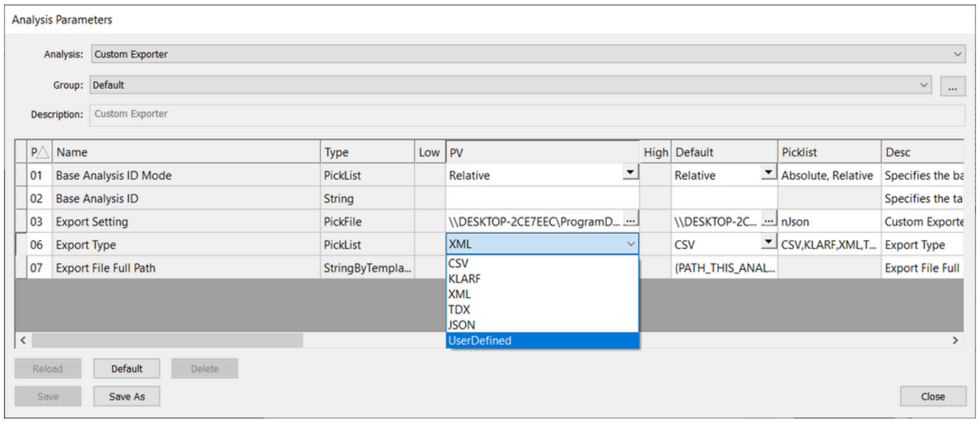
This guide assume familiarity with Python f-string formatting. nfmt is an implementation of {fmt} C++ library. We've developed a custom syntax-highlighting extension for VS Code to aid in creating **nfmt** files. Contact support@nanotronics.ai for access to this custom VS extension.

Formatting a DB

Formatting a SQL row

Custom Exporter Usage

To use the custom string template formatter in **Custom Exporter**, you must select **UserDefined** as the **Export Type**.



Analysis Parameters

Analysis: Custom Exporter

Group: Default

Description: Custom Exporter

P	Name	Type	Low	PV	High	Default	Picklist	Desc
01	Base Analysis ID Mode	PickList		Relative		Relative	Absolute, Relative	Specifies the ba
02	Base Analysis ID	String						Specifies the ta
03	Export Setting	PickFile		\\DESKTOP-2CE7EEC\ProgramD...		\\DESKTOP-2C...	nJson	Custom Exporte
06	Export Type	PickList		XML		CSV	CSV,KLARF,XML,T...	Export Type
07	Export File Full Path	StringByTempla...				{PATH_THIS_ANAL...		Export File Full

When selecting **UserDefined** export type, you must provide a nfmt file to format your export. You must point to this nfmt file using the field `CustomTypeFile` in the **Export Setting** nJson file.

Below is an example nJson file. Note that the `CustomTypeFile` is `nanofmt.nfmt` and the `CustomTypeExtension` is `txt`.

```
{
  "Custom Exporter": {
    "inputTablesNames": "src",
    "CustomTypeExtension": "txt",
    "CustomTypeFile": "nanofmt.nfmt",
    "Views" : [
      {
        "Title": "srcScanID",
        "Query": "SELECT ScanID FROM vwAnalysis WHERE AnalysisID = (SELECT AnalysisID FROM src LIMIT 1)"
      },
      {
        "Title": "vwSrcScan",
        "Query": "SELECT ScanID, Timestamp As StartTime, EndTime, (SELECT COUNT(*) FROM vwImages) AS NumImages , (SELECT PropertyData / 1000 FROM ScanProperties WHERE PropertyName = 'Scan Min X Microns')  AS 'X_mm', (SELECT PropertyData / 1000 FROM ScanProperties WHERE PropertyName = 'Scan Min Y Microns')  AS 'Y_mm', (SELECT PropertyData / 1000 FROM ScanProperties WHERE PropertyName = 'Scan Width Microns')  AS 'Width_mm', (SELECT PropertyData / 1000 FROM ScanProperties WHERE PropertyName = 'Scan Height Microns') AS 'Height_mm', Result, (SELECT PropertyData FROM ScanProperties WHERE PropertyName = 'SampleID') AS SampleName FROM Scans WHERE ScanID = (SELECT ScanID FROM srcScanID)"
      },
      {
        "Title": "vwSrcAnalysis",
        "Query": "SELECT AnalysisID, AnalyzerMenuText AS Analyzer, Timestamp AS StartTime, EndTime, NumDefects, AnalyzerName, Result FROM vwAnalysis WHERE AnalysisID = (SELECT AnalysisID FROM src LIMIT 1)"
      }
    ],
    "Queries": [
      {
        "Title": "scans",
        "Query": "SELECT * FROM Scans"
      }
    ]
  }
}
```

Example nfmt formatting file

Below is an example nfmt file. Anything not contained in braces `{` `}` is considered literal text, and brace characters can be escaped by doubling `{{` `}}`.

Note that within the braces, the nfmt file references and accesses the SQL database queries made in the nJson Export Setting file, e.g. `scans` and `vsSrcScan`.

```
User-Defined Report Sample (from Query)
=======================================
Scans ID : {scans:e{"\t"}:ScanID}
Scans StartTime : {scans:e{"\t"}:Timestamp}
Scans EndTime : {scans:e{"\t"}:EndTime}
Scans Result : {scans:e{"\t"}:Result}
{db:sql{scan, SELECT * FROM vwSrcScan}:e{"\n"}:f{
"
Defined Report Sample (from views)
=======================================
Scan ID : {scan:ScanID}
Scan StartTime : {scan:StartTime}
Scan EndTime : {scan:EndTime}
Number of Images : {scan:NumImages}
X(mm) : {scan:X_mm}
Y(mm) : {scan:Y_mm}
Width(mm) : {scan:Width_mm}
Height(mm) : {scan:Height_mm}
Scan Result : {scan:Result}
SampleName : {scan:SampleName}
{db:
sql{property,
  f{"SELECT * FROM ScanProperties WHERE ScanID = {scan:ScanID}"} }
  :e{"\n"}
  :f{"{property:PropertyName} : {property:PropertyData}"} }

{db:sql{analysis, SELECT * FROM vwAnalysis WHERE AnalysisID = (SELECT AnalysisID
FROM src LIMIT 1)}
  :e{"\n"}
  :f{
"
Analyzer
--------
StartTime : {analysis:Timestamp}
EndTime : {analysis:EndTime}
Defects : {analysis:NumDefects}
AnalyzerName : {analysis:AnalyzerName}
"} }

Devices
-------
{db:
sql{device, f{"SELECT * FROM vwDevices WHERE ScanID = {scan:ScanID} ORDER BY
DeviceID"} }
:e{"\n"}
:f{
"
DeviceID : {device:DeviceID}
X : {device:X}
Y : {device:Y}
width : {device:width}
height : {device:height}
Images
------
{db:sql{image, f{"
SELECT * FROM vwImages WHERE ImageID IN
(SELECT ImageID FROM DevicesInImages WHERE DeviceID = {device:DeviceID})
ORDER BY ImageID"} }
:e{"\n"}
:f{
"
ImageID : {image:ImageID}
  X : {image:X}
  Y : {image:Y}
  width : {image:wMicrons}
  height : {image:hMicrons}

Defects
-------
DefectID X Y W H Area
{db:sql{d, f{"SELECT * FROM src WHERE ImageID = {image:ImageID} ORDER BY DefectID"}
}
::e{" {d:DefectID:<11} {d:X:<6.5g} {d:Y:<6.5g} {d:W:<6.5g} {d:H:<6.5g}
{d:Area:<9.8g}\n"
} }"
} }"
} }"
} }

```

Example Export File

The following export file was generated via **Custom Exporter** using the example nfmt file above. The data is sample data, but typically the data draws from the nSpec scan database. Only a portion of the `Defects` have been included for brevity.

```
User-Defined Report Sample (from Query)
=======================================
Scans ID        : 1 2   3   4   5   6
Scans StartTime : 2024-09-08 22:45:10.624   2024-09-08 22:47:04.214 2024-09-08 22:48:05.204 2024-09-08 22:50:10.931 2024-09-08 22:51:09.385 2024-09-08 22:53:06.674
Scans EndTime   : 2024-09-08 22:47:03.977   2024-09-09 12:48:39.323 2024-09-08 22:50:08.973 2024-09-09 12:55:33.344 2024-09-08 22:53:04.566 2024-09-09 13:00:17.962
Scans Result    : Success   Success Success Success Success Success

Defined Report Sample (from views)
=======================================
Scan ID          : 6
Scan StartTime   : 2024-09-08 22:53:06.674
Scan EndTime     : 2024-09-09 13:00:17.962
Number of Images : 7982
X(mm)            : 15.254580095
Y(mm)            : 15.538067214
Width(mm)        : 310.29911172
Height(mm)       : 310.501818577
Scan Result      : Success
SampleName       : 300mm_Wafer
Alignment Angle : 0.789400
Alignment File : \\DESKTOP\Alignments\300mm_Wafer_Alignment.csv
Autofocus Set : 300mm_Wafer_AF
Autofocus Type : Automatic Predictive
Autoloader Set : None
CenterX : 170384.977373
CenterY : 170668.930430
DiePitchX : 64498.265301
DiePitchY : 90001.686035
Edge Exclude : 3000.000000
Exposure Time : 1
Filter Slider Status : None
FlatOffsetAngle : 0.000000
FlatSegmentLength : 0.000000
Focus Point Pattern : 300mm 9 Point
Focus Predictor : PreFoc Polynomial Standard
Golden Tile Number of Devices : 8
Golden Tile Scan : 1
Golden Tile Tiles per Device : 88
Illumination : Bright Field
Image Height Microns : 7410.389169
Image Height Pixels : 4268
Image Width Microns : 7888.396686
Image Width Pixels : 4398
Initiator : Manual
Install Build Version : 0.24.2.0
```

```
JobName : 300mm_Wafer_Demo_Job
JobUpdateTime : 2024-09-08 23:42:31.428
KLARFMode : 1
Layout File : D:\Scans\300mm_Wafer\Scan_006\Layout.csv
Light Intensity Control 1 : Setpoint
Light Intensity Control 2 : Setpoint
Light Intensity Control Value 1 : 0
Light Intensity Control Value 2 : 1000
Light Source 1 : Nano:Transmitted
Light Source 2 : Nano:Reflected
Mosaic Name : 300mm_Wafer_Mosaic.png
Objective : 2.5X - CFI L Plan 2.5X
OriginOffsetX : 0.000000
OriginOffsetY : 0.000000
Pattern : WholeStage
Pattern Type : 2
Radius : 149988.238372
SampleCenterX : 172401.665016
SampleCenterY : 172685.624342
SampleID : 300mm_Wafer
SampleLength : 300.000000
Scan Height Microns : 309401.818577
Scan Min X Microns : 16256.183319
Scan Min Y Microns : 16348.184435
Scan Tilt Angle : 0.000000
Scan Width Microns : 308409.111720
Stage Height Microns : 343179.700000
Stage Width Microns : 344681.400000
XOffset : -17537.000000
YOffset : -18344.000000

Analyzer
--------
  StartTime     : 2024-09-09 17:20:57.937
  EndTime       : 2024-09-09 17:21:31.650
  Defects       : 23189
  AnalyzerName  : nrad_rangeselect

Devices
-------
  DeviceID : 1
  X        : 28645.193836
  Y        : 117102.611014
  width    : 63391.820591
  height   : 77005.699667

  Images
  ------
  ImageID  : 2001
    X      : 28642.416191
    Y      : 117095.278032
    width  : 4461
    height : 4169

    Defects
    -------
      DefectID    X      Y      W      H      Area

  ImageID  : 2002
    X      : 36569.712877
    Y      : 117096.278032
    width  : 4461
    height : 4169

    Defects
    -------
      DefectID    X      Y      W      H      Area

  ImageID  : 2003
    X      : 44498.009564
    Y      : 117096.278032
    width  : 4461
    height : 4169

    Defects
    -------
      DefectID    X      Y      W      H      Area

ImageID  : 5750
    X      : 138607.349836
    Y      : 82548.104671
    width  : 4461
    height : 4169

    Defects
    -------
      DefectID    X      Y      W      H      Area
      97734       2134.8 2252.4 5.6254 3.9378 22.468003
      97735       1714.6 2124.7 6.0588 3.3427 20.88575
      97736       534.98 2172.5 166.51 102.38 9194.793
      97737       895    2134.8 32.057 1.636  24.050257
      97738       2349.7 2105   7.5578 8.3532 54.429529
      97739       547.35 2070.7 4.7733 4.7733 21.518651
      97740       895    2040.9 1.1251 37.127 24.050257
      97741       534.98 2045.9 166.51 93.381 6940.3979
      97742       1630.8 1974.5 1.1251 50.628 23.100905
      97743       296.46 1921.1 7.16   11.933 74.365926
      97744       895    1911.5 1.1251 50.628 35.126033
      97745       534.41 1919.4 165.95 101.82 9144.4774
      97746       895    1845.1 1.1251 57.941 33.54378
      97747       232.89 1797.9 5.0629 6.1879 31.328624
      97748       1630.8 1856.4 1.1251 125.45 58.543389
      97749       534.41 1793.4 165.95 92.819 9597.6348
      97750       2462.8 1754.6 24.263 9.5844 164.23794
```

Basic Pieces of Syntax

We only add new syntax to the {fmt} library for format-specifiers; these are the parts of a `{variable_name:format_spec}` to the right of the first colon. There are a couple of basic ideas:

Joining format-specifiers

Instead of using a single block of characters from a `:` to a `}` to denote how to format some typed thing, we will allow a sequence of these to iteratively turn the thing into progressively easier-to-format things. This is not required in regular f-strings, which never permit a `:` to appear in a format-specifier.

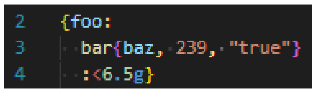
Iterables

If you have some iterable variable containing things of type `T`, then it is formatted with a joiner to become something that is formatted with a format-specifier for something of type `T`. So for example, if we had `scan_ids,` was a list `{1, 2, 3}`, and it was formatted with `{scan_ids:, :03}`, that would produce the string `001, 002, 003`.

Note that this is not quite the same as the range-based syntax extension described in the library, because we can add joiners.

Function calls

In some places, we embed something that should be read as a function call. Function calls are a name matching `[A-Za-z_][A-Za-z_0-9]*`, followed by a `{}`-wrapped, `,`-delimited sequence of arguments. Whitespace before and after is ignored. For example:

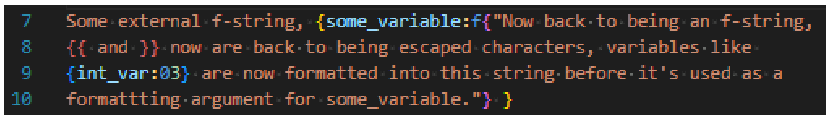


```
{foo:
  bar{baz, 239, "true"}
  :<6.5g}
```

Would require `foo` and `bar` to be variables in the surrounding context, `foo` to understand how to find a function `bar`, and implicitly that function must return a floating point number to be correctly formatted by the regular format specifier `:<6.5g`.

Escaped f-strings

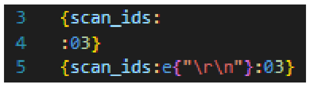
Anywhere in a format specifier that requires a string, we can *recursively* have an f-string. This is done with the reserved functions `f` and `e`. The basic syntax for this is to wrap in `""` and `{}:`



```
Some external f-string, {some_variable:f{"Now back to being an f-string,
{{ and }} now are back to being escaped characters, variables like
{int_var:03} are now formatted into this string before it's used as a
formattting argument for some_variable."} }
```

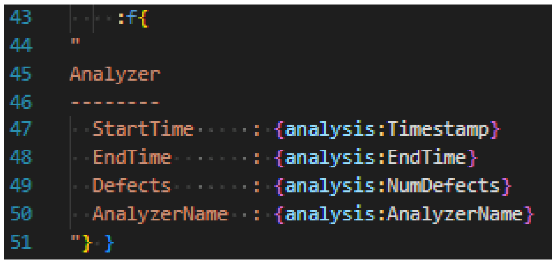
Note, critically, the space after the magenta-highlighted `}`. **Some trailing whitespace after this function call is mandatory for distinguishing closing two scopes** and intending to embed a raw `}` into the embedded f-string.

The function `e` has the same semantics, but additionally unescapes C-style `\<char>` characters. The main ones of use are `\t`, `\r`, `\n`, `\0` (tab, carriage return, line feed, null). All but a null can technically be embedded in a string without escaping, but they can be hard to read. The following two lines express the same intent, but the latter is much clearer:



```
{scan_ids:
:03}
{scan_ids:e{"\r\n"}:03}
```

For these embedded `e` and `f` strings, whitespace between the `{` and `"` and `"` and `}` can be freely added. If whitespace between the `{` and `"` matches exactly with whitespace at the beginning or end of the quoted string, it is removed; this allows for clean syntax separating the management of a block of text to be embedded and the text to be embedded. For example:



```
    :f{
"
Analyzer
--------
  StartTime     : {analysis:Timestamp}
  EndTime       : {analysis:EndTime}
  Defects       : {analysis:NumDefects}
  AnalyzerName  : {analysis:AnalyzerName}
"} }
```

Embeds an f-string which starts with `A` and ends immediately after the `AnalyzerName`, without any trailing newline (for now, don't worry about what the `analysis` variable is).

SQL formatting

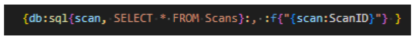
Formatting a DB

For now, a SqlDB exposes exactly one callable function, `sql{row_name, sql_string}`, which runs the query in `sql_string` and returns an iterable of rows, each of which will be exposed to subsequent formatting as a variable named `row_name`. For now, this means that to produce anything useful, the row must be formatted with some embedded f-string, since it is **named**.

Currently we are in the context of file exports for an analysis, there's only one natural DB (the scanDB), which is exposed as a variable named `db`. As in other Exporters, the `.njson` file may have a number of queries to produce named views or other iterable rows that were returned by a SQL query.

Formatting a SQL row

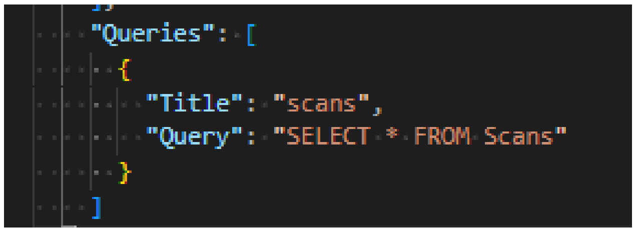
Rows are dictionaries, indexed by their column titles. So something like:



```
{db:sql{scan, SELECT * FROM Scans}:, :f{"{scan:ScanID}"} }
```

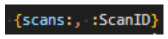
Will produce a list of the `ScanID`s for every scan in the `Scans` table, separated with `", "`.

If a query is embedded in the `.njson` file, e.g. as



```
"Queries": [
    {
        "Title": "scans",
        "Query": "SELECT * FROM Scans"
    }
]
```

then the entire **iterable** of results will be named scans, and so can be formatted like:



```
{scans:, :ScanID}
```

This is structurally less flexible, but is simpler syntax in the `.nfmt` file.

Note that in either case, the format specifier here is simply producing some integer that is then default formatted; if this needed to be controlled with a further specifier for width or padding that occurs exactly as for any other integer.

New Features

Highlights

NSPEC-7252 Fix incorrect exposure times for nSpec systems with Bonito cameras

For nSpec systems with Bonito cameras, exposure times will increase for all scans. This is due to a difference found between the manufacturer's stated exposure times and actual measured exposure times. All jobs will be automatically adjusted to run at the same speeds as before, so although exposure times will increase, scan times should stay the same. See **v0.24.2.0 Deprecations** for more on this change.

NSPEC-8099 Custom Export File Formatting in Custom Exporter using String Templates

Users can now fully customize export file formats using user-defined `nfrmt` files using **Custom Exporter.** See the **Major Enhancements** section of release notes for more information on how to create and use custom formatters.

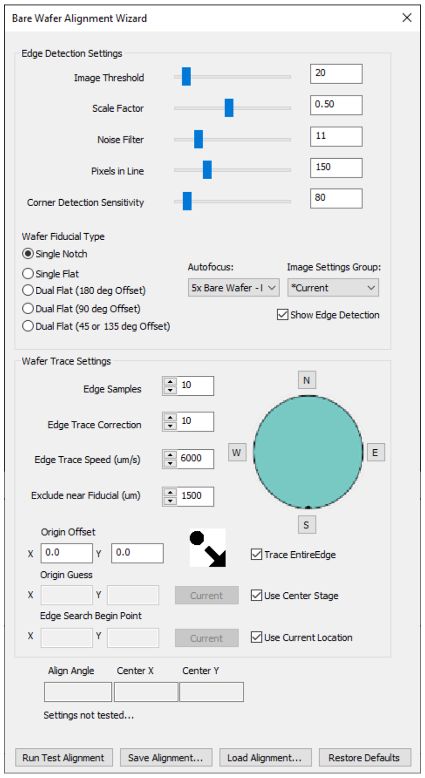
NSPEC-8374: Deprecate 0-based indexing for bare wafer image tiles scanned via Continuous Scanning Mode

See **v0.24.2.0 Deprecations** for more on this change, which affects the naming convention for image tiles scanned via bare wafer continuous scans.

NSPEC-8482 Shorten Bare Wafer Alignment Process

There is a new option in the **Bare Wafer Alignment Wizard** to **Trace Entire Edge** of the sample when performing alignment. By default, this behavior is enabled. This matches the legacy behavior of bare ware alignment.

If you would like to use new improvements that reduce the speed of bare wafer alignment by 2-3x, uncheck the **Trace Entire Edge** box. **Note** that this new improvement assumes that the camera is already directed at the sample, and that the sample has not been manually loaded on the far ends of the stage.


Bare Wafer Alignment Wizard

Edge Detection Settings

Image Threshold	20
Scale Factor	0.50
Noise Filter	11
Pixels in Line	150
Corner Detection Sensitivity	80

Wafer Fiducial Type
- [✓ Single Notch]
- Single Flat
- Dual Flat (180 deg Offset)
- Dual Flat (90 deg Offset)
- Dual Flat (45 or 135 deg Offset)

Autofocus: 5x Bare Wafer -I
Image Settings Group: *Current
[✓] Show Edge Detection

Wafer Trace Settings

Edge Samples	10
Edge Trace Correction	10
Edge Trace Speed (um/s)	6000
Exclude near Fiducial (um)	1500

Origin Offset X 0.0 Y 0.0
[✓] Trace EntireEdge
Origin Guess X Y
[✓] Use Center Stage
Edge Search Begin Point X Y
[✓] Use Current Location

Align Angle Center X Center Y

Settings not tested...

NSPEC-8666 Add Device Name as a string template in Cropped Images analysis

Defect device names can be used to name export files in Cropped Images analysis using string template `{DEFECT_DEVICE_NAME}`.

New Features Changelog

T	Key	Release Notes Summary
	NSPEC-7252	Fix incorrect exposure times for nSpec systems with Bonito cameras
	NSPEC-8099	Custom Export File Formatting in Custom Exporter using String Templates
	NSPEC-8374	Deprecate 0-based indexing for bare wafer and custom scan image tiles via Continuous Scanning Mode
	NSPEC-8482	Shorten Bare Wafer Alignment Process
	NSPEC-8666	Add Device Name as a string template in Cropped Images Analysis

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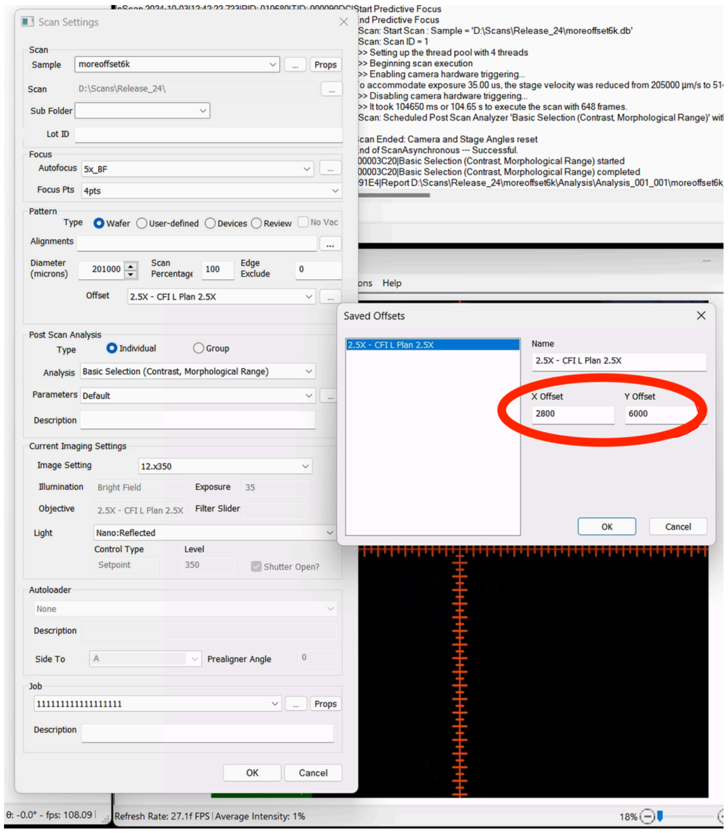
Bug Fixes

Highlights

NSPEC-7685 Cannot scan 8 inch wafer at 1.25x

Previously, users had difficulty scanning larger wafers at low magnification objectives. Now, users can enter a positive X and Y offset when inputting a wafer-type pattern in order to capture the entire wafer in a scan using a low magnification objective.



Scan Settings

Scan
Sample: moreoffset6k
Scan: D:\Scans\Release_24\
Sub Folder:
Lot ID:

Focus
Autofocus: 5x_BF
Focus Pts: 4pts

Pattern
Type: [✓ Wafer] User-defined Devices Review No Vac
Alignments:
Diameter (microns): 201000 Scan Percentage: 100 Edge Exclude: 0
Offset: 2.5X - CFI L Plan 2.5X

Post Scan Analysis
Type: [✓ Individual] Group
Analysis: Basic Selection (Contrast, Morphological Range)
Parameters: Default
Description:

Current Imaging Settings
Image Setting: 12.x350
Illumination: Bright Field Exposure: 35
Objective: 2.5X - CFI L Plan 2.5X Filter Slider:
Light: Nano:Reflected
Control Type: Setpoint Level: 350 [✓ Shutter Open?]

Autoloader
None
Description:
Side To: A Prealigner Angle: 0

Job
11111111111111111
Description:

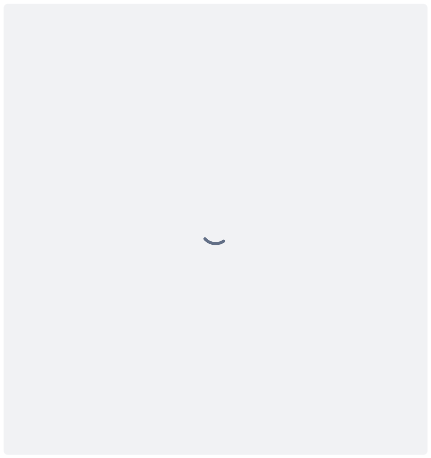
Saved Offsets
2.5X - CFI L Plan 2.5X
Name: 2.5X - CFI L Plan 2.5X
X Offset: 2800 Y Offset: 6000

```
Start Predictive Focus
End Predictive Focus
Scan: Start Scan : Sample = 'D:\Scans\Release_24\moreoffset6k.db'
Scan: Scan ID = 1
>> Setting up the thread pool with 4 threads
>> Beginning scan execution
>> Enabling camera hardware triggering...
To accommodate exposure 35.00 us, the stage velocity was reduced from 205000 µm/s to 51
>> Disabling camera hardware triggering...
>> It took 104650 ms or 104.65 s to execute the scan with 648 frames.
Scan: Scheduled Post Scan Analyzer 'Basic Selection (Contrast, Morphological Range)' wit

Scan Ended: Camera and Stage Angles reset
End of ScanAsynchronous --- Successful.
00003C20|Basic Selection (Contrast, Morphological Range) started
00003C20|Basic Selection (Contrast, Morphological Range) completed
91E4|Report D:\Scans\Release_24\moreoffset6k\Analysis\Analysis_001_001\moreoffset6k
```

θ: -0.0° - fps: 108.09 | Refresh Rate: 27.1f FPS | Average Intensity: 1%

The resulting scan encompasses all edges of the wafer.



NSPEC-8708 Suffix always appended to Cropped Images stacked TIFF export files

When running **Cropped Images** analysis with parameter **Export Many Images As Single File** set to `TRUE`, every export file has the suffix `.tiffCroppedDefects.tiff` appended to the file name.

Changelog

T	Key	Release Notes Summary
🟥	NSPEC-7658	Cannot scan 8 inch wafer at 1.25x
🟥	NSPEC-8556	GEM host cannot start autoloader job immediately after connecting to host
🟥	NSPEC-8572	nSpec hangs when closing Golden Die Utility after saving a template mask and opening a new template
🟥	NSPEC-8595	Old Bare Wafer Alignment Files Cannot Load Autofocus
🟥	NSPEC-8602	Align Angle field in Bare Wafer Alignment Wizard is empty when doing test alignments
🟥	NSPEC-8604	Deprecate Use of User-Defined Focus Point Patterns in Scans
🟥	NSPEC-8620	GEM Jobs send ACK before all parameters are updated
🟥	NSPEC-8689	Opening multiple device inspection templates in the golden die utility causes nSpec to freeze
🟥	NSPEC-8708	Suffix always appended to Cropped Images stacked TIFF export files
🟥	NSPEC-8804	Handle Leaks in nAnalyzerManager
🟥	NSPEC-8855	Subfolder field ignored in group job if set to {OCR}
🟥	NSPEC-8868	OCR string template in sample ID not functioning as expected
🟥	NSPEC-8891	Virtual Device Inspection scans cannot be generated from layouts with certain device counts
🟥	NSPEC-8923	Lights do not turn back on after shutting off when program option "Shutoff lights after scan completes" = 1

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Appendix

Multi-Type Device Inspection Workflow

Overview

nSpec supports scanning patterned wafers with multiple device types in a single scan. This article will walk through how to create a multi-device layout using the **Create Device Layout** dialog.

Note that in this workflow, the devices **must** be the same shape and size, otherwise, users with samples with devices of different sizes will need to run a scan and create a unique device layout for **each** device type.

Prerequisites

Prior to creating any device layout, you must create in the following order:

1. Image settings group
2. Autofocus group
3. North-south-origin alignment

Layout Creation

After creating and gathering all prerequisites, navigate to **nScan - Stage View** > **Scan** > **Create Device Layout**.

For general guidance on creating a device layout, see Create Device Layout. We recommend reading this article first before continuing this guide if you have never created a device layout before.

Create a layout as you would with a single type device layout, measuring the die and pitch and generating a layout using either rectangular or circular extrapolation.

When finished, **Export Device Layout**, then open the resulting CSV file.

Create a column named “Type”. Assign each device to a number representing its device type. We recommend using a 1-based index for type. In this example, there are 36 different types of devices, so we will use 1-36 to indicate the 36 device types.

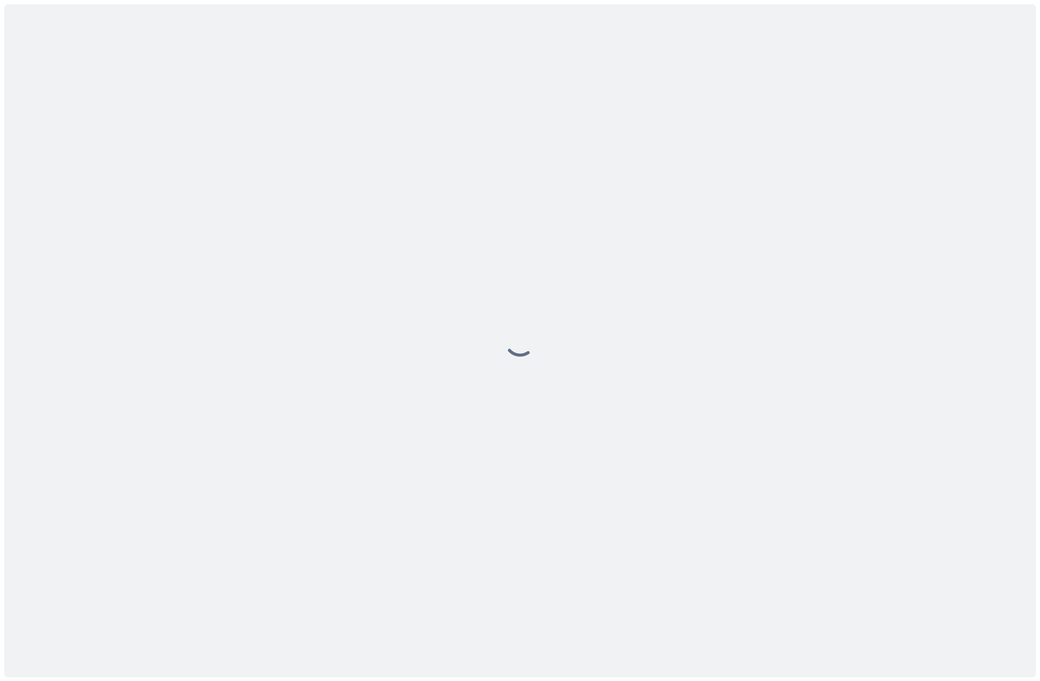
The X, Y columns represent the location of each device on the stage relative to the origin selected in the alignment file. The Xindex and Yindex represent the device’s position in units of devices, also relative to the origin. The Xindex and Yindex of each device can be seen in the **nScan - Camera View**.

Scan Setup

The last step is setup the device inspection scan. Setting up a multi-type device scan is almost identical to the procedure described in Device Inspection Analysis, with some small changes.

First, all devices types will be scanned and analyzed, unless using the **Device Type Filter** parameter for **Device Inspection**.

If you'd like to analyze just a subset of device types, you can input a regular expression in the **Device Type Filter** to indicate which types should be analyzed. The regular expressions should follow ECMA-262 regex patterns. For example, `([1-9]|1[0-8])` would analyze device types 1-18.



Note, that you cannot use **both** the **Device Type Filter** and **Optional: GTS Device Numbers to Analyze** parameters. Using both will cause the analysis to fail.

Previously, **Optional: GTS Device Numbers to Analyze** enabled a more difficult multi-type device workflow which required users to enter in every device ID to be analyzed, instead of using types.