Nutshell – PALM Rendering





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PALM Rendering Scope and recommended previous knowledge.

Here we cover rendering as one of the tools in PALM / dSTORM process. **Previous knowledge** on PALM / dSTORM and ELYRA is recommended. In particular:

Drift correction / Grouping / Filtering •



300 nm





10 nm







Overview



1 Why? What is PALM Rendering?

- 2 How does it work? Definitions
- 3 Additional Remarks

PAL-Drift PAL-Grouping PAL-Statistics PAL-Filter PAL-Rendering					
Pixel Resolution XY 10 1 nm/pixel					
Display Mode Gauss					
Expansion factor 1,00 🗘 x PSF					
✓ Render auto dynamic range HR Scale 99,00 \$ %					
Render auto dynamic range SWF Scale 100,00 🗘 %					
☐ Render Localized Precision x/y: 120.0 nm z: 40.0 nm ✓ Render Best Quality					

PALM Rendering - the last step in the process

Simply put, rendering is for viewing only...





2 ^{3n X}	Position Y [nm]	Precision [nm]	Number Photons	Ва
667.3	842.6	8.1	1966	
659.8	840.4	8.2	1968	
673.0	837.1	8.0	1741	
2502.8	1022.1	11.5	1066	
684.9	833.8	8.4	2411	
2508.2	1032.1	11.1	1806	
2185.8	2604.4	14.8	1534	
2153.6	2530.7	8.3	3396	
2501.0	1022.5	16.7	841	





Recording Data: Acquisition Laser Intensities / Gain Peak finding



Editing Data: Filtering Statistics Drift / Group / Filtering



Viewing Data: Rendering Display Brightness / Contrast

PALM Rendering - the last step in the process

Rendering generates an image from the table. Rendering does <u>not</u> affect the table.





Single emitter patterns (original data)

Acquisition	Processing	🔎 Maintai				
Peak Finder Peak Mask Size Peak Intensity to Noise		Pixel				
Localizer Fit Model x,y 2D Gauss Fit Average before Localization PSF File E:\train the trainer 2\PSF\PSF_63x14_1min_488r						

Acquisition settings Peak finding Accounting for overlap Has influence on the data Not covered in this presentation

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Position and parameter table (raw data)



Data analysis Statistics Drift / Group / Filtering Has influence on the data Not covered in this presentation



Rendered image (visualization)



Rendering Display Brightness / Contrast NO INFLUENCE on the data

Mainstay of this presentation



1 Why? What is PALM Rendering?

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Tip of
the day:Read also the notes in the presentationfor (even) more information

PALM Rendering – Parameters

Main parameters: Pixel size, Gaussian, etc...

In ZEN the rendering options are defined in the PAL-Rendering tab:



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Pixel size: Follow Nyquist reasoning





Pixel size: Follow Nyquist reasoning



- FAQ: Why am I allowed to set the resolution* (pixel size) how I want?
 Answer: The image is rendered from a table <u>not</u> related to the camera pixel size
- When you halve the pixel size, the files get 4 times bigger.
- If you don't know what to do: Look up precision** statistics, use half of the peak value.



* Attention: Some people use pixel size (or quantity) interchangeably with resolution.

** Attention: Precision is not equal to resolution. It's the best case, if the labelling density sufficiently high (see PAL-Statistics)

Display mode: Depends on the application





Render Localized Precision x/y: 120.0 nm z: 40.0 nm

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Special case: see next slides

Display mode: Special case – Molecule Density



ZEINS

Display mode: Special case – Molecule Density



Brightness is not necessarily equal to quantity:

Few bright molecules can "outshine" many dim ones.

Many dim molecules <u>can</u> be more crowded than few bright ones.

=> The brightest spot is <u>not necessarily</u> the most crowded!



Expansion Factor: A matter of confidence





The user can choose to expand the Gaussians by any factor. For example to display results with decreased resolution but with increased confidence level. (In the example above the confidence levels are increased from 68.2% using σ to 95.4% using 2 σ .) In case of doubt leave factor as 1x.

Dynamic Range: HR and SWF



The dynamic range is (per default) **scaled** from the highest intensity to the lowest.

In 16-bit the highest greyscale value is 65535 (white) and the lowest is 0 (black)

This range is insufficient when one object (like a fiducial marker) – is more than 65,325 times brighter than the structures of interest.



Dynamic Range: HR and SWF





Note: Similar result can be obtained by adjusting brightness and contrast values. However this only works up to a certain limit (dictated by the 16-bit depth). If the brightness discrepancy is too large, the better option is to use the dynamic range option in the PAL-Render tab.

Dynamic Range: HR and SWF





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Dynamic Range: HR and SWF





Note: The left image has 4-bit depth (16 greyscale values), and the arrows point to dim objects that vanish due to the rescaling of the brightest object (their peak values after rescaling are below 1) the crosses for the center of mass are still there. In the right image with 8-bit depth (256 greyscale values) but scaled to the 97-th brightest percentile, the patterns remain clearly visible.

Render Localized Precision



Localized Precision renders all patterns with the largest localization precision value set in PAL-Filter. This value can be adjusted in the PAL-Filter tab and will be used even if left unticked in PAL-Filter). The same applies to precision in z.





Render Localized Precision



Localized Precision uses the largest localization precision value set in PAL-Filter for all patterns. **The reason for this:** Despite the high precision (e.g. 5 nm) of each individual pattern, this is of little use if the density of patterns is low (i.e. if the object is sparsely labelled or if there are no other patterns nearby to fill the gaps). The resolution therefore must be decreased to appear less spotty.



Less "blur" but more "spotty"

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More "blur" but less "spotty"

Render Best Quality

Only for pixel sizes above 10 nm





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Remark 1: Molecule Density

Warning: Readout may be confusing





Dimensions	Display	Graphics	PAL-Drift	PAL-Grouping	PAL-Statistics	PAL-Filter	PAL-Render
Pixel Resolu		0			- <u>5</u> n		
Display Mode		Molecule	e Density	Ð			
Binning [Pixel]			-0		4		
✔ Render auto dynamic range HR			Scal	e 100,00 🗘 %			
🖌 Render auto dynamic range SWF				e 100,00 🗘 %			

Note 1:

Density is given in "molecules" per square micron (µm²)

(1) "molecules" is the count of fitted events, under the assumption that an event corresponds to a molecule.

(2) To obtain the number of events per pixel bin, the LUT value has to be multiplied by the square of the pixel size times the binning.

For a white pixel in the depicted case: 212500 multiplied by $(0.005\mu m * 4)^2$ - or 0.0004, gives: 85 events per pixel bin

Note 2:

The LUT is affected by brightness and contrast as well as by rendering of the dynamic range. For best results, keep dynamic range at 100% (see red arrows)

All HR 1 SWF 1 Auto Min/Max Best fit 0,40 0 0,40 0	Reset
Black 0 3 Gamma 1,00 3 0.45 1.0	White 65535

Remark 2: Profiles

Overlay and images are offset (known issue as of 9 / 2015).

Profile overlay and image are offset (typically the image is more to the top left)



The red profile line is displayed at the "wrong position"



Remark 3: Gauss + Cross / Gauss + Centroid

Overlay is mismatched (known issue as of 9 / 2015).



Gauss + cross (or Gauss + Centroids) are offset (typically the dots and crosses are more to the top left)



The cross is displayed at the "wrong position"



We make it visible.