Nutshell – PALM Grouping





PALM Grouping Scope and recommended previous knowledge.



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

• single-molecule fluorescence behavior (on/off and blinking)



• positioning accuracy and the involved scales of length



• basic knowledge of the PALM / dSTORM workflow in ELYRA



Overview



1 Why? What is PALM Grouping?

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

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PAL-Drift PAL-Grouping PAL-Statistic	s PAL-Filter PAL-Renderîng	-
Max On Time	1 frames 0 frames	
Capture Radius	1,0 🗘 pixels	
	Group Ungroup	

PALM Grouping *Why group?*



PALM is based on the frame-by-frame localization of single emitter patterns.



Are these patterns coming from the same identical molecule? If so, can I join the information from these positions?



PALM Grouping Tool



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PALM Grouping – Three parameters

Capture radius, Max On Time and Off Gap.



	Dimensions	Display	Graphics	PAL-Grouping		-
2	Max On Tir Off Gap		0		4	framesframes
	Capture Ra	dius	-0-		0,9	🗧 🗧 pixels
-					Group	Ungroup
					Ungrou Undo th	o button: e grouping
				Group b Do the g	outton: grouping	

Data must be drift free or drift corrected (see also PALM-Drift)

- 1 Capture radius: Starting from a given molecule position the SW will look for molecules within only that <u>radius</u> in the time sequence. (This radius is typically around 10 nm).
- 2 Max On Time: After step 1 the time sequence is analyzed. A molecule can be <u>on</u> for this number of subsequent frames. If it is on for <u>longer</u> than this value then it is completely erased.
- **3 Off Gap**: Allows for an off gap (due to e.g. blinking) of this maximum length. If equal or shorter then the sequence is joined. If longer then it is not joined.

PALM Grouping – Capture radius

First of all: Molecule has to be within a small radius.



Max On Time) 4 🗘 frames	Pixel Resolution XY
Off Gap	0 🗘 frames	Display Mode Gauss
Capture Radius	0,9 🗘 pixels	Expansion factor 1,00 🗘 x PSF
	Group Ungroup	✓ Render auto dynamic range HR Scale 95,00 \$ %
		Render auto dynamic range SWF Scale 100,00 🗘 %

Attention! Radius is in units of <u>rendered image pixels</u> (set in the PAL-Render Tab) Here the radius is 9 nm (if pixel resolution is set to 20 nm/pixel, then the radius will be 18 nm) Attention! We assume that the data is drift free !!! (see PAL - Drift)

PALM Grouping – on/off times

Molecules within the radius have an on/off behaviour



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PALM Grouping – on/off times (consecutive)

On/off times are always in <u>consecutive</u> frames



ZEINS

Max On Time sets an upper limit. Removes molecules on for <u>unreasonably long</u> time.





Attention! It affects only consecutive on frames (i.e. green blocks).

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PALM Grouping – Off Gap (consecutive)

Molecules that remain off for too long are unreasonable



Attention! It affects only <u>consecutive</u> frames. Attention! The molecules are SPLIT (not removed).

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1 Why? What is PALM Grouping?

- 2 How does it work? Definitions
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After understanding how **grouping** works, a few questions remain open:

- How important is this step? When do I have to use it?
 - How do I set the values for Capture Radius, Max On Time and Off Gap?

PALM Grouping

Importance and influence of grouping on the data.

ZEISS

(1) Grouping affects the positioning accuracy. A large group results in better precision



(2) To count molecules (e.g. proteins at a binding site) grouping must be used to avoid double counting the same molecule





(3) If the number of molecules is of no relevance, only the structure matters, then grouping may be disregarded.





After understanding how **grouping** works, a few questions remain open:

- How important is this step? When do I have to use it?
 - How do I set the values for Capture Radius, Max On Time and Off Gap?

PALM Grouping – And Statistics

Not easy to find on / off times. Given in Statistics is <u>sum total.</u>

Index	First Frame	Number Frames	Frames Missing	Position X [nm]	Position Y [nm]	Pre [nr
4001	3895	2	0	756.3	906.9	
4002	3911	2	1	1665.2	1867.9	
4003	3929	2	0	2438.7	2830.3	
4004	3929	4	2	931.4	949.8	
4005	3932	2	1	2158.5	2617.8	
4006	3933	3	1	2162.7	2602.6	
4007	3941	2	0	498.4	793.5	
4008	3943	2	2	1809.6	909.3	

PAL-Drift PAL-Statistics PAL-Filter PAL-Rendering						
Display	Table	Statistic Plot	Peak Tracker			
Plot type	Histogram					
Histogram Source	Number Frames					
🖌 Auto Histogram Rang	ge		Scale 100,00 🔹 %			
PAL-Drift PAL-Statistics	PAL-Filter PAL-Rer	nderîng				
PAL-Drift PAL-Statistics	PAL-Filter PAL-Rer Table	nderîng Statistic Plot	Peak Tracker			
PAL-Drift PAL-Statistics Display Plot type	PAL-Filter PAL-Rer Table Histogram	nderîng Statistic Plot	Peak Tracker			
PAL-Drift PAL-Statistics Display Plot type Histogram Source	PAL-Filter PAL-Rer Table Histogram Frames Missing	nderîng Statistic Plot	Peak Tracker			
PAL-Drift PAL-Statistics Display Plot type Histogram Source Auto Histogram Range	PAL-Filter PAL-Rer Table Histogram Frames Missing	nderîng Statistic Plot	Peak Tracker Scale 100,00 🔹 %			

Max On Time ≠ Number Frames Off Gap ≠ Frames Missing

Dimensions	Display	Graphics	PAL-Grouping
		0	
Max On Tin	ne	0	
Off Gap		0	

It is not possible to infer from the statistics what the typical on and off time for the molecules is. This is so because the numbers given are the sum total of all on times and all off times. For an example see next slide.

// H K K

PALM Grouping – And Statistics Not easy to find on / off times. Given is sum total.





✓ Auto Histogram Range

PALM Grouping – And Statistics Not easy to find on / off times. Given is sum total.





Auto Histogram Range

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Frames Missing

PALM Grouping – And Statistics

Not easy to find on / off times. Given in Statistics is <u>sum total.</u>



So how to find on/off times?

- (1) With control specimens: With diluted molecules, so that each molecule can be addressed individually (virtually no spatial overlap) then characterizing on / off times with external software (Origin, MatLab, XL, etc.)
- (2) Try and error: Starting from restrictive settings (small on times, no off gap), gradually increasing on times and then gradually allowing for longer off gaps – then characterizing the histograms (using external software, Origin, MatLab, XL, etc.)



We make it visible.

PALM Grouping – Extreme examples

Special cases that are unlikely to exist





A molecule could be on for 2 frames then blink for 1 frame (like above) indefinetly. In this case there is no maximum number of frames, no maximum number of frames missing.

The statistics don't stop at Max On Time The statistics don't stop at Off Gap

PALM Grouping – Capture radius

Going back to theory... Just a bit





Camera Image

PALM Image

Same Zoom

Each camera pixel is 100 nm in size. The positioning accuracy is much better than that!



PALM / dSTORM (Localization Microscopy)

Molecules may persist over a few frames or blink.



It is reasonable to assume that these highlighted patterns in each frame originate from one molecule. In that case, the retrieved positions can be assigned to one and the same molecule - These patterns can be **grouped**.

ZEX





I want to count molecules. To do that: I need to control grouping properly. Example:

12 molecules or 6?



PALM Grouping *Why group?*



If I want to count molecules, I need to control grouping properly. Example:

12 molecules or 6?

