Torrent Scout Raw Data Analysis

Table of Contents
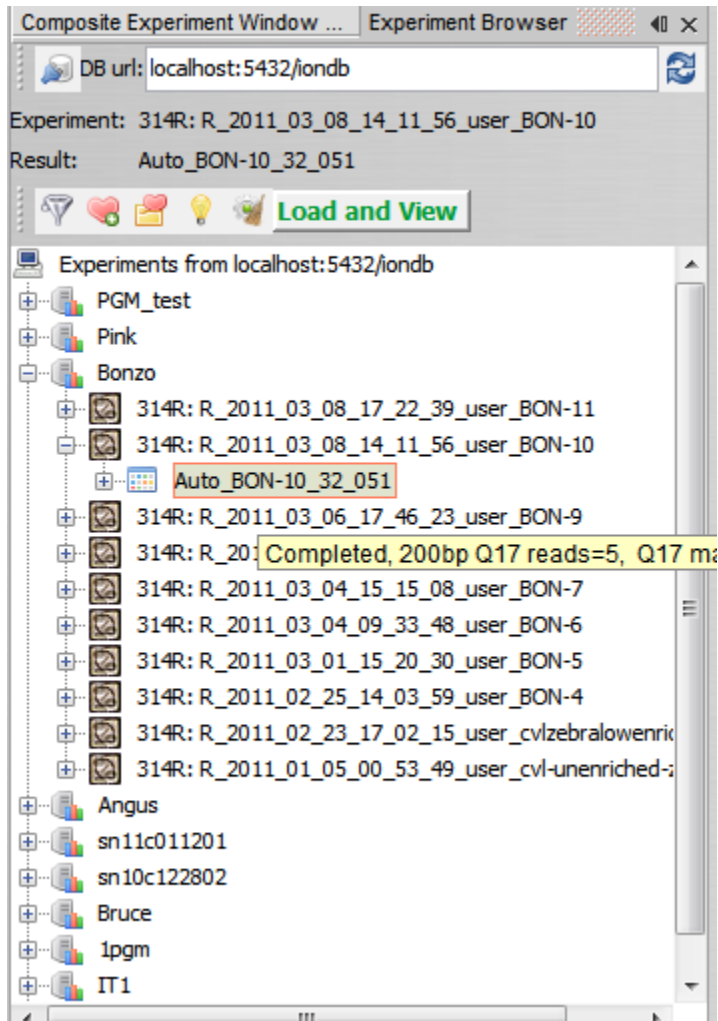
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Summary

This tutorial shows you how to work with raw data and masks.

Opening an Experiment

First, as usual, open an experiment either via database (**Experiment Browser**)

or, if you have an experiment that is not in the database (maybe you only have a raw .dat file), you can use the **Offline Component** to open it (See other tutorials for details).
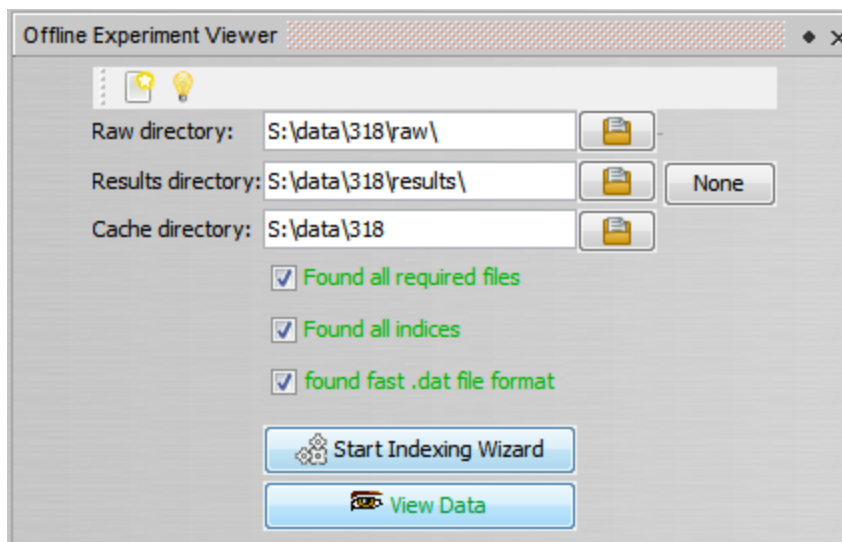
Whole Chip View

In Menu Windows, select the "Whole Chip View" if it is not already open.

Here you can select the frame you want to see, the flow and the type of raw .dat file. The image below shows frame 15 of flow 0 from an acquisition file:
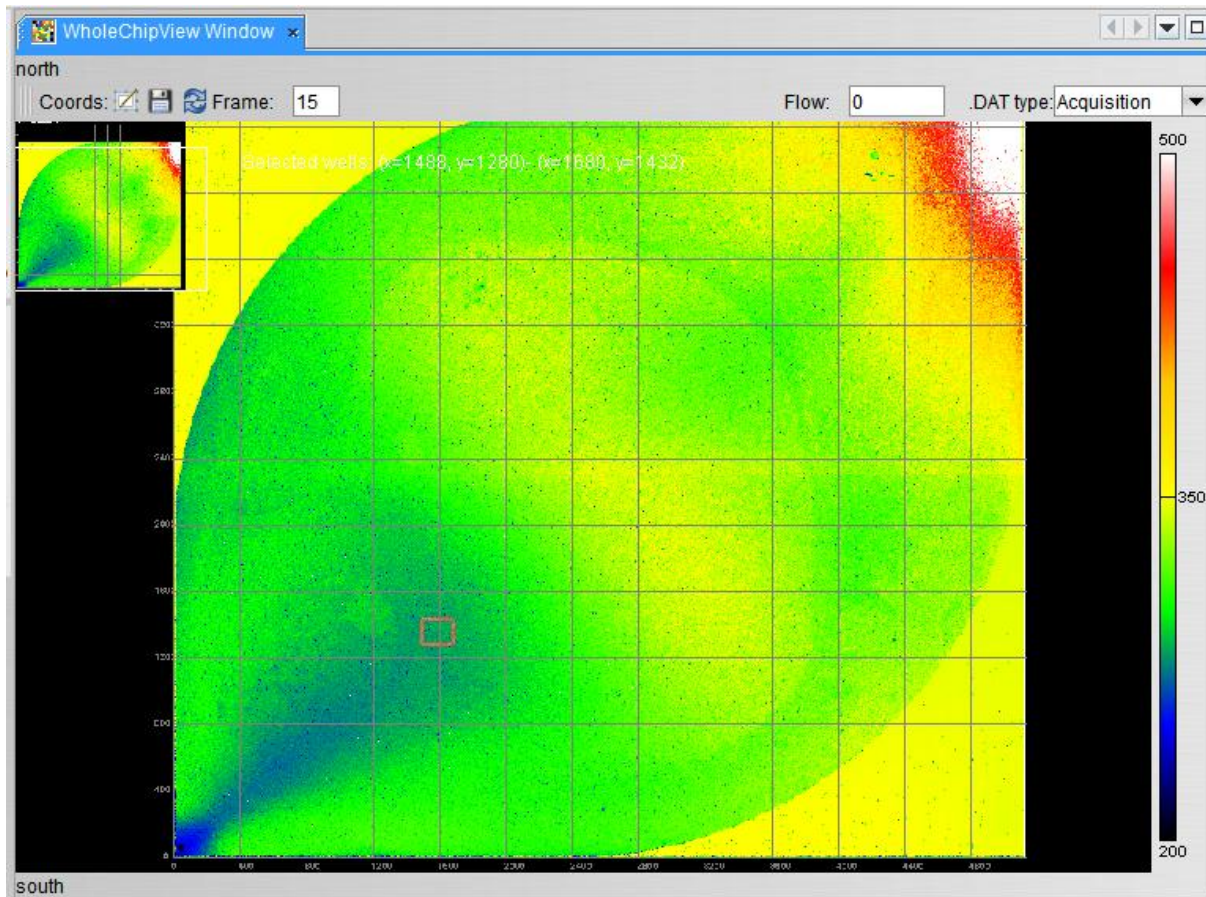
By right clicking into the color gradient on the right you can change the color scale (min/max).

To start looking at raw data, pick an area by clicking into the chip image (or by drawing a rectangle).

It will ask you if you are sure because you might lose already edited masks .

Mask Editor Component

Select Menu Windows/ Mask Editor if not already open. You might want to maximize this component, or drag it to another screen to give it more space.
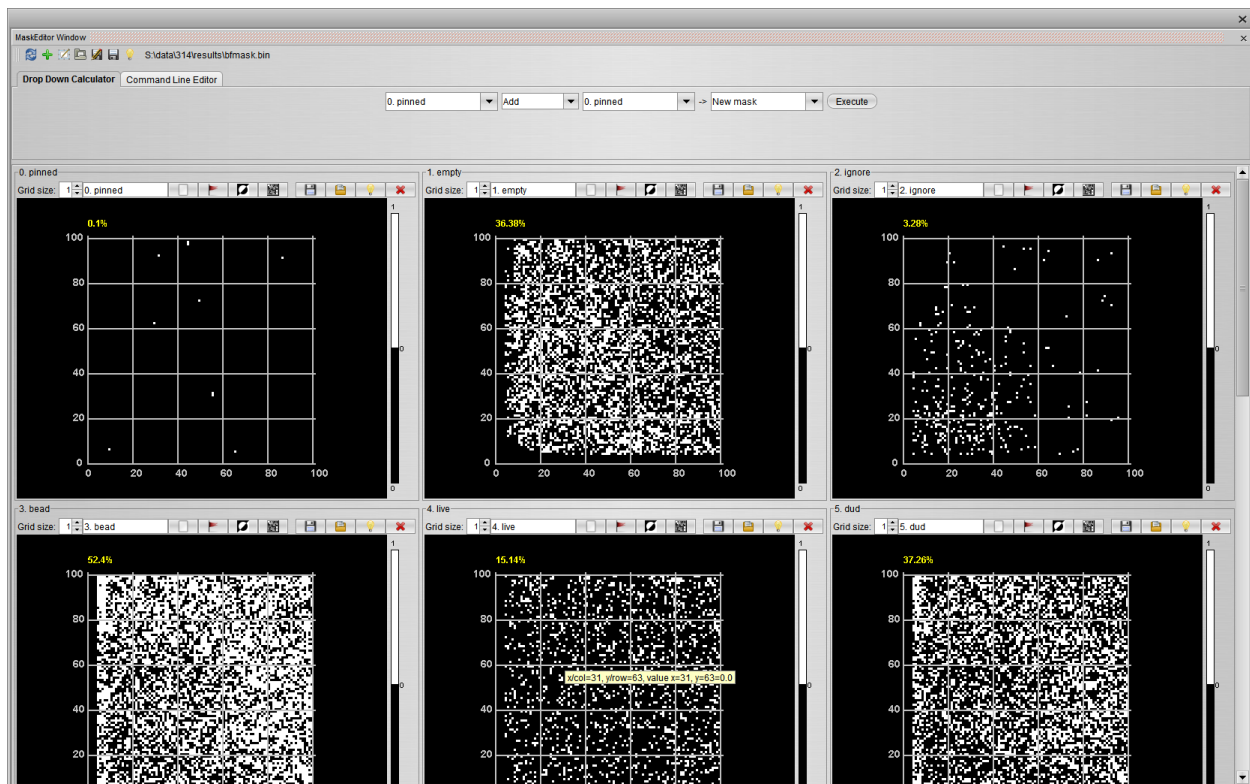
If you do have a bfmask.bin file (in the results folder), it will populate the masks with that data as a start.

If you do not have anything other than the .dat file, it will create two masks, one with pinned pixels, and one the inversion if it.

Operations on one single mask
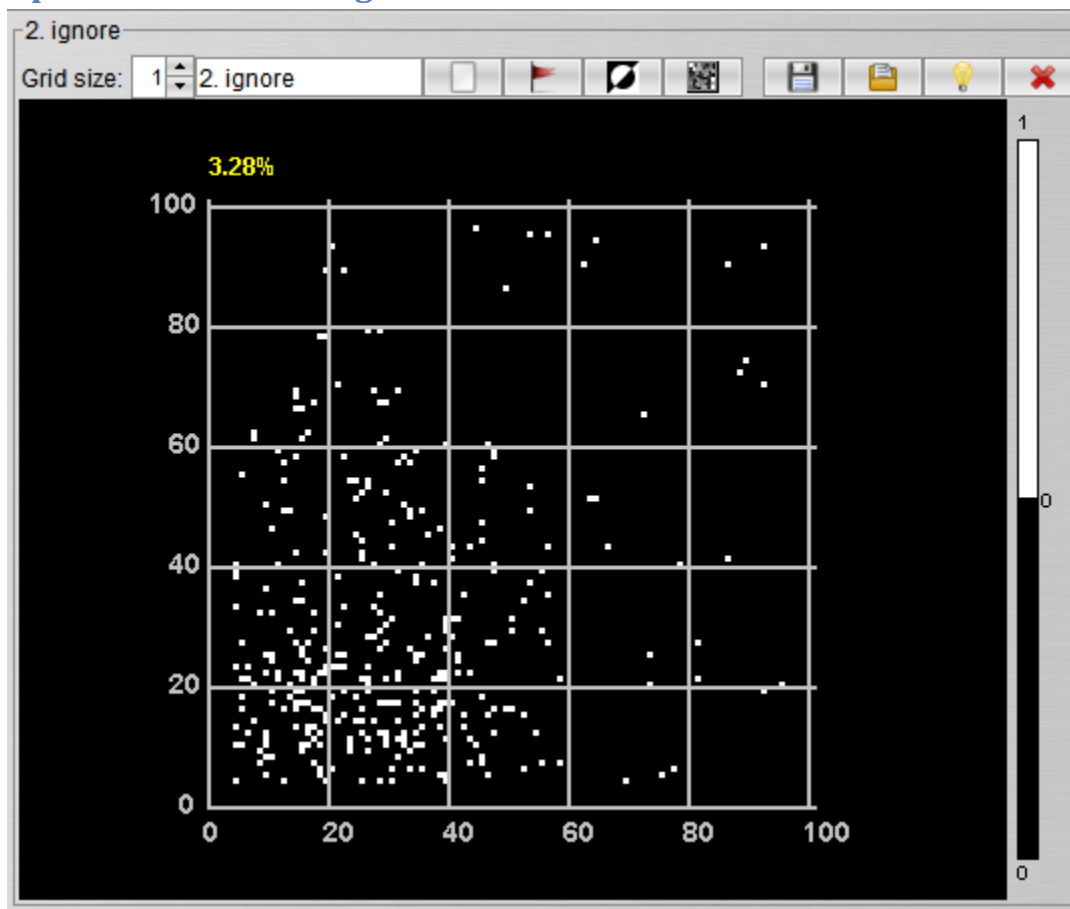
Finding pinned pixels

If you want you can add wells that are pinned, meaning that the signal is either above or below a certain value, or else if the value is the same for all frames.

Use the red flag to find pinned pixels, and enter the values for the limit:

Eingabe ✕

❓ Minimum acceptable value in current data (note: may be nn and OFFSET subtracted...)

-100

OK   Abbrechen
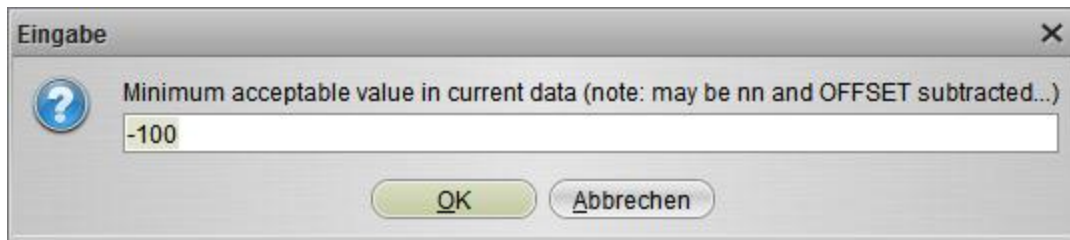
It will tell you how many pixels it has flagged

Nachricht ✕

ℹ️ Flagged 9 additional pixels

OK
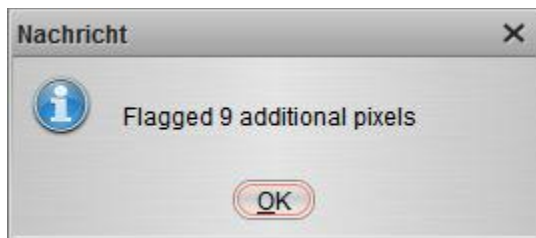
Inverting the mask

The black and white icon inverts the mask

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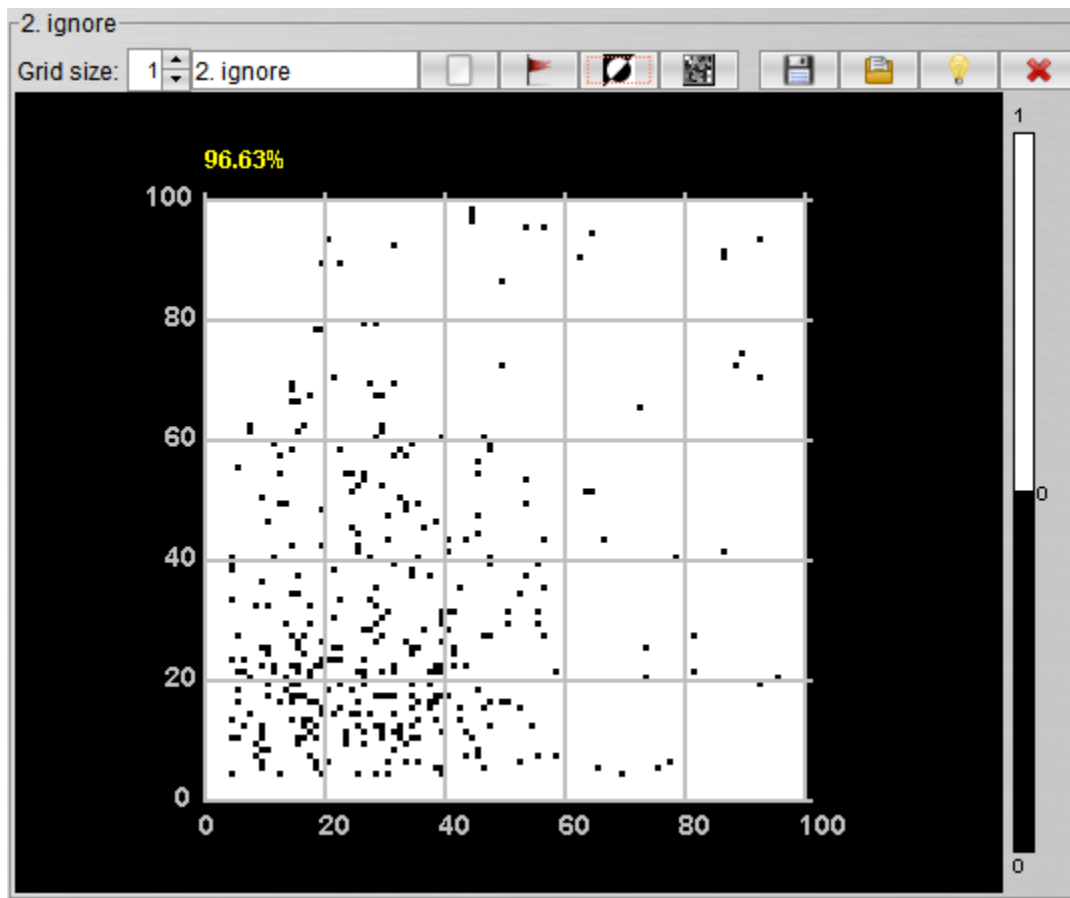
Renaming

Just in the text field to rename the mask (the numbers are optional and are part of the name)

Saving/Loading

You can save and load this particular mask, but you can also save all masks at once in the tool bar of the MaskEditor component. If the coordinate is different when loading, it will ask you if you want to move your view there.

Zooming and other heat map operations

You can do everything you can do with any of the heat maps, including moving the mask around (right mouse button), zooming in and out (wheel), and also selecting wells for viewing in the table (but currently this also moves the selected location to that position).
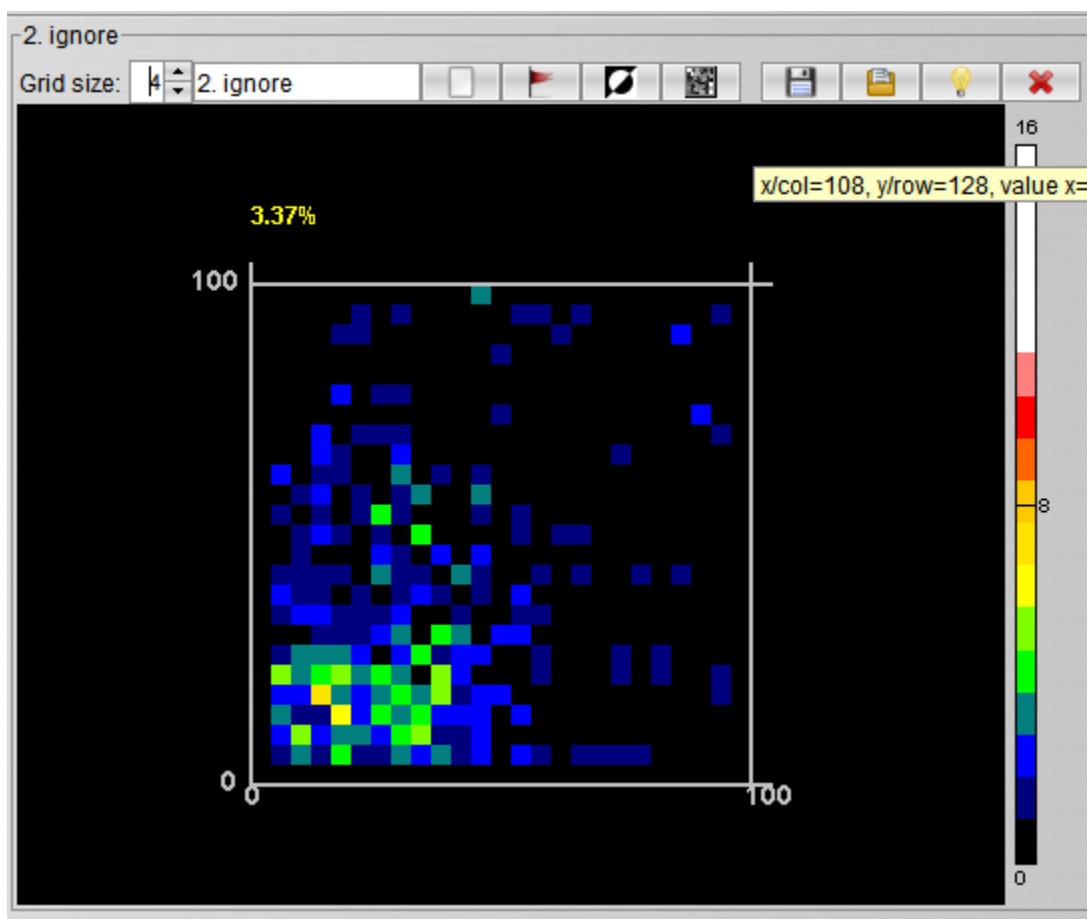
Removing map

You can also remove this map with the x icon from the view

Operations with multiple masks

Drop Down Calculator

In the top Drop Down Calculator you can combine masks in various ways to create new masks or to replace existing masks:
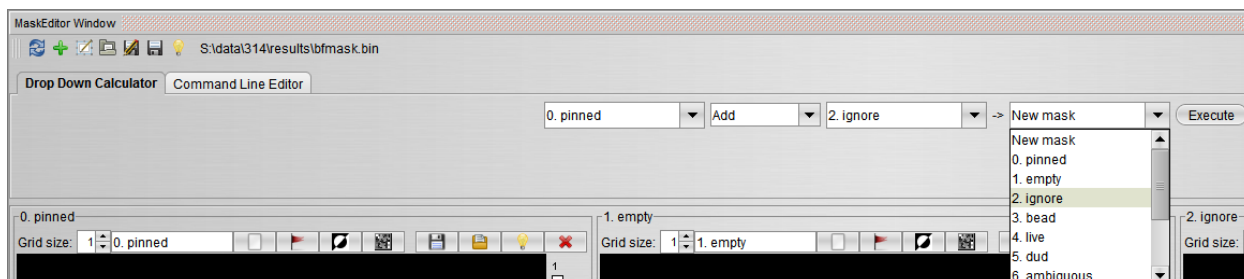
Currently supported operations:

- Not: invert a mask
- Add: combine flags of a mask (Boolean or)
- Subtract: remove flags of one mask from another
- Shift: shift the mask in any direction (used for instance to see if neighboring wells have some effect)
- Intersect: Boolean and
- Copy : just copy the entire mask
- Xor

Command Line Editor

In the command line editor you can type in operations and combine as many operations as you like. There are multiple ways to reference masks, and each operation has multiple accepted versions:

Mask names:

- Use the number as they appear in the gui (starting with 0)
- Use the full name (1. ignore)
- Use the part after a space if there is one (such as ignore of 1. ignore)
- Use the beginning of the name (after the space) – it will use whatever matches first

Use the light bulb icon to see what operations are supported and what the accepted names of them are (such minus, subtract and – for "subtract").

MaskEditor Window — S:\data\314\results\b

Drop Down Calculator | **Command Line Editor**

2 = (0 or 1)

0. pinned

Grid size: 1 | 0. pinned

0.1%

Nachricht

You can do the following things here:

- General commands: new, clear
- Mask names: (say the mask is 1. ignore)
  - you can use the number 1
  - the full mask name 1. ignore
  - just the part aftr the space ignoree
  - just the beginning of the name 1. ig
  (it will pick the first it finds)
- And operation: and, &
- Or operation: or, |
- Plus operation: add, +
- Subtract operation: minus, subtract, -
- Not operation: not, !, ~
- Copy operation: copy, duplicate
- Shift diagonal: shift, diag, shiftdiag;
- Shift left: shiftleft, left, <
- Shift right: shiftright, right, >
- Shift up: shiftup, up, ^
- Shift down: shiftdown, down, v
- Example: ignore = (empty or pinned)
- Example: newbg = (empty minus somemask)
- Example: c = (a | b) & (c | d)
- Example: c = !a and (b > 4) (shifting be to the right by for, combining with not a)
- Example:0 = 0 shift 4 4 (shifting mask by 4 in x and 4 in y direction)

OK

Recreate default masks

If you want to start again fresh with the default masks, or if for some reasons the masks were not loaded properly and are all empty, or for whatever other reason, you can use the blue refresh icon to reload the masks

Storing all masks (and location)

With the load and save icon on top, you can load all masks plus the currently selected coordinate to a file and reload it back later (it has to be for the same experiment).

Process Component

The process component allows you to compute masked neighbor subtraction, view all data of one flow of any file type of a particular area, view the time series of selected wells, overlay masks and specify a function (such as a peak function) to fit the data to (with the Fit component).

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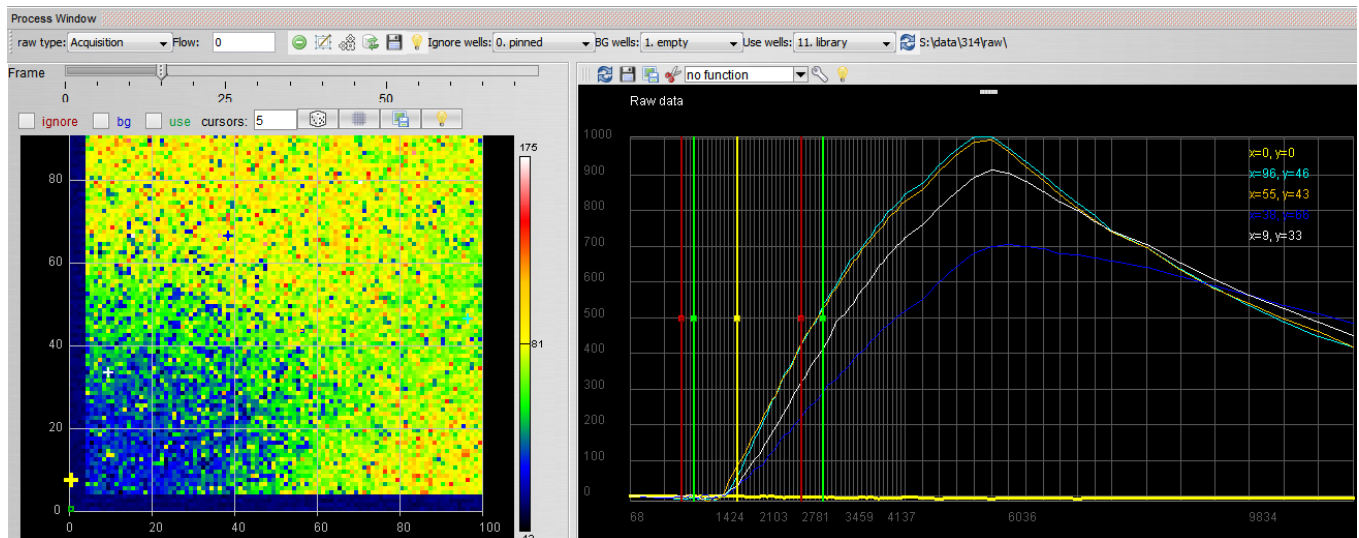
Changing frames

The frame slider on top, and also the yellow vertical line in the time series view moves the frame and updates the graphics immediately:
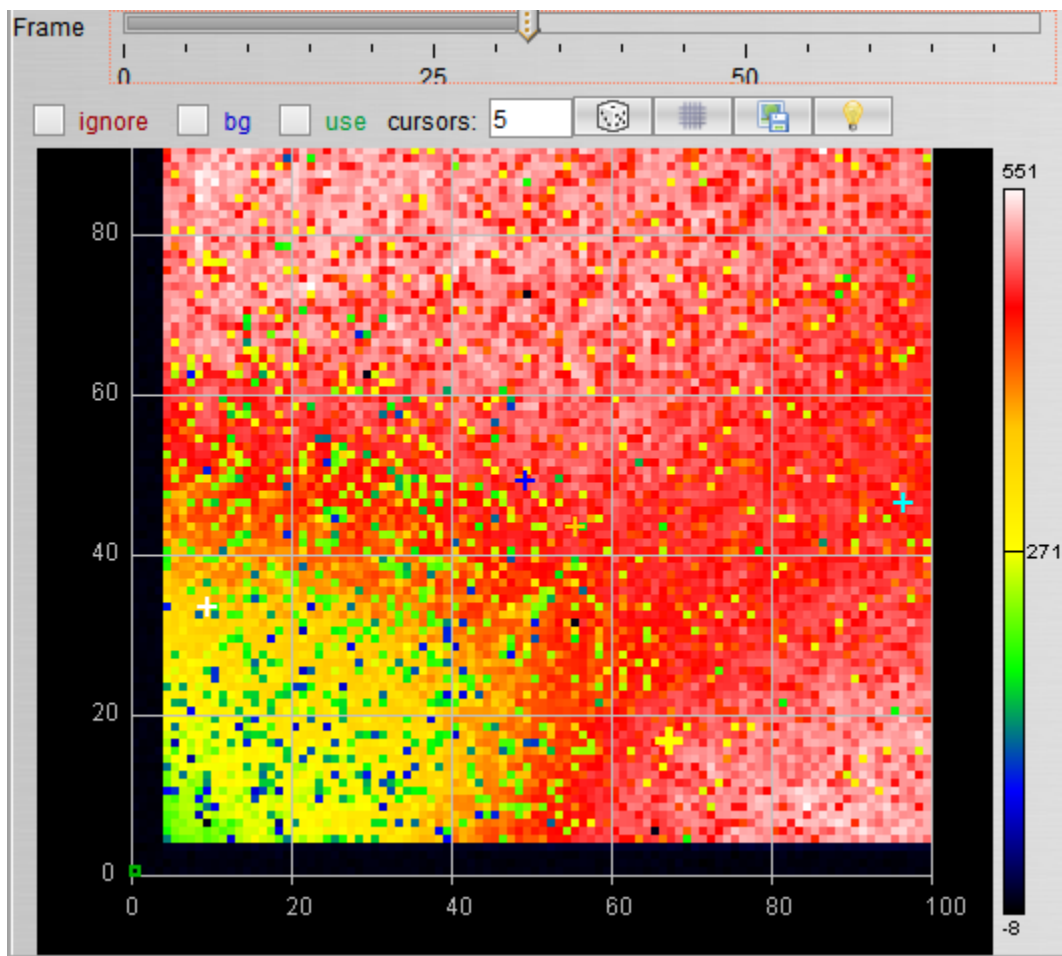
Selecting wells
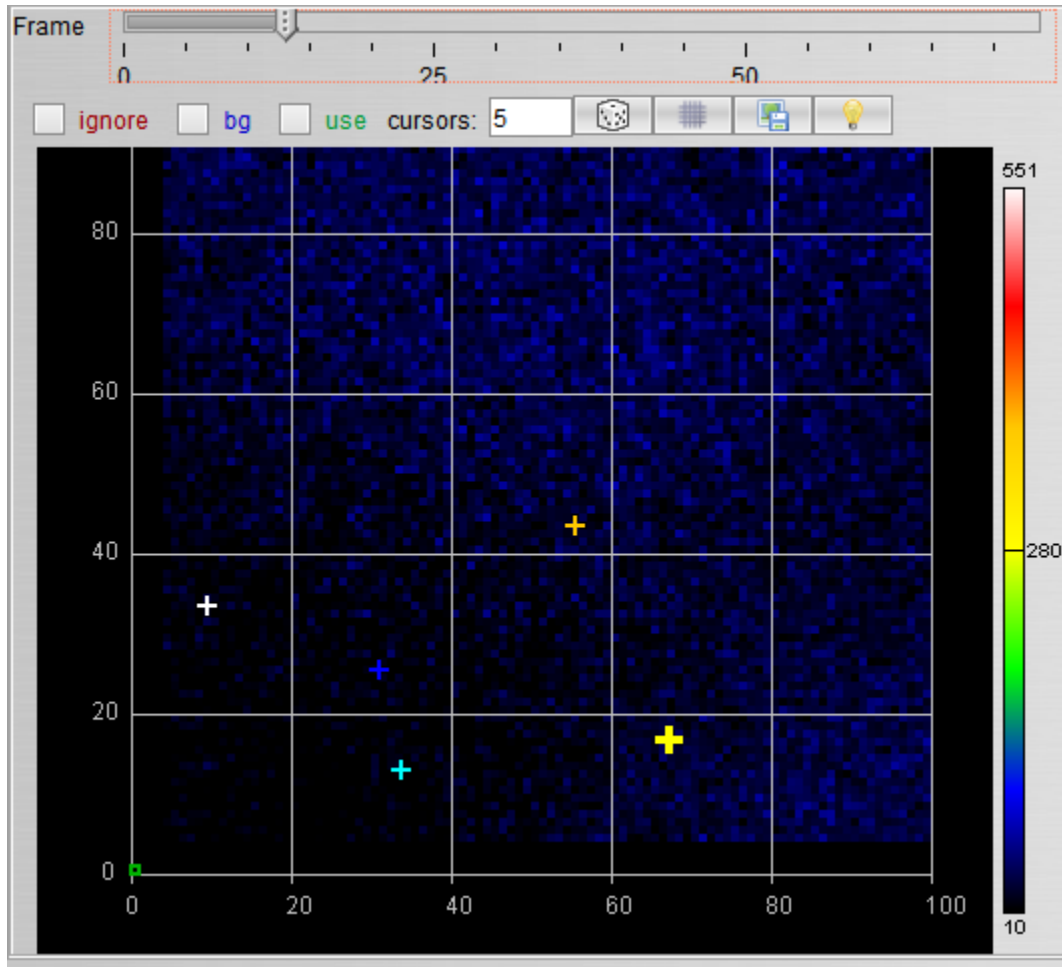
Move the frame so you can see the cursors

Background subtraction

To see the actual signal, the first thing we want to do is subtract the background.

To do this, select a mask in the BG wells dropdown box. Either check it in the mask editor first to see if it looks ok, or else overlay it into the Process area view:

Select the blue check box labeled "bg". This will draw all wells flagged as blue rectangles from the selected bg mask (you might want to move to a frame to see it better, or change the minimum value in the color gradient).

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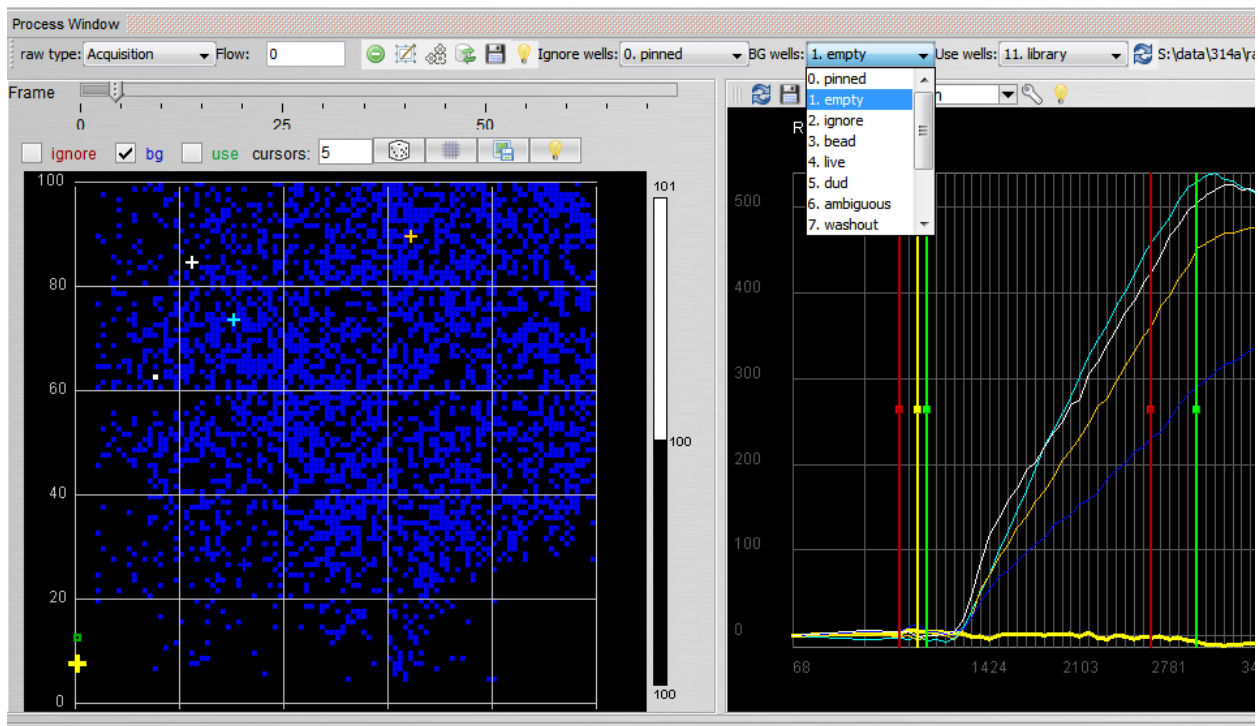
When ready, click the wheels icon to compute the masked neighbor subtraction. It does the following:

- For each well in the entire area, do this:
    - Compute the average signal of all wells +- the span size (see Menu Options/Explorer), which do **not** have the ignore flag and **do** have the flag set in the bg mask.
    - Subtract the average bg signal from the time series data of the current well

The result will look similar to this if you have chosen an acquisition file where you expect an incorporation:

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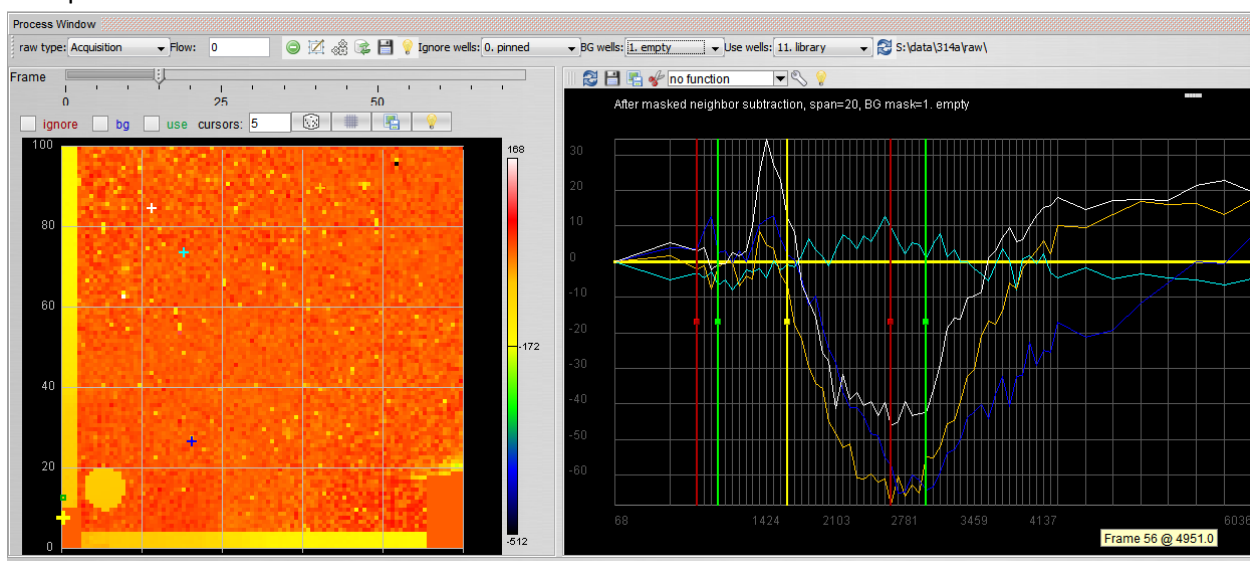
The white, blue and yellow cursors show an incorporation signal, while the light blue/cyan cursor does not.

Pick a "good" mask (such as live wells) in the use wells drop down box, and check the green use check box.

When you now click on the little grid icon, all cursors will snap to the use mask, so you can see only wells that should have a signal:
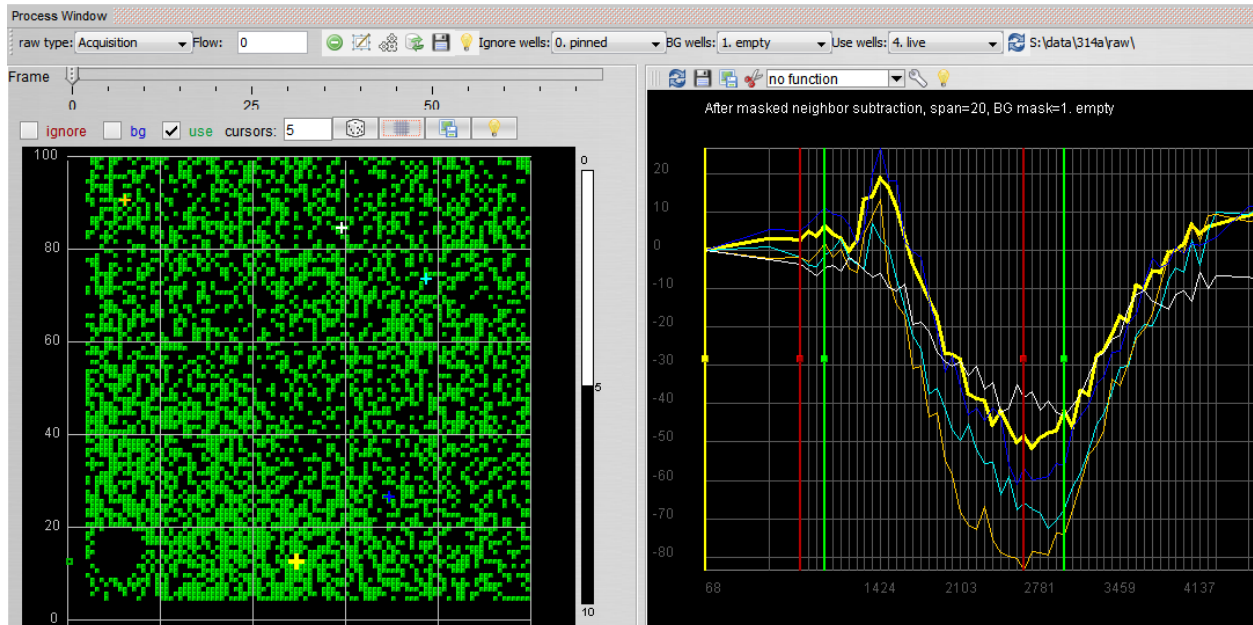
If you click the yellow light bulb icon of the left area view, you get more information on what you can do here:
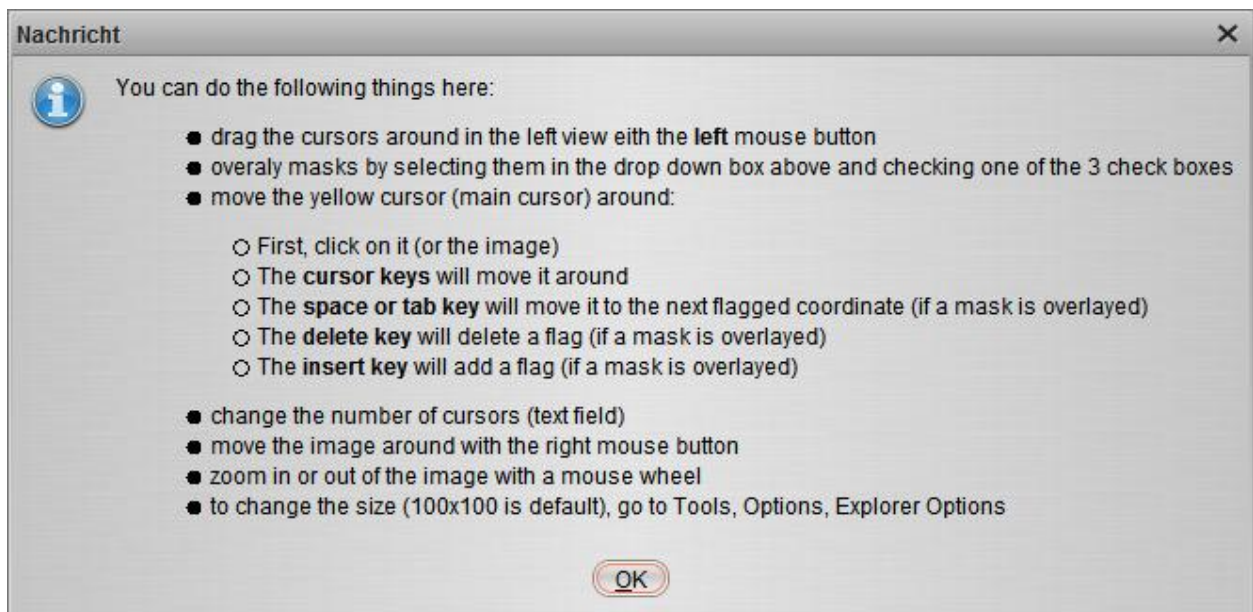
For instance you can move the main cursor around with keyboard cursor keys, and you can change the nr of cursors. For instance in the image below, I have chosen 50 cursors and fit them to a mask that has good signal wells:
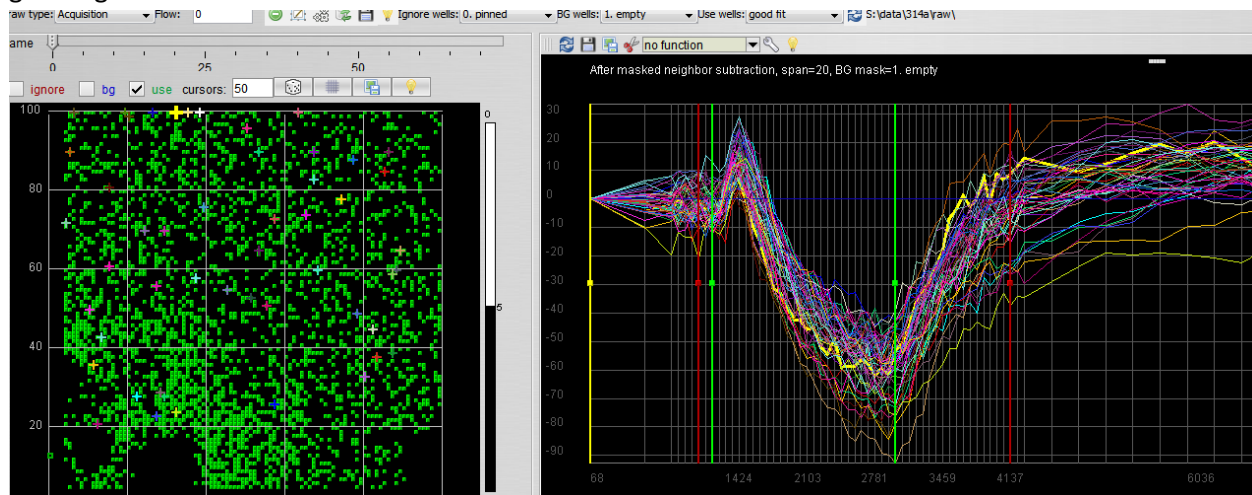
Again to find out more about what you can do on the right side, click the yellow light bulb icon:
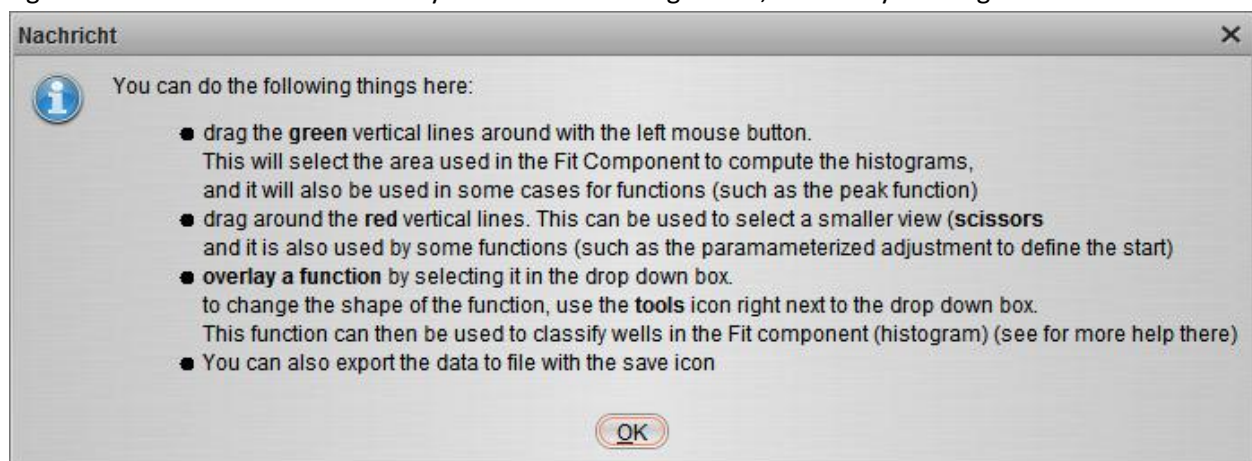
For instance you can overlay a function. Let us overlay both a peak function, and adjust the background. Select the "Peak and Parametric Adjustment" from the drop down box.
A red line appears in the chart:

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After masked neighbor subtraction, span=20, BG mask=1. empty

. To make it fit better to the data, click on the tools icon right next to the drop down box, and select the parametric adjustment function:

Each function can have parameters. The peak function start t0 can be set with the vertical green line. The other parameters can be set either by typing into the text boxes (any value is allowed), or by using

the sliders

Select the parameters for the plot functions   ✕

Peak function	⚪ root mean square of function compared to data ⚪ data minus function value
Parametric Adjust...	
Peak function+Par...	m [0.0050] k [0.0090]
Integral	
max-end height	x-scale [1.3702] y-scale [0.841]
RSM	**Peak function**
count	Compute how well data fits the peak function
slope	[exp(-kt) - exp(-mt)]/(m-k),

where t0 starts at the left **green** frame.
The result in the histogram view is the RMS of the difference

m=0.0050
k=0.0090
x-scale=1.3702
y-scale=0.841

Examples for various t (ms):
  f(0) = 0.0
  f(500) = 0.0
  f(1000) = 0.0
  f(1500) = 44.77062965067427

m	▭▭▭▭▭▭▭▭▭▭	0.0050
k	▭▭▭▭▭▭▭▭▭▭▭	0.0090
x-scale	▭	1.3702
y-scale	▭	0.841

The red function will update immediately as you change the values.

Do the same for the parametric adjustment function so that you get a nice fit as show above.

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## Fit Component

We can now use this function to find wells that fit this function particularly well (or bad).

Go to the fit component. Here, you can pick a function – pick the peak+parametric function that we have adjusted above. Pick a mask (all wells is fine), then to compute the histogram, click on the histogram icon.

To change the min/max in the view, click on the icon with blue-red dots.
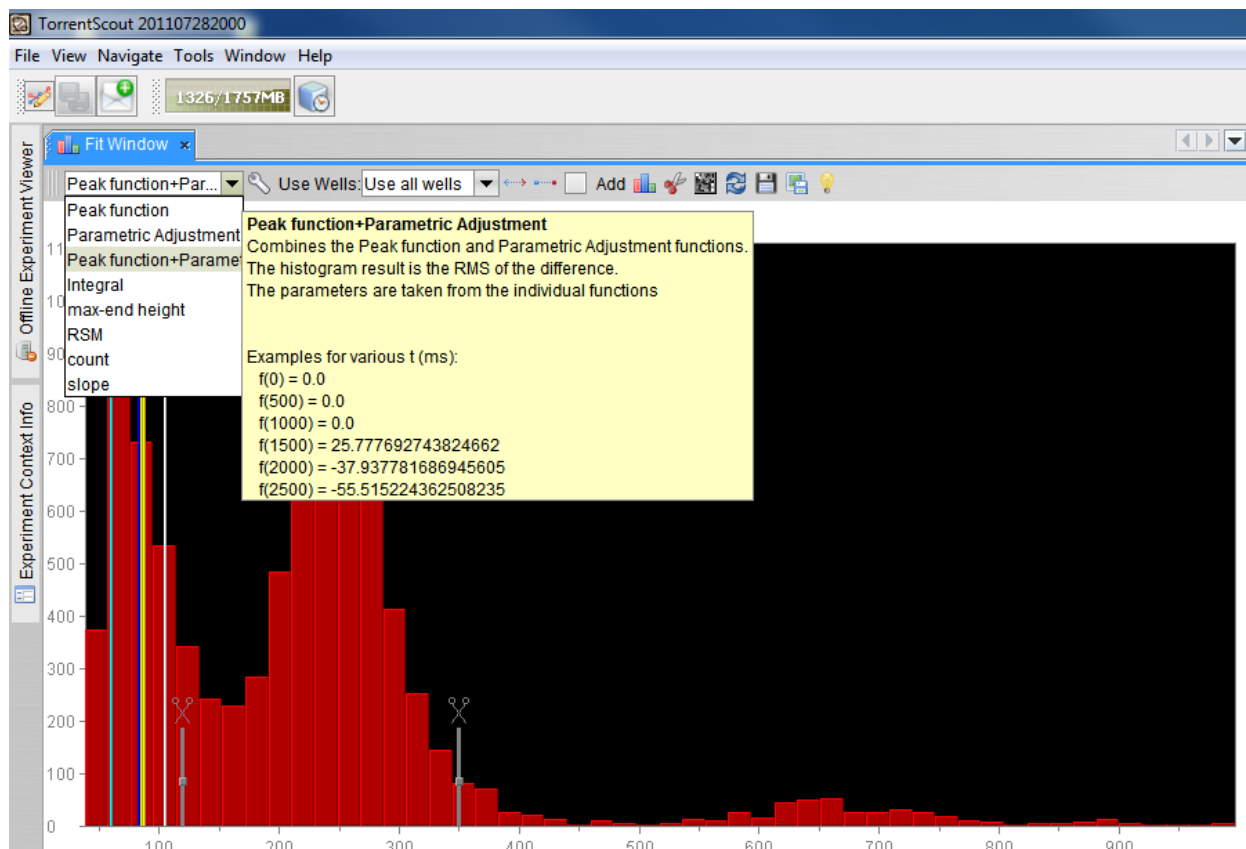
In this example, we have chosen the root of the sum of the error squared. The "error" in this context means the difference between the data (for each well), and the red function that we have adjusted.

So a perfect fit would have a value of 0, quite good fits below 100, and very bad fits have large values.

Notice the vertical colored lines. These are the values of the chosen coordinates. For instance our main yellow coordinate seemed to fit quite well, so it has a low value.

Move the scissors to 0 and say 100. Now we can cut out a portion of the histogram, and create a new mask that we call "good fit". These will include all wells where the RMS of the difference between red function and data is between 0 and 100.

Note that the histogram is computed between the green vertical lines in the Process component.

The green vertical lines define the start and end frame for the computation.

To create a mask with the chosen values, pick the gray/black mask icon and give it a name:
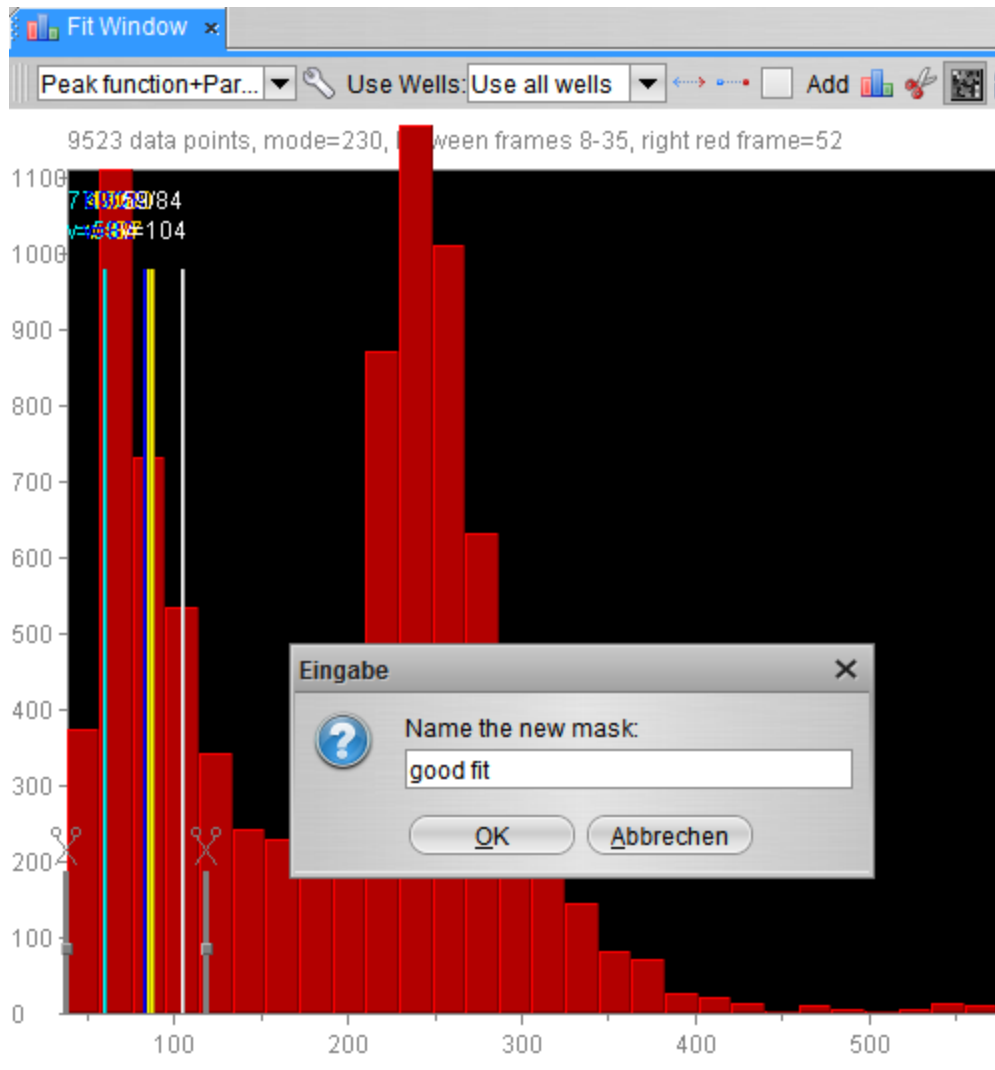
RMS versus difference

In the config panel you can specify how the histogram should be computed for the peak and similar functions. The default is RMS (root mean square), but you can also chose the difference between function and data:
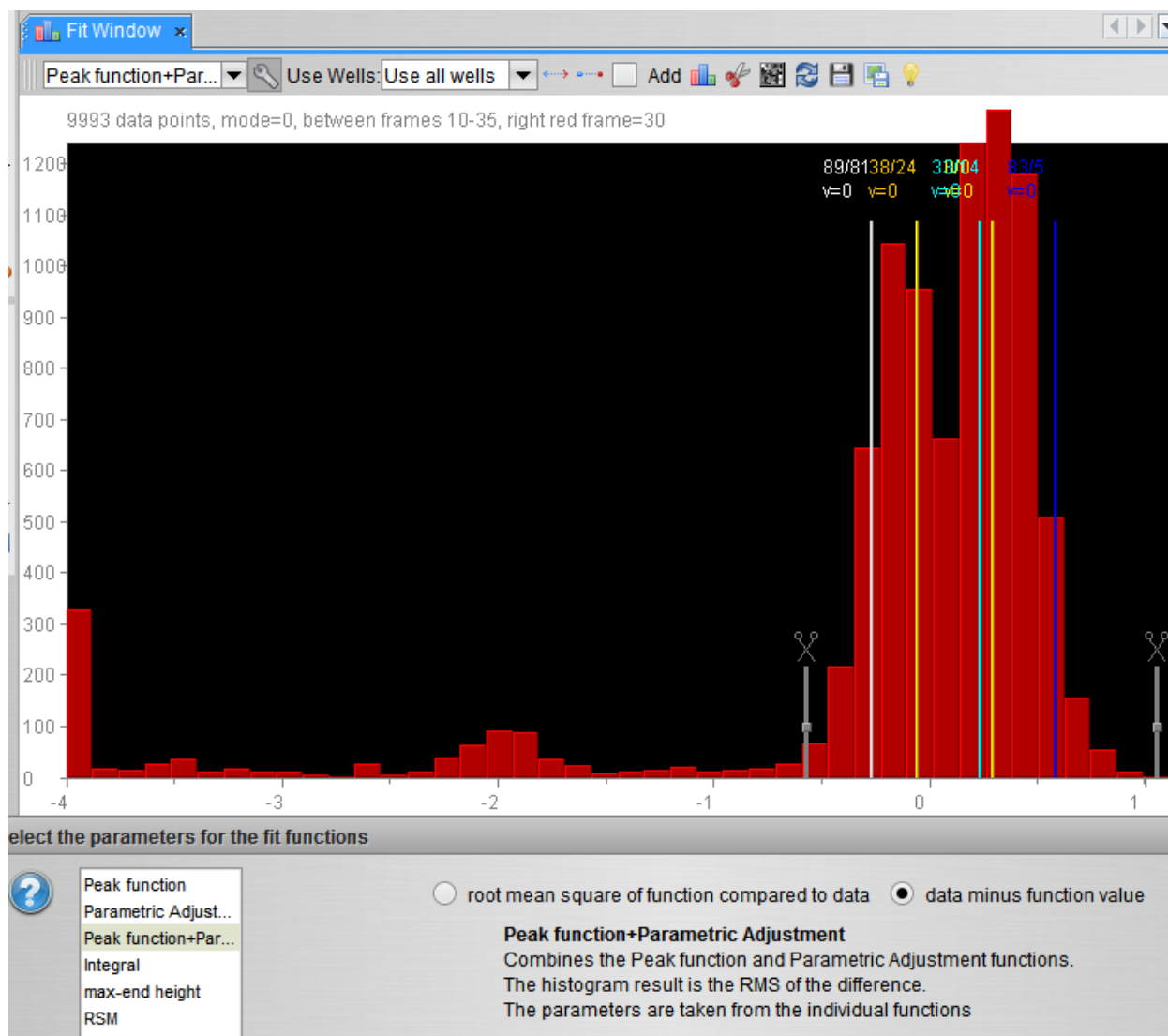
That way you can find data that is better than your red "baseline". In particular for peaks, you might want to find wells that fit your function, but also want to include larger peaks. In the image above, the peak +adjustment function was chosen but with the data minis function value. Our good data lies between -0.5 and 2 (the difference is averaged over the chosen time span).

Overlaying a second histogram

By selecting the add check box, you can overlay a second histogram (blue). In the example below, the red histogram was computed with the live mask, and the blue with the empty mask to see the

difference between the two.
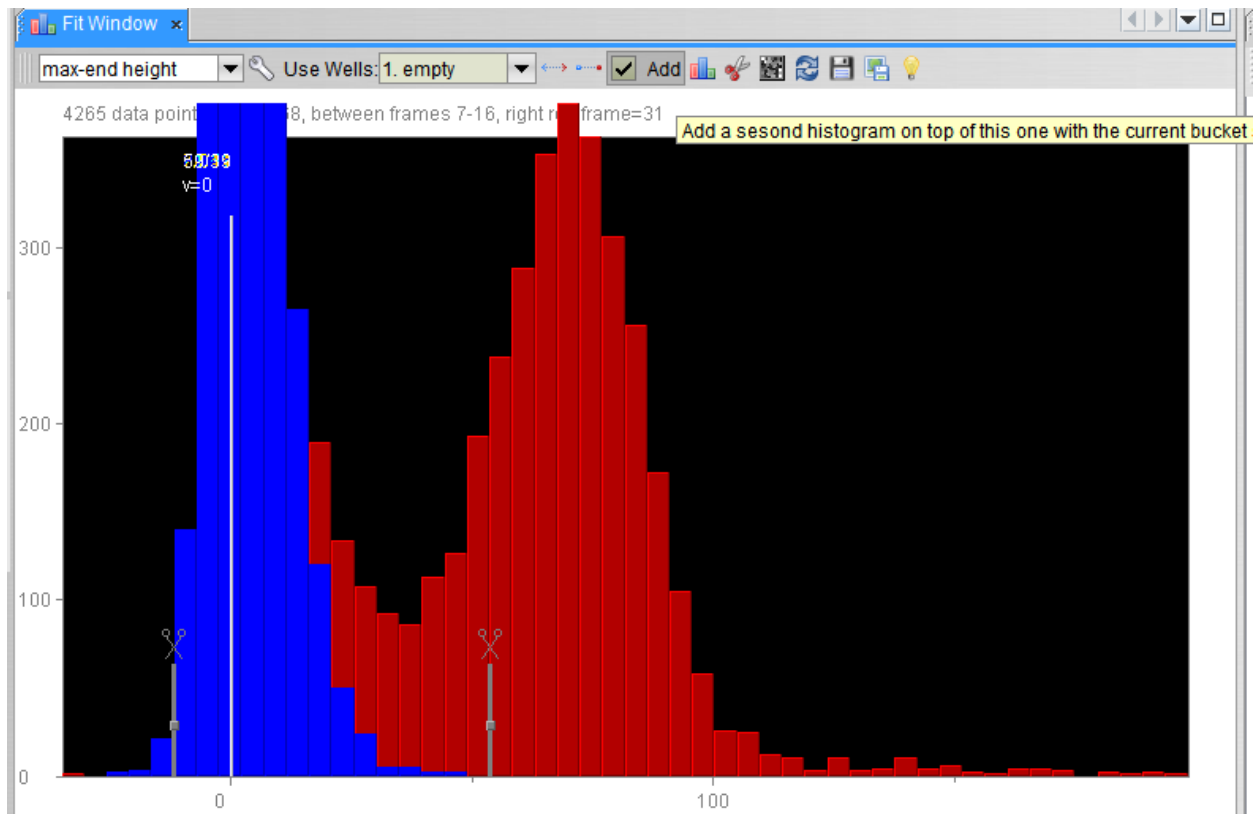
Max – end height

The max – end height function is useful to find peaks: the function takes the maximum value between the two green cursors (the peak), and subtracts the value at the right red frame.

For more tips, use the yellow light bulb icon

Fit Window ×

Peak function+Par... | Use Wells: Use all wells | → ···· □ Add

9523 data points, mode=230, between frames 8-35, right red frame=52

Nachricht ×

ℹ You can do the following things here:

- Pick a function to classify wells.
  Some cases (integral), it will simply compute the value based on the data as you would expect from the name of the function
 Where functions are used such as peak or parameterized adjustment, it will usually compute the **root of the sum of error squared**
  where error means simply the difference between value from the function and value from the data
- You can then move the scissors around to define the area you want to use to create a mask from
- To create a mask with these wells, click on the mask icon. It will then use all wells that are:
  - in the selected mask (from the drop down)
  - and are in the selected range (scissors)
- You can change the min and max x coordinate in the view eith the blue and red line icons
- by clicking the add button, it will add the next histogram to the existing histogram,
  this helps to see differences between functions or between masks
- You can also export the data to file with the save icon
- In menu tools, options, explorer options you can change the y axis (percent or absolute value) and the nr of bins
- with the tools icon you can change the parameters and shapes of some functiosn (see also process component)

OK

Let's now go back to the process component, and look at this new mask we called "good fit":

Pick the mask good fit, select the green use check box, and snap the cursors to this mask to see how well the data fits:
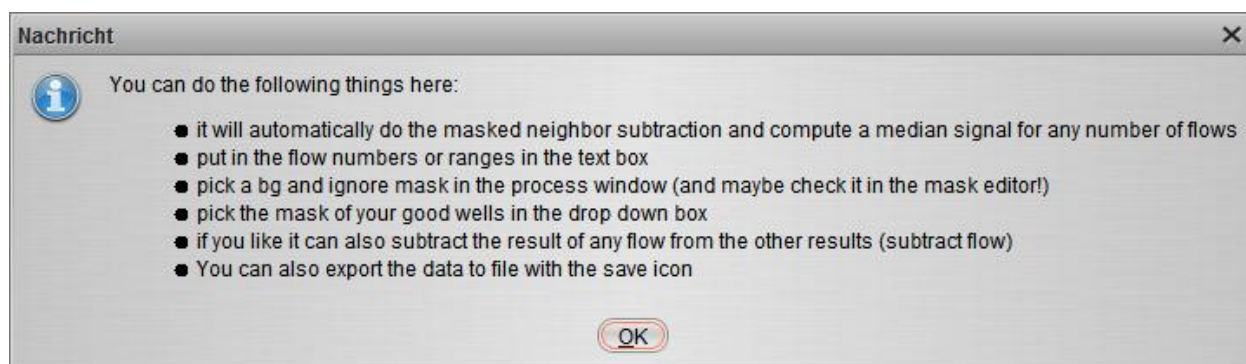
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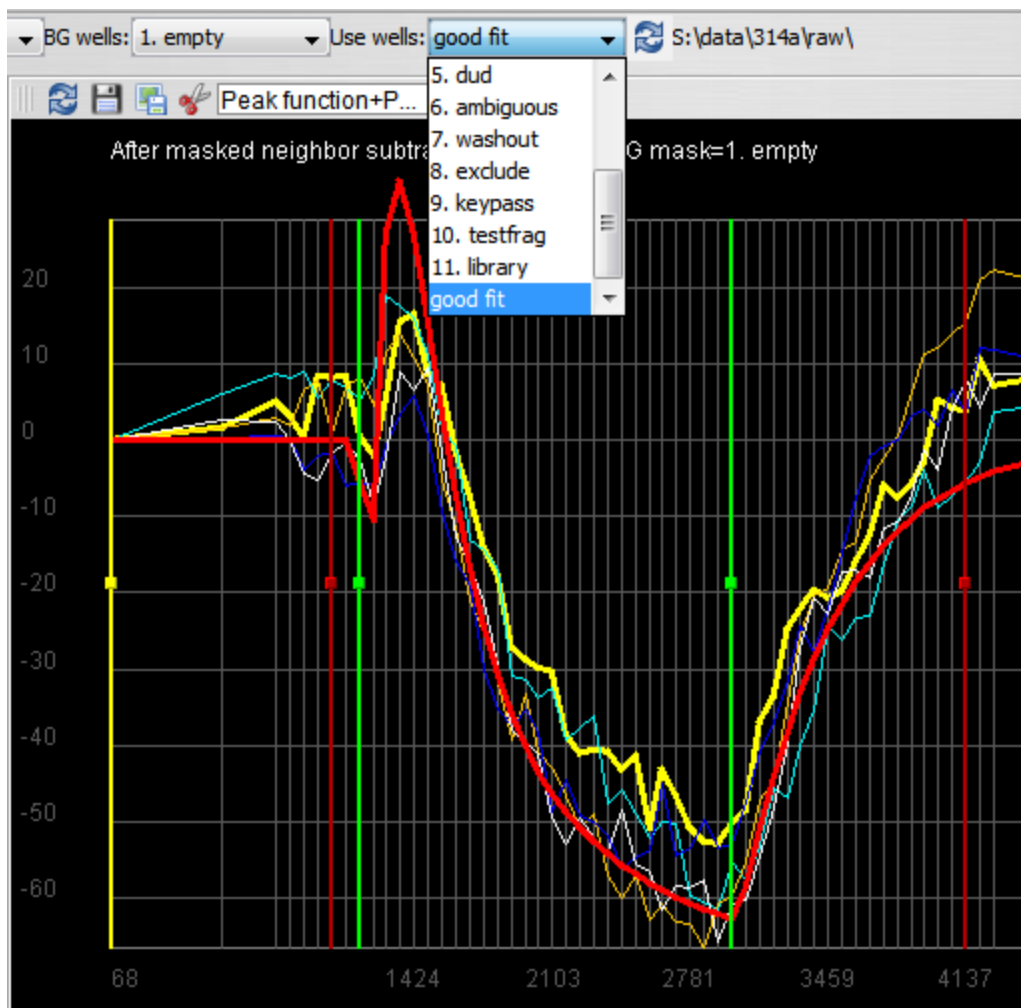
Automate Component

Now that we have found "good wells", we can use those wells to compute the overall mean signal. Select the Windows/Automate Component.
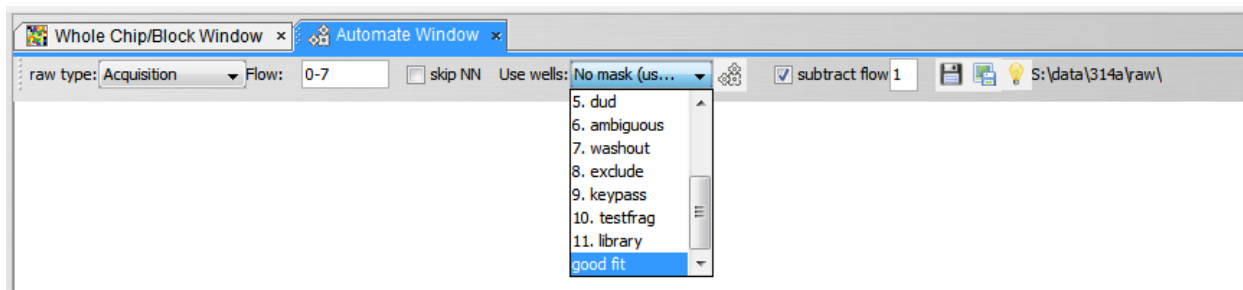
Here you can pick the file type, flows to compute, and what mask to use. Pick the good wells mask.

You can also chose to subtract a flow that has no incorporation signal. The light bulb gives you more information:

Below is the result of computing the signal for 0-2 flows and subtracting flow 0:

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Area 0/0+100, flows 1 2 AC

good fit, 27.47% wells, signal
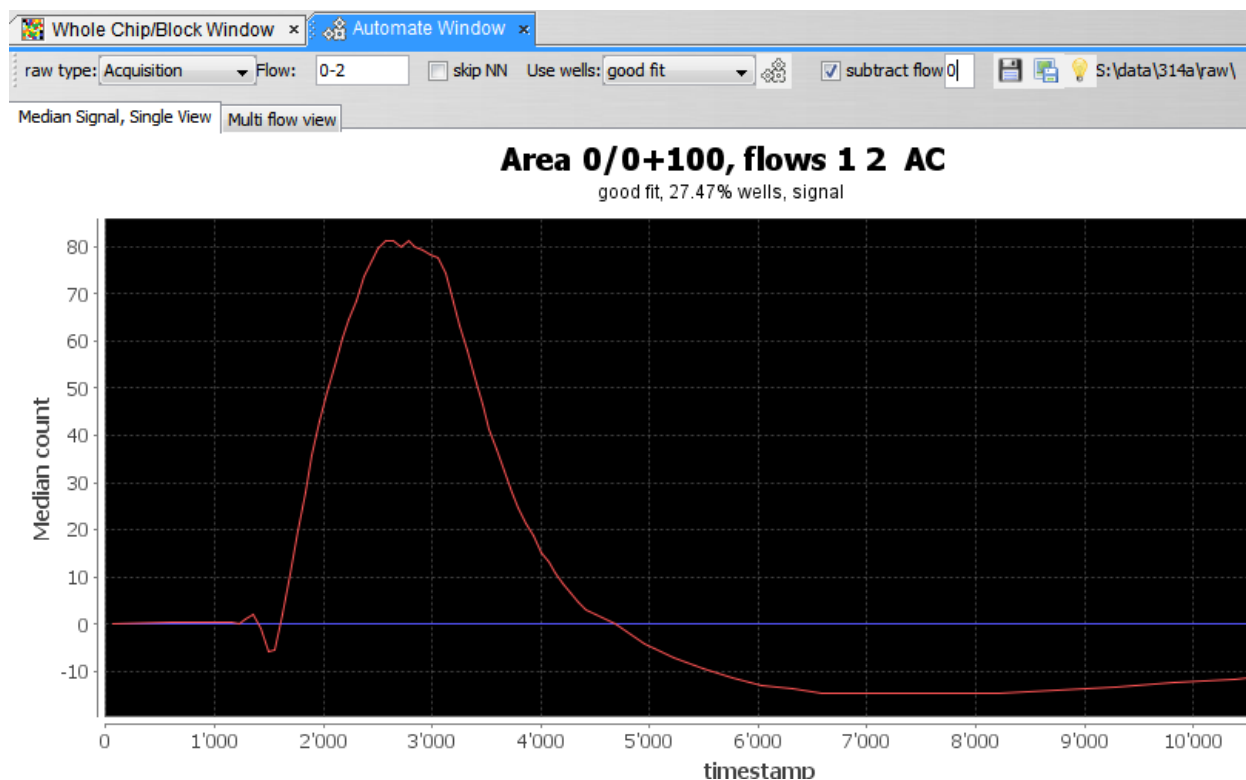
The data can be exported to a file. The second tab can show you multiple flows next to each other

Questions

For questions, suggestions and feedback, please feel free to post a question on the ion community, or contact Chantal.roth@lifetech.com

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