Objects - cell array containing frames

Frame 1 | Frame 2 | Frame 3 | ...

legend:
- class: scalar of single
- class: vector of single
- class: matrix of single
  first row: value
  second row: error
- class: vector of cells
  type: matrix of single

- time [sec] — creation time of the frame
- center_x [nm], center_y [nm] — position of center of object
- com_x [nm], com_y [nm] — center of mass of object (with error)
- orientation [rad] — orientation and error
- length [nm] — total length and its error
- width [nm] — width and its error – averaged for stretched Gauss and filaments, otherwise width of peak
- height [counts] — height and its error – averaged for filaments, otherwise height of peak
- background [counts] — background and its error – averaged for filaments
- data — results from interpolation

data for symmetric Gauss function → empty

data for stretched Gauss function →

axis	width [nm]
major	xxx
minor	xxx

data for symmetric Gauss functions with additional Gaussian rings →

ring	radius [nm]	width [nm]	height [counts]
1	xxx	xxx	xxx
(2)	xxx	xxx	xxx

data for filaments →

point	x-position [nm]	y-position [nm]	distance [nm]	width [nm]	height [counts]	background [counts]
1	xxx	xxx	0	xxx	xxx	xxx
2	xxx	xxx	xxx	xxx	xxx	xxx
...	xxx	xxx	xxx	xxx	xxx	xxx

- widths are given in FWHM values (the units are pixels times the given scaling)
- angles are given in counter-clockwise orientation in the interval [0,2*pi), 0 pointing to the right
- background and height are given in the scale of the input image
- the height is the maximum height of the object at this point minus the background

Molecule – vector of structure containing molecule track data

Molecule 1 | Molecule 2 | Molecule 3 | …

legend:
- class: vector of char
- class: scalar of double
- class: vector of double
- class: matrix of single

- **Name** – name of the molecule
- **File** – filename of the image stack
- **Directory** – directory of the image stack
- **Type** – type of molecule: 'symmetric','stretched','ring1','ring2'
- **Selected** – flag if molecule is selected
- **Visible** – flag if molecule is visible
- **Drift** – flag if molecule is drift corrected
- **PixelSize [nm]** – original size of pixel for scaling
- **Color** – color code of line color for plotting tracks [R G B]
- **Results** – results of complete track as table – see variations for different types

Type='symmetric'

frame	time [sec]	x-position [nm]	y-position [nm]	distance [nm] *(to origin)*	width [nm]	height [counts]	ΔR [nm]
xxx	xxx	xxx	xxx	0	xxx	xxx	xxx
xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx

+

Type='stretched'

width [nm] *(major axis)*	width [nm] *(minor axis)*	orientation [rad]
xxx	xxx	xxx
xxx	xxx	xxx

Type='ring1'

radius [nm] *(inner ring)*	width [nm] *(inner ring)*	height [counts] *(inner ring)*
xxx	xxx	xxx
xxx	xxx	xxx

Type='ring2'

radius [nm] *(outer ring)*	width [nm] *(outer ring)*	height [counts] *(outer ring)*
xxx	xxx	xxx
xxx	xxx	xxx

- **PathData** – results of path statistics

x-position [nm] *(of path)*	y-position [nm] *(of path)*	distance [nm] *(along path)*	sideways [nm] *(to path)*
xxx	xxx	xxx	xxx
xxx	xxx	xxx	xxx

- **PlotHandles** – graphics handles for plotting the tracks

- widths are given in FWHM values (the units are pixels times the given scaling)
- angles are given in counter-clockwise orientation in the interval [0,2*pi), 0 pointing to the right
- background and height are given in the scale of the input image
- the height is the maximum height of the object at this point minus the background

Filament – vector of structure containing filament track data

Filament 1 | Filament 2 | Filament 3 | …

legend:
- class: vector of char
- class: scalar of double
- class: vector of double
- class: matrix of single
- class: vector of cells type: matrix of single

- **Name** — name of the filament
- **File** — filename of the image stack
- **Directory** — directory of the image stack
- **Selected** — flag if molecule is selected
- **Visible** — flag if molecule is visible
- **Drift** — flag if molecule is drift corrected
- **PixelSize [nm]** — original size of pixel for scaling
- **Color** — color code of line color for plotting tracks [R G B]
- **Results** — results of complete track as table – see variations for different types

frame	time [sec]	x-position [nm]	y-position [nm]	distance [nm] *(to origin)*	length [nm]	height [counts]	orientation [rad]
xxx	xxx	xxx	xxx	0	xxx	xxx	xxx
xxx	xxx	xxx	xxx	xxx	xxx	xxx	xxx

- **PosStart** — position of first filament point
- **PosCenter** — position of center filament point
- **PosEnd** — position of last filament point

x-position [nm]	y-position [nm]
xxx	xxx
xxx	xxx

- **Data** — all filament positions and interpolated results – see Objects (page 1)
- **PathData** — results of path statistics

x-position [nm] *(of path)*	y-position [nm] *(of path)*	distance [nm] *(along path)*	sideways [nm] *(to path)*
xxx	xxx	xxx	xxx
xxx	xxx	xxx	xxx

- **PlotHandles** — graphics handles for plotting the tracks

- widths are given in FWHM values (the units are pixels times the given scaling)
- angles are given in counter-clockwise orientation in the interval [0,2*pi), 0 pointing to the right
- background and height are given in the scale of the input image
- the height is the maximum height of the object at this point minus the background