

SIMPLE 2.0 command line dictionary

<i>acf</i>	autocorrelation function
<i>amsklp</i>	automask low-pass limit (in Å)
<i>bin</i>	binarize (yes no)
<i>box</i>	image size in pixels (image assumed to be <i>box*box</i> array)
<i>boxpd</i>	padded box size (default is $2*box$)
<i>center</i>	center(yes no)
<i>clsdoc</i>	Spider format clustering document
<i>cure</i>	cure or not (yes no), for curing NaN:s and normalize
<i>cwd</i>	current working directory
<i>debug</i>	debug mode (yes no)
<i>deterministic</i>	deterministic search (yes no)
<i>discrete</i>	discrete option (yes no)
<i>doalign</i>	do alignment (yes no)
<i>dopca</i>	do PCA (yes no)
<i>doprint</i>	do print (yes no)
<i>e1</i>	first Euler angle
<i>e2</i>	second Euler angle
<i>e3</i>	third Euler angle
<i>edge</i>	edge size for softening molecular envelope (in pixels)
<i>eo</i>	even-odd test (yes no)
<i>even</i>	even (yes no)
<i>fbody</i>	file body (<body>.ext)
<i>filter</i>	filter (yes no)
<i>frac</i>	fraction [0,1]
<i>fromp</i>	from particle index
<i>froms</i>	from state index
<i>gw</i>	Gaussian half width (in pixels)
<i>hp</i>	high-pass limit (in Å)
<i>kmeans</i>	do kmeans (yes no)
<i>local</i>	local refinement (yes no)
<i>lp</i>	low-pass limit (in Å)
<i>matched</i>	use matched Wiener filter (yes no)
<i>maxits</i>	maximum number of iterations
<i>minp</i>	minimum number of particle images (in a cluster)
<i>moldiam</i>	molecular diameter (in Å)
<i>msk</i>	circular or spherical mask radius (in pixels)
<i>mskfile</i>	external mask file (*.spi)
<i>mul</i>	multiplication (scaling) factor (for shifts)
<i>mw</i>	molecular weight (in kD)
<i>navgs</i>	number of averages
<i>ncls</i>	number of clusters
<i>ndiscrete</i>	number of discrete (orientations)
<i>ndocs</i>	number of documents
<i>newbox</i>	new box size

<i>noise</i>	noise (yes no)
<i>noris</i>	number of orientations
<i>norm</i>	normalize (yes no)
<i>npart</i>	number of partitions
<i>npeaks</i>	number of peaks (=number of nonzero orientation weights)
<i>nptcls</i>	number of particle images
<i>nran</i>	number of images in random sample
<i>nspace</i>	number of projection directions in search space
<i>nstates</i>	number of discrete state groups
<i>nthr</i>	number of openMP threads
<i>nvars</i>	number of eigenvectors or hidden variables
<i>nvox</i>	number of voxels
<i>oritab</i>	SIMPLE orientations file (*.txt)
<i>outfile</i>	SIMPLE output file (*.txt)
<i>outstk</i>	output Spider image stack (*.spi suffix required)
<i>outvol</i>	output Spider volume (*.spi suffix required)
<i>part</i>	partition number
<i>pgrp</i>	point-group symmetry (c1, c2, c3, ..., or d1, d2, d3, ...)
<i>phrand</i>	phase randomize (yes no)
<i>phranlp</i>	phase randomization low-pass limit (in Å)
<i>ppca</i>	probabilistic pca (yes no)
<i>ring1</i>	inner ring in polar image representation
<i>ring2</i>	outer ring in polar image representation
<i>rnd</i>	random (yes no)
<i>roalgn</i>	rotational alignment (yes no)
<i>shalgn</i>	shift alignment (yes no)
<i>smpd</i>	sampling distance (in Å)
<i>snr</i>	signal-to-noise ratio
<i>space</i>	space (real fourier)
<i>startit</i>	starting iteration (if different than 1)
<i>state</i>	discrete state group
<i>stk</i>	spider image stack name (*.spi suffix required)
<i>stk2</i>	second spider image stack name (*.spi suffix required)
<i>stk3</i>	third spider image stack name (*.spi suffix required)
<i>tau</i>	temperature parameter
<i>time_per_image</i>	per particle time indicator
<i>top</i>	to particle index
<i>tos</i>	to state index
<i>tres</i>	threshold
<i>trs</i>	origin shift search range parameter [- <i>trs</i> , <i>trs</i>]
<i>trsstep</i>	translation step size
<i>utst</i>	unit test number
<i>var</i>	variance
<i>vol1</i>	spider volume 1 name (*.spi suffix required)
<i>wfun</i>	weighting function or interpolation kernel
<i>winsz</i>	window size for interpolation

zero

zero (yes|no)