Param Structure CellOrganizer v2.0

Training

Minimum requirements: 1. At least 2 single cell images of what you would like to learn a model for (nuc, nuc+cell, nuc+cell+protein). 2. Resolution at which images were acquired.

Training call:

img2slml(dimensionality,dnaPath,cellPath,protPath,param);
Dimensionality = ‘2D’,’3D’
dnaPath,cellPath,protPath = wildcard string (e.g. ‘cell*ch0*.tif’)
Param = struct defined below

Field	**type**	**Allowed values**	**Default value**
Required fields			
model.filename	string	[Anystring,’.mat’]	N/A
model.resolution	1x3double array	Any double 1x3double	N/A
Defaulted fields			
model.downsampling	1x3doublt array	Any double 1x3double	[5,5,1]
nucleus.type	string	(‘medial axis’,’diffeomorphic’)	‘medial axis’
cell.type	string	(‘ratio’,’diffeomorphic’)	‘ratio’
protein.type	string	(‘vesicle’) note: network models training not currently supported	‘vesicle’
protein.cytonuclearflag	string	(‘cyto,‘nuc’,’all’)	‘cyto’
Verbose	boolean	(True,False)	True
Debug	boolean	(True,False)	False

model.proteinUpsampleZ	double	Any double	[]
masks	string	Any string	[]
Display	boolean	(True,False)	False
train.flag	string	(‘all’,’nuclear’,‘framework’)	‘all’
Optional fields			
model.name	string	Any string	[]
model.id	string	Any string	[]
nucleus.name	string	Any string	[]
nucleus.id	string	Any string	[]
cell.name	string	Any string	[]
cell.id	string	Any string	[]
Cell.model	string	Any string	[](not used in current implementation)
protein.name	string	Any string	[]
protein.id	string	Any string	[]
protein.class	string	Any string	[]
documentation.author	string	Any string	[]
documentation.email	string	Any string	[]
documentation.description	string	Any string	[]

Synthesis

Minimum requirements: A valid CellOrganizer model
Synthesis call: slml2img(modelPaths, param);
modelPaths = cell array of paths to models from which to synthesize (e.g. {‘./endosome.mat’, ’./diffeomorphic.mat’})
List of ‘param’ struct fields for synthesis using slml2img.m

Field	type	Allowed values	Default value
Required fields			
Defaulted fields			
targetDirectory	string	Any string	‘./’
prefix	string	Any string	‘demo’
numberOfSynthesizedImages	int	Any int >=1	1
compression	string	(‘none’,’lzw’,’packbits’)	‘none’
debug	boolean	(True,False)	False
display	boolean	(True,False)	False
verbose	boolean	(True,False)	True
microscope	string	(‘none’,’lzw’)	‘none’

synthesis	string	(‘nuclear’,’framework’,’all’)	‘all’
protein.cytonuclearflag	string	(‘cyto’,’nucleus’,’all’)	‘all’
sampling.method	string	(‘disc’,’sampled’)	‘disc’
savePDF	boolean	(True,False)	False
Spherical_cell	boolean	(True,False)	False
Synthesis.diffeomorphic.maximum_iterations	int	Any int	100
randomwalk	Boolean	(True,False)	False
framefolder	string	Any string	[]
walksteps	int	Any int	1
overlapsubsize	double	Any non-negative double	0.3
Overlapthresh	Double	Any non-negative double	2
Optional fields			
sampling.method.density	int	Any int	[]
resolution.cell	1x3 double array	Any 1x3 double array	[]
resolution.objects	1x3 double array	Any 1x3 double array	[]
Instance.cell	2D or 3D binary cell image	Binary valued image	[]

Instance.nucleus		2D or 3D binary nuclear image	Binary valued image	[]
tempdir		string	Any string	'./temp'
Walk_type		string	('brownian','willmore','density')	'willmore'
output		struct of Boolean flags	Fields:(tifimages,indexedimages,SBML,blenderfile,blender.downsample)	True,**(only if no other output specified)**
	tifimages	boolean	(True,False)	[]
	indexedimage	boolean	(True,False)	[]
	SBML	boolean	(True,False)	[]
	blenderfile	boolean	(True,False)	[]**(required if output.blenderfile =True)**
	Blender.downsample	Double	Any non negative double	[]

Parameter fields other than slml2img

Downsample(for syn2blender)	Double or 1xD double array	Any double or 1xD double	1, (only called through syn2blender, not slml2img. Same as param.blender.downsample)
Method (for syn2projection)	string	'mean'	[]
Includenuclear (for slml2report)	Boolean	(True,False)	True
Includecell (for slml2report)	Boolean	(True,False)	True
Includeprot (for slml2report)	Boolean	(True,False)	True