

# Package ‘LOMAR’

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**Type** Package

**Title** Localization Microscopy Data Analysis

**Version** 0.2.1

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**Description** Read, register and compare point sets from single molecule localization microscopy.

**URL** <https://git.embl.de/heriche/lomar>

**Depends** R (>= 3.6.0)

**biocViews**

**Imports** Rcpp, FNN, stats, data.table, parallel, doParallel, foreach,  
proxy, reshape2, pracma, transport, RANN, ff, aws, dbscan,  
EBImage

**LinkingTo** BH (>= 1.78.0-0), Rcpp

**Suggests** testthat

**License** GPL-3

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**ByteCompile** true

**RoxygenNote** 7.1.2

**SystemRequirements** C++14, gmp, fftw3

**NeedsCompilation** yes

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## R topics documented:

apply_transformation . . . . .	2
ary2ps . . . . .	3
circle_hough_transform . . . . .	3
costWd . . . . .	4

cpd . . . . .	5
crop_point_set . . . . .	7
downsample . . . . .	7
find_elbow . . . . .	8
Gaussian_Wd . . . . .	8
get_kernel_matrix . . . . .	9
get_persistence_diagrams . . . . .	10
GMM_Wd . . . . .	11
gradientWd . . . . .	12
icp . . . . .	12
idx2rowcol . . . . .	14
img2ps . . . . .	14
jrmpe . . . . .	15
local_densities . . . . .	17
locprec2cov . . . . .	18
locs2ps . . . . .	18
locs_from_csv . . . . .	19
points2img . . . . .	20
points_from_roi . . . . .	21
point_sets_from_locs . . . . .	21
point_sets_from_tiffs . . . . .	23
ps2ary . . . . .	24
pssk . . . . .	24
q2dr . . . . .	25
q2r . . . . .	25
restore_coordinates . . . . .	26
rotx . . . . .	26
roty . . . . .	27
rotz . . . . .	27
sliced_Wd . . . . .	28
standardize_coordinates . . . . .	28
tr . . . . .	29
wgmmreg . . . . .	29

**Index** **32**

---

apply\_transformation    *apply\_transformation*

---

**Description**

Apply rotation and translation to a point set

**Usage**

apply\_transformation(X, R, t, s)

**Arguments**

X	a point set as an N x D matrix
R	D x D rotation matrix
t	1 x D translation vector
s	scaling factor

**Value**

transformed point set as a N x D matrix

---

 ary2ps

---

*ary2ps*


---

**Description**

Convert a 4d array to a list of 3d point sets. The points are formed by extracting the coordinates of array values strictly above the given cut-off (default 0).

**Usage**

```
ary2ps(ary, bkg = 0)
```

**Arguments**

ary	a 4d array with last dimension indexing instances.
bkg	Extract points for array values strictly above this (default = 0)

**Value**

a list of point sets.

---

 circle\_hough\_transform

---

*Circle Hough transform*


---

**Description**

Extract coordinates of the centres of circles from a 2D image using the Hough transform

**Usage**

```
circle_hough_transform(
  pixels,
  rmin,
  rmax,
  threshold,
  resolution = 360,
  ncpu = 1
)
```

**Arguments**

pixels	input data, either a matrix representing a 2D image or a data frame of signal coordinates with columns x, y. For images, background is expected to be 0 and signal to have positive values.
rmin	minimum search radius.
rmax	maximum search radius.
threshold	score threshold between 0 and 1.
resolution	number of steps in the circle transform (default: 360). This represents the maximum number of votes a point can get.
ncpu	number of threads to use to speed up computation (default: 1)

**Value**

a data frame with columns x, y, r and score

**Examples**

```
point.set <- data.frame(x = c(-9.8, -5.2, 12.5, 2.5, 4.5, 1.3, -0.2, 0.4, 9.3, -1.4, 0.5, -1.1, -7.7),
  y = c(-4.2, 1.5, -0.5, 12, -3, -7.2, 10.9, 6.7, -1.3, 10, 6.7, -6.2, 2.9))
circles <- circle_hough_transform(pixels = point.set, rmin = 3, rmax = 6, resolution = 100,
  threshold = 0.1, ncpu = 1)
```

---

costWd

*costWd*

---

**Description**

Objective function to minimize when using GMMs

**Usage**

```
costWd(Tr, X, Y, CX, CY, w1 = NULL, w2 = NULL, S = NULL)
```

**Arguments**

Tr	Transformation vector as translation vector + rotation (angle in 2d, quaternion in 3d))
X	matrix of means of first GMM (i.e. reference point set)
Y	matrix of means of second GMM (i.e. moving point set)
CX	array of covariance matrices of first GMM such that X[i,] has covariance matrix CX[:,i]
CY	array of covariance matrices of second GMM such that Y[i,] has covariance matrix CY[:,i]
w1	(optional) vector of mixture weights of first GMM.
w2	(optional) vector of mixture weights of second GMM.
S	(optional) array of pre-computed $\sqrt{\text{sqrtm}(\text{CX}[:,i]) \%*\% \text{CY}[:,j] \%*\% \text{sqrtm}(\text{CX}[:,i])}$

**Value**

cost value

---

cpd

*cpd*

---

**Description**

Affine and rigid registration of two point sets using the coherent point drift algorithm. See: Myronenko A., Song X. (2010): "Point-Set Registration: Coherent Point Drift", IEEE Trans. on Pattern Analysis and Machine Intelligence, vol. 32, issue 12, pp. 2262-2275.

**Usage**

```
cpd(
  X,
  Y,
  w = 0,
  weights = NULL,
  scale = FALSE,
  maxIter = 100,
  subsample = NULL,
  tol = 1e-04
)
```

**Arguments**

<code>X</code>	reference point set, a $N \times D$ matrix
<code>Y</code>	point set to transform, a $M \times D$ matrix,
<code>w</code>	noise weight in the range $[0, 1)$
<code>weights</code>	a $M \times N$ matrix of point correspondence weights
<code>scale</code>	logical (default: <code>FALSE</code> ), whether to use scaling
<code>maxIter</code>	maximum number of iterations to perform (default: 100)
<code>subsample</code>	if set, use this randomly selected fraction of the points
<code>tol</code>	tolerance for determining convergence

**Value**

a list of

- `Y`: transformed point set,
- `R`: rotation matrix,
- `t`: translation vector,
- `s`: scaling factor,
- `P`: matrix of correspondence probabilities between the two point sets,
- `sigma`: final variance,
- `iter`: number of iterations performed,
- `converged`: boolean, whether the algorithm has converged.

**Examples**

```
data.file1 <- system.file("test_data", "parasaurolophusA.txt", package = "LOMAR",
  mustWork = TRUE)
PS1 <- read.csv(data.file1, sep = '\t', header = FALSE)
data.file2 <- system.file("test_data", "parasaurolophusB.txt", package = "LOMAR",
  mustWork = TRUE)
PS2 <- read.csv(data.file2, sep = '\t', header = FALSE)
transformation <- cpd(PS1, PS2, maxIter = 10, tol = 1e-3)
## Not run:
# Visualize registration outcome
library(rgl)
plot3d(PS1, col = "blue")
points3d(PS2, col = "green")
points3d(transformation[['Y']], col = "magenta")

## End(Not run)
```

---

crop_point_set	<i>crop_point_set</i>
----------------	-----------------------

---

**Description**

Retain points in the set that are within the given distance from the geometric median of the set. Using the geometric median is more robust than using the centre of mass (i.e. mean).

**Usage**

```
crop_point_set(point.set, size)
```

**Arguments**

point.set	a point set as a matrix with columns x,y,z.
size	vector of distances from the geometric median of the points along each axis. Points are discarded if they are outside the ellipsoid defined by size and centred on the geometric median of the points.

**Value**

point set as a matrix with columns x,y,z.

---

downsample	<i>downsample</i>
------------	-------------------

---

**Description**

Weighted downsampling of a point set. If point weights are not provided, they are computed to be proportional to the local density around each point.

**Usage**

```
downsample(point.set, n = NULL, k = NULL, weights = NULL)
```

**Arguments**

point.set	a point set
n	integer, sample size.
k	integer, number of nearest neighbours to consider to estimate local density
weights	a vector of probability weights

**Value**

a point set

---

find_elbow	<i>find_elbow</i>
------------	-------------------

---

**Description**

Find elbow in a 2D curve represented by a list of ordered values

**Usage**

```
find_elbow(values)
```

**Arguments**

values	vector of values in decreasing order
--------	--------------------------------------

**Details**

This function finds the point with maximum distance from the line between the first and last points. Adapted from StackOverflow: <http://stackoverflow.com/questions/2018178/finding-the-best-trade-off-point-on-a-curve>

**Value**

index and value of the selected point

---

Gaussian_Wd	<i>Gaussian_Wd</i>
-------------	--------------------

---

**Description**

Compute 2-Wasserstein distance between two Gaussian distributions

**Usage**

```
Gaussian_Wd(m1, m2, S1, S2, S = NULL)
```

**Arguments**

m1	mean of first distribution
m2	mean of second distribution
S1	variance of first distribution
S2	variance of second distribution
S	(optional) matrix of pre-computed $\sqrt{\text{S1}}$ %*% $\text{S2}$ %*% $\sqrt{\text{S1}}$

**Value**

distance value



---

```
get_kernel_matrix      get_kernel_matrix
```

---

## Description

Compute kernel/distance matrix between persistence diagrams.

## Usage

```
get_kernel_matrix(  
  Diag = NULL,  
  method = c("sWd", "pssk"),  
  dimensions = NULL,  
  return.dist = FALSE,  
  M = NULL,  
  sigma = NULL,  
  ncpu = 1  
)
```

## Arguments

Diag	list of persistence diagrams as n x 3 matrices
method	which kernel or distance to compute. One of sWd (for sliced Wasserstein kernel) or pssk (for the persistence scale-space kernel)
dimensions	vector of the dimensions of the topological features to consider, if NULL (default) use all available dimensions
return.dist	logical (default: FALSE) for method sWd, whether to return the sliced Wasserstein distance matrix instead of the kernel.
M	number of slices for the sliced Wasserstein kernel
sigma	kernel bandwidth
ncpu	number of parallel threads to use for computation

## Value

a matrix

## Examples

```
PS <- list(data.frame(x = c(2.4, -6.9, 4.6, -0.7, -3.3, -4.9, -3.5, -3.5, 4.2, -7),  
                      y = c(5.7, 1.9, 4.8, 3.4, -3, -2.1, 7.2, 1.8, 6.1, -1.6),  
                      z = c(2.7, -0.1, -0.7, -0.6, 0.4, -1.5, -0.6, -0.9, 2.2, 0.7)),  
           data.frame(x = c(0, 0, 3.1, -5.6, -5, -7.4, -0.7, -7.7, -6.7, 4, 4.2, 0.2, 5.8, 3.9, 3.9),  
                      y = c(6.3, -6.1, -3.5, 4.6, -4.1, 0.3, 8.8, -2.3, 2.9, 3.7, -1.4, -3.9, 5.5, -1.2, -6.7),  
                      z = c(-1.5, 1.7, -0.4, -1.4, 1.8, 1.7, -0.9, -1.8, -0.5, 1.7, 1.3, 0.5, -1.4, 1.6, -0.1)),  
           data.frame(x = c(-9.8, -5.2, 12.5, 2.5, 4.5, 1.3, -0.2, 0.4, 9.3, -1.4, 0.5, -1.1, -7.7),  
                      y = c(-4.2, 1.5, -0.5, 12, -3, -7.2, 10.9, 6.7, -1.3, 10, 6.7, -6.2, 2.9),
```

```

z = c(3.4,-3.8,-1.4,1.8,3.5,2.5,2.6,-4.8,-3.8,3.9,4.1,-3.6,-4))
Dgs <- get_persistence_diagrams(point.sets = PS, maxdimension = 1, maxscale = 5, ncpu = 1)
K <- get_kernel_matrix(Diag = Dgs, method = 'sWd', dimensions = c(0,1), M = 10, sigma = 5)

```

---

```
get_persistence_diagrams
```

```
get_persistence_diagrams
```

---

## Description

Compute persistence diagrams for a list of point sets. By default, compute persistent homology from the Vietoris-Rips filtration. If `use.dtm` is `TRUE`, compute instead the persistent homology of the sublevel set of the distance to measure evaluated over a grid.

## Usage

```

get_persistence_diagrams(
  point.sets = NULL,
  maxdimension = NULL,
  maxscale = NULL,
  use.dtm = FALSE,
  m0 = NULL,
  grid.by = NULL,
  ncpu = 1
)

```

## Arguments

<code>point.sets</code>	list of point sets, each as a data frame with columns <code>x,y,z</code>
<code>maxdimension</code>	maximum dimension of the homological features to be computed
<code>maxscale</code>	limit of the Vietoris-Rips filtration
<code>use.dtm</code>	logical (default: <code>FALSE</code> ), whether to use the distance to measure function
<code>m0</code>	parameter for the dtm function
<code>grid.by</code>	vector of space between points of the grid for the dtm function along each dimension
<code>ncpu</code>	number of parallel threads to use for computation

## Value

a list of persistence diagrams as  $n \times 3$  matrices. Each row is a topological feature and the columns are dimension, birth and death of the feature.

**Examples**

```
PS <- list(data.frame(x = c(2.4, -6.9, 4.6, -0.7, -3.3, -4.9, -3.5, -3.5, 4.2, -7),
  y = c(5.7, 1.9, 4.8, 3.4, -3, -2.1, 7.2, 1.8, 6.1, -1.6),
  z = c(2.7, -0.1, -0.7, -0.6, 0.4, -1.5, -0.6, -0.9, 2.2, 0.7)),
  data.frame(x = c(0, 0, 3.1, -5.6, -5, -7.4, -0.7, -7.7, -6.7, 4, 4.2, 0.2, 5.8, 3.9, 3.9),
  y = c(6.3, -6.1, -3.5, 4.6, -4.1, 0.3, 8.8, -2.3, 2.9, 3.7, -1.4, -3.9, 5.5, -1.2, -6.7),
  z = c(-1.5, 1.7, -0.4, -1.4, 1.8, 1.7, -0.9, -1.8, -0.5, 1.7, 1.3, 0.5, -1.4, 1.6, -0.1)))
Diags <- get_persistence_diagrams(point.sets = PS, maxdimension = 1, maxscale = 5, ncpu = 1)
```

GMM\_Wd

*GMM\_Wd***Description**

Compute 2-Wasserstein distance between two Gaussian mixture models See: Delon J, Desolneux A. (2019) A Wasserstein-type distance in the space of Gaussian Mixture Models. hal-02178204v2

**Usage**

```
GMM_Wd(m1, m2, S1, S2, w1 = NULL, w2 = NULL, S = NULL)
```

**Arguments**

m1	matrix of means of first GMM
m2	matrix of means of second GMM
S1	array of covariance matrices of first GMM such that m1[i,] has covariance matrix S1[,i]
S2	array of covariance matrices of second GMM such that m2[i,] has covariance matrix S2[,i]
w1	(optional) vector of mixture weights of first GMM.
w2	(optional) vector of mixture weights of second GMM.
S	(optional) array of pre-computed $\sqrt{\text{sqrtm}(\text{sqrtm}(S1[,i]) \%*\% S2[,j] \%*\% \text{sqrtm}(S1[,i]))}$

**Value**

list of distance value d and optimal transport matrix ot

---

 gradientWd

*gradientWd*


---

### Description

Gradient of the objective function with respect to rotation and translation parameters

### Usage

```
gradientWd(Tr, X, Y, CX, CY, w1 = NULL, w2 = NULL, S = NULL)
```

### Arguments

Tr	Transformation vector as translation vector + rotation (angle in 2d, quaternion in 3d))
X	matrix of means of first GMM (i.e. reference point set)
Y	matrix of means of second GMM (i.e. moving point set)
CX	array of covariance matrices of first GMM such that X[i,] has covariance matrix C1[:,i]
CY	array of covariance matrices of second GMM such that Y[i,] has covariance matrix C2[:,i]
w1	(optional) vector of mixture weights of first GMM.
w2	(optional) vector of mixture weights of second GMM.
S	(optional) array of pre-computed $\sqrt{\text{C1}[i,j] \%*\% \text{C2}[i,j] \%*\% \text{C1}[i,j]}$

### Value

gradient vector

---

icp

*icp*


---

### Description

Rigid registration of two point sets using the iterative closest point algorithm.

**Usage**

```
icp(
  X,
  Y,
  weights = NULL,
  iterations = 100,
  subsample = NULL,
  scale = FALSE,
  tol = 0.001
)
```

**Arguments**

X	reference point set, a N x D matrix
Y	point set to transform, a M x D matrix,
weights	vector of length nrow(Y) containing weights for each point in Y. Not implemented.
iterations	number of iterations to perform (default: 100)
subsample	if set, use this randomly selected fraction of the points
scale	logical (default: FALSE), whether to use scaling.
tol	tolerance for determining convergence

**Value**

a list of

- Y: transformed point set, a M x D matrix,
- R: rotation matrix,
- t: translation vector,
- s: scaling factor,
- iter: number of iterations performed,
- conv: boolean, whether the algorithm has converged.

**Examples**

```
data.file1 <- system.file("test_data", "parasaurolophusA.txt", package = "LOMAR",
  mustWork = TRUE)
PS1 <- read.csv(data.file1, sep = '\\t', header = FALSE)
data.file2 <- system.file("test_data", "parasaurolophusB.txt", package = "LOMAR",
  mustWork = TRUE)
PS2 <- read.csv(data.file2, sep = '\\t', header = FALSE)
transformation <- icp(PS1, PS2, iterations = 10, tol = 1e-3)
## Not run:
# Visualize registration outcome
library(rgl)
plot3d(PS1, col = "blue")
```

```

points3d(PS2, col = "green")
points3d(transformation[['Y']], col = "magenta")

## End(Not run)

```

---

idx2rowcol

*idx2rowcol*


---

### Description

Convert indices into a dist object to row, column coordinates of the corresponding distance matrix

### Usage

```
idx2rowcol(idx, n)
```

### Arguments

idx	vector of indices
n	size of the n x n distance matrix

### Value

a matrix with two columns nr and nc

---

img2ps

*img2ps*


---

### Description

Read an image into a point set. The points are formed by extracting the coordinates of voxel values strictly above the given cut-off (default 0).

### Usage

```
img2ps(img = NULL, bkg = 0, crop.size = NULL)
```

### Arguments

img	either a 2d or 3d array or a path to a file containing a 2d or 3d image.
bkg	Extract points for values strictly above this (default = 0).
crop.size	vector (of length 2 or 3) containing the desired reduced size of the images along each dimension, e.g. c(30,30,30).

**Value**

a point set as matrix with columns x,y[,z]

**Examples**

```
img.file <- system.file("test_data/img", "alien1_3d.tif", package = "LOMAR",
  mustWork = TRUE)
point_set <- img2ps(img = img.file, bkg = 0)
```

---

 jrmpc

*jrmpc*


---

**Description**

Joint registration of multiple point sets See: G. D. Evangelidis, D. Kounades-Bastian, R. Horaud, and E. Z. Psarakis. A generative model for the joint registration of multiple point sets. In European Conference on Computer Vision, pages 109–122. Springer, 2014

**Usage**

```
jrmpc(
  V,
  C = NULL,
  K = NULL,
  g = NULL,
  initialPriors = NULL,
  updatePriors = TRUE,
  maxIter = 100,
  fixedVarIter = 0,
  tol = 0.01,
  initializeBy = NULL,
  model.selection = FALSE,
  model.selection.threshold = NULL,
  rotation.only = FALSE
)
```

**Arguments**

- |   |                                                                                                                          |
|---|--------------------------------------------------------------------------------------------------------------------------|
| V | list of point sets as N x D matrices                                                                                     |
| C | (optional) list of arrays of covariance matrices with C[[j]][,i] the covariance matrix associated with point i of set j. |
| K | (optional) number of components of the GMM, defaults to the average number of points in a set.                           |
| g | (optional) proportion of noisy points, defaults to 1/K. If set, priors will be initialized uniformly.                    |

<code>initialPriors</code>	(optional) vector of length $K$ of prior probabilities. Defaults to uniform distribution using $g$ . If set, will determine $g$ so it is an error to specify $g$ with <code>initialPriors</code> .
<code>updatePriors</code>	logical, whether to update priors at each iteration (default: <code>TRUE</code> ).
<code>maxIter</code>	maximum number of iterations to perform (default: 100).
<code>fixedVarIter</code>	number of iterations before starting variance updates
<code>tol</code>	tolerance for determining convergence (default: $1e-2$ ).
<code>initializeBy</code>	(optional) how to initialize the GMM means. Defaults to distributing the means on the surface of the sphere enclosing all (centred) sets. Currently supported values are: <ul style="list-style-type: none"> <li>• 'sampling': sample from the data,</li> <li>• a <math>K \times D</math> matrix of points</li> </ul>
<code>model.selection</code>	whether to perform model selection (default: <code>FALSE</code> ). If set to <code>TRUE</code> , GMM components with no support in the data are deleted.
<code>model.selection.threshold</code>	value below which we consider a GMM component has no support, set to $1/K$ if not explicitly given
<code>rotation.only</code>	if set to <code>TRUE</code> , no translation is performed (default: <code>FALSE</code> )

## Value

a list of

- `Y`: list of transformed point sets as  $N \times d$  matrices,
- `R`: list of  $d \times d$  rotation matrices, one for each point set in  $V$ ,
- `t`: list of translation vectors, one for each point set in  $V$ ,
- `M`: centres of the GMM,
- `S`: variances of the GMM.
- `a`: list of posterior probabilities as  $N \times K$  matrices
- `iter`: number of iterations
- `conv`: error value used to evaluate convergence relative to `tol`
- `z`: support scores of the GMM components

## Examples

```
X <- read.csv(system.file("test_data", "parasaurolophusA.txt", package="LOMAR",
  mustWork = TRUE), sep = "\t")
Y <- read.csv(system.file("test_data", "parasaurolophusB.txt", package="LOMAR",
  mustWork = TRUE), sep = "\t")
Z <- read.csv(system.file("test_data", "parasaurolophusC.txt", package="LOMAR",
  mustWork = TRUE), sep = "\t")
PS <- list(X, Y, Z)
C <- list()
for(i in 1:3) {
```



```

cv <- diag(0.1, ncol(PS[[i]])) + jitter(0.01, amount = 0.01)
cv <- replicate(nrow(PS[[i]]), cv)
C[[i]] <- cv
}
transformation <- jrmpc(PS, C = C, K = 100, maxIter = 20, tol = 0.01,
model.selection = TRUE)
## Not run:
# Visualize registration outcome
library(rgl)
colours <- c("blue", "green", "magenta")
Yt <- transformation[['Y']]
plot3d(Yt[[1]], col = colours[1])
for(i in 2:length(Yt)) {
  points3d(Yt[[i]], col = colours[i])
}
# Visualize GMM centres highlighting those with high variance
GMM <- as.data.frame(cbind(transformation[['M']], transformation[['S']]))
colnames(GMM) <- c("x", "y", "z", "S")
colours <- rep("blue", nrow(GMM))
# Find high variance components
threshold <- quantile(transformation[['S']], 0.75)
high.var.idx <- which(transformation[['S']]>threshold)
colours[high.var.idx] <- "red"
plot3d(GMM[, c("x", "y", "z")], col = colours, type = 's', size = 2, box = FALSE, xlab = '',
  ylab = '', zlab = '', xlim = c(-0.15,0.15), ylim = c(-0.15, 0.15),
  zlim = c(-0.15, 0.15))

## End(Not run)

```

---

local\_densities

*local\_densities*


---

## Description

Compute local point density at each point of a point set

## Usage

```
local_densities(X, k = NULL)
```

## Arguments

X	point set, a N x D matrix
k	(optional) number of nearest neighbors used (defaults to all points).

## Details

Local density is computed as in Ning X, Li F, Tian G, Wang Y (2018) An efficient outlier removal method for scattered point cloud data. PLOS ONE 13(8):e0201280. <https://doi.org/10.1371/journal.pone.0201280>

**Value**

vector of density value for each point

---

locprec2cov	<i>locprec2cov</i>
-------------	--------------------

---

**Description**

Converts localization precision columns to a list of arrays of covariance matrices

**Usage**

```
locprec2cov(point.sets, scale = FALSE)
```

**Arguments**

point.sets	a list of n point sets with locprec columns (locprecz column required for 3D data)
scale	logical, whether to scale the localization precision by the variance of the coordinates

**Value**

a list of 2x2xn or 3x3xn arrays.

---

locs2ps	<i>locs2ps</i>
---------	----------------

---

**Description**

Cluster localizations into point sets using DBSCAN

**Usage**

```
locs2ps(
  points,
  eps,
  minPts,
  keep.locprec = TRUE,
  keep.channel = TRUE,
  cluster.2d = FALSE
)
```

**Arguments**

points	a point set as a data frame of coordinates with columns x,y,z.
eps	DBSCAN parameter, size of the epsilon neighbourhood
minPts	DBSCAN parameter, number of minimum points in the eps region
keep.locprec	logical (default: TRUE), whether to preserve the localization precision columns
keep.channel	logical (default: TRUE), whether to preserve channel information column
cluster.2d	logical (default: FALSE), whether to cluster only using x,y (and ignore z)

**Value**

a list of matrices with columns x,y,z and eventually locprec[z] and names set to the cluster indices.

---

locs_from_csv	<i>locs_from_csv</i>
---------------	----------------------

---

**Description**

Reads and filters single molecule localization events from a csv file as typically output by the SMAP software. The main columns of interest are the coordinates (x, y, z), point set membership (site) and localization precision (locprec and locprecz).

**Usage**

```
locs_from_csv(
  file = NULL,
  roi = NULL,
  channels = NULL,
  frame.filter = NULL,
  llrel.filter = NULL,
  locprec.filter = 0,
  locprecz.filter = 0
)
```

**Arguments**

file	a csv file with columns x[nm], y[nm], z[nm] and optionally site[numbers], channel, locprec[nm] and locprecz[nm], other columns are ignored.
roi	region of interest, keep points within the specified volume. Must be a data frame with columns x,y,z and rows min and max defining a bounding box.
channels	vector of integers indicating which channel(s) of a multicolour experiment to get data from.
frame.filter	vector of min and max values, filter out points from frames outside the specified range.
llrel.filter	vector of min and max values, filter out points on log-likelihood (for fitted data).

`locprec.filter` filter out points with `locprec` value greater than the specified number. Points with `locprec == 0` are also removed.

`locprecz.filter` filter out points with `locprecz` value greater than the specified number. Points with `locprecz == 0` are also removed.

### Value

a data frame with columns `x,y,z`, optionally `site`, `locprec` and `locprecz`.

### Examples

```
data.file <- system.file("test_data", "simulated_NUP107_data.csv", package = "LOMAR",
  mustWork = TRUE)
locs <- locs_from_csv(file = data.file, locprec.filter = 20)
```

---

points2img

*points2img*

---

### Description

Convert a data frame of point coordinates into an image. Expected photon count at each voxel is computed as in: F. Huang, S. L. Schwartz, J. M. Byars, and K. A. Lidke, "Simultaneous multiple-emitter fitting for single molecule super-resolution imaging," *Biomed. Opt. Express* 2(5), 1377–1393 (2011).

### Usage

```
points2img(points, voxel.size, method, channels = NULL, ncpu = 1)
```

### Arguments

<code>points</code>	a point set as a data frame of coordinates with columns <code>x,y,z</code> .
<code>voxel.size</code>	a numeric vector of length 3 indicating the size of the voxel along <code>x,y</code> and <code>z</code> in the same unit as the coordinates (e.g. nm)
<code>method</code>	how to calculate voxel values. Available methods are: <ul style="list-style-type: none"> <li>• <code>'histogram'</code>: value is the number of points (i.e. emitters) in the voxel</li> <li>• <code>'photon'</code>: value is the expected number of photons from the points in the voxel. Input data frame must have columns <code>locprec</code>, <code>locprecz</code> and <code>phot[on]</code>.</li> </ul>
<code>channels</code>	vector of channels to consider, must be values present in the input data frame channel column
<code>ncpu</code>	number of threads to use to speed up computation (default: 1)

### Value

an array of dimensions `x,y,z` and channels if applicable

**Examples**

```
point.set <- data.frame(x = c(-9.8,-5.2,12.5,2.5,4.5,1.3,-0.2,0.4,9.3,-1.4,0.5,-1.1,-7.7),
  y = c(-4.2,1.5,-0.5,12,-3,-7.2,10.9,6.7,-1.3,10,6.7,-6.2,2.9),
  z = c(3.4,-3.8,-1.4,1.8,3.5,2.5,2.6,-4.8,-3.8,3.9,4.1,-3.6,-4))
img <- points2img(point.set, voxel.size = c(2,2,2), method = 'histogram')
```

---

points\_from\_roi      *points\_from\_roi*

---

**Description**

Extract points within given bounding box. Points are translated so that (0,0,0) correspond to the bounding box corner defined by roi['min',c('x','y','z')]

**Usage**

```
points_from_roi(points, roi)
```

**Arguments**

points            a point set as a data frame of coordinates with columns x,y,z.  
 roi                a data frame with columns x,y,z and rows min and max defining a bounding box

**Value**

a data frame with same columns as input

---

point\_sets\_from\_locs    *point\_sets\_from\_locs*

---

**Description**

Extracts list of point sets from a data frame of single molecule localization coordinates. By default, uses point set membership indicated in the site column.

**Usage**

```
point_sets_from_locs(
  locs = NULL,
  channels = NULL,
  min.cardinality = NULL,
  max.cardinality = NULL,
  crop.size = NULL,
  keep.locprec = TRUE,
  sample.size = NULL,
```

```

    ignore.site = FALSE,
    cluster.points = FALSE,
    eps = NULL,
    minPts = NULL
  )

```

### Arguments

<code>locs</code> ,	a data frame with columns <code>x[nm]</code> , <code>y[nm]</code> , <code>z[nm]</code> and optionally <code>site[numbers]</code> , <code>locprec[nm]</code> and <code>locprecz[nm]</code> , other columns are ignored.
<code>channels</code>	vector of integers indicating which channel(s) of a multicolour experiment to extract point sets from.
<code>min.cardinality</code>	filter out point sets with less than the specified number of points.
<code>max.cardinality</code>	filter out point sets with more than the specified number of points.
<code>crop.size</code>	remove points from a set if they are further away than the specified distance from the center of the set.
<code>keep.locprec</code>	logical (default:TRUE). Whether to keep locprec information for each point.
<code>sample.size</code>	returns this number of randomly selected point sets. Selects the point sets after applying eventual filtering.
<code>ignore.site</code>	logical (default: FALSE), set to TRUE if point set membership is not present or needed.
<code>cluster.points</code>	logical (default: FALSE), whether to cluster the points using DBSCAN (only if <code>ignore.site</code> is also TRUE).
<code>eps</code>	DBSCAN parameter, size of the epsilon neighbourhood
<code>minPts</code>	DBSCAN parameter, number of minimum points in the eps region

### Value

a list of matrices with columns `x,y,z`, optionally `locprec` and `name` set to the value of the `site` column (if applicable).

### Examples

```

data.file <- system.file("test_data", "simulated_NUP107_data.csv", package = "LOMAR",
  mustWork = TRUE)
locs <- locs_from_csv(file = data.file, locprec.filter = 20)
point.sets <- point_sets_from_locs(locs, keep.locprec = TRUE, min.cardinality = 15)

```

---

point\_sets\_from\_tiffs *point\_sets\_from\_tiffs*

---

### Description

Read in single molecule localization events from a series of 3D images in TIFF files where each image file represents a point set.

### Usage

```
point_sets_from_tiffs(  
  image_dir = NULL,  
  pattern = NULL,  
  image.size = NULL,  
  sample.size = NULL,  
  sample.first = FALSE,  
  min.cardinality = NULL,  
  max.cardinality = NULL,  
  crop.size = NULL  
)
```

### Arguments

<code>image_dir</code>	path to a directory containing the TIFF files.
<code>pattern</code>	regular expression, select images whose file path matches the given pattern.
<code>image.size</code>	vector of length 3 containing the size of the images along each dimension, e.g. <code>c(40,40,40)</code> .
<code>sample.size</code>	if set, selects this number of images at random. A sample size larger than the available number of samples produces a warning and is ignored.
<code>sample.first</code>	if TRUE, samples are selected before applying any eventual filtering. This is more efficient as it avoids reading all data files.
<code>min.cardinality</code>	if set, filter out all point sets with less than the specified number of points.
<code>max.cardinality</code>	if set, filter out all point sets with more than the specified number of points.
<code>crop.size</code>	vector of length 3 containing the desired reduced size of the images along each dimension, e.g. <code>c(30,30,30)</code> .

### Value

a list with two elements:

- `point.sets`: a list of point sets as matrices with columns x,y,z and
- `file.names`: a vector of paths to the TIFF files from which the point sets were extracted.

**Examples**

```
data.dir <- system.file("test_data/img", package = "LOMAR", mustWork = TRUE)
point_sets <- point_sets_from_tiffs(image_dir = data.dir, pattern = "\\..tiff?$",
  image.size = c(64, 64, 4), min.cardinality = 10)
```

---

ps2ary                      *ps2ary*

---

**Description**

Convert a list of 3d point sets to a 4d array. Also works for 2d point sets to 3d array conversion.

**Usage**

```
ps2ary(point.sets, dims)
```

**Arguments**

`point.sets`            a list of point sets.  
`dims`                    vector of dimensions of the axes (x,y in 2d, x,y,z in 3d).

**Value**

a 3d or 4d array.

---

pssk                              *pssk*

---

**Description**

Compute the persistence scale-space kernel on persistence diagrams. Reference: Jan Reininghaus, Stefan Huber, Ulrich Bauer, and Roland Kwitt. A stable multi-scale kernel for topological machine learning. In Proceedings of the IEEE conference on computer vision and pattern recognition (CVPR), pages 4741–4748, 2015.

**Usage**

```
pssk(Dg1 = NULL, Dg2 = NULL, sigma = NULL, dimensions = NULL)
```

**Arguments**

`Dg1`                    a persistence diagram as a  $n1 \times 3$  matrix where each row is a topological feature and the columns are dimension, birth and death of the feature.  
`Dg2`                    another persistence diagram as a  $n2 \times 3$  matrix  
`sigma`                   kernel bandwidth  
`dimensions`            vector of the dimensions of the topological features to consider, if NULL (default) use all available dimensions



**Value**

kernel value

**Examples**

```
D1 <- matrix(c(0,0,0,1,1,0,0,0,1.5, 3.5,2,2.5,3, 4, 6), ncol = 3, byrow = FALSE)
D2 <- matrix(c(0,0,1,1,0, 0, 1.2, 2, 1.4, 3.2,4.6,6.5), ncol = 3, byrow = FALSE)
K <- pssk(Dg1 = D1, Dg2 = D2, sigma = 1)
```

q2dr

*Get derivative of 3D rotation matrix from quaternion***Description**

Get derivative of 3D rotation matrix from quaternion

**Usage**

q2dr(q)

**Arguments**

q                    quaternion

**Value**

derivative of rotation matrix

q2r

*Convert quaternion to rotation matrix  
[http://en.wikipedia.org/wiki/Quaternions\\_and\\_spatial\\_rotation](http://en.wikipedia.org/wiki/Quaternions_and_spatial_rotation)***Description**Convert quaternion to rotation matrix [http://en.wikipedia.org/wiki/Quaternions\\_and\\_spatial\\_rotation](http://en.wikipedia.org/wiki/Quaternions_and_spatial_rotation)**Usage**

q2r(q)

**Arguments**

q                    quaternion

**Value**

rotation matrix

restore\_coordinates    *restore\_coordinates*

---

**Description**

Restore coordinates from mean 0 and standard deviation 1 to their original distribution

**Usage**

```
restore_coordinates(X, mu, sigma)
```

**Arguments**

X	standardized point set as N x D matrix
mu	1 x D vector of means
sigma	standard deviation

**Value**

N X D matrix of unstandardized coordinates

---

rotx                    *rotx*

---

**Description**

Create a rotation matrix representing a rotation of theta radians about the x-axis

**Usage**

```
rotx(theta)
```

**Arguments**

theta	angle in radians
-------	------------------

**Value**

a 3x3 rotation matrix

---

roty

*roty*

---

**Description**

Create a rotation matrix representing a rotation of theta radians about the y-axis

**Usage**

roty(theta)

**Arguments**

theta            angle in radians

**Value**

a 3x3 rotation matrix

---

rotz

*rotz*

---

**Description**

Create a rotation matrix representing a rotation of theta radians about the z-axis

**Usage**

rotz(theta)

**Arguments**

theta            angle in radians

**Value**

a 3x3 rotation matrix

---

sliced\_Wd

*sliced\_Wd*


---

### Description

Compute sliced Wasserstein distance or kernel. Reference: Mathieu Carriere, Marco Cuturi, and Steve Oudot. Sliced Wasserstein kernel for persistence diagrams. In Proceedings of the 34th International Conference on Machine Learning, volume 70 of Proceedings of Machine Learning Research, pages 664–673, 2017.

### Usage

```
sliced_Wd(Dg1, Dg2, M = 10, sigma = 1, dimensions = NULL, return.dist = FALSE)
```

### Arguments

Dg1	a persistence diagram as a $n_1 \times 3$ matrix where each row is a topological feature and the columns are dimension, birth and death of the feature.
Dg2	another persistence diagram as a $n_2 \times 3$ matrix
M	number of slices (default: 10)
sigma	kernel bandwidth (default: 1)
dimensions	vector of the dimensions of the topological features to consider, if NULL (default) use all available dimensions
return.dist	logical (default: FALSE). Whether to return the kernel or distance value.

### Value

kernel or distance value

### Examples

```
D1 <- matrix(c(0,0,0,1,1,0,0,0,1.5, 3.5,2,2.5,3, 4, 6), ncol = 3, byrow = FALSE)
D2 <- matrix(c(0,0,1,1,0, 0, 1.2, 2, 1.4, 3.2,4.6,6.5), ncol = 3, byrow = FALSE)
K <- sliced_Wd(Dg1 = D1, Dg2 = D2, M = 10, sigma = 1, return.dist = TRUE)
```

---

standardize\_coordinates

*standardize\_coordinates*


---

### Description

Transform coordinates to have mean 0 and standard deviation 1

**Usage**

```
standardize_coordinates(X)
```

**Arguments**

*x*                    point set as N x D matrix

**Value**

a list of X: standardized matrix, mu: vector of means, sigma: standard deviation

---

<i>tr</i>	<i>tr</i>
-----------	-----------

---

**Description**

Compute the trace of a matrix

**Usage**

```
tr(x)
```

**Arguments**

*x*                    matrix

**Value**

trace of the matrix

---

<i>wgmmreg</i>	<i>wgmmreg</i>
----------------	----------------

---

**Description**

Rigid registration of two point sets by minimizing the Wasserstein distance between GMMs

**Usage**

```
wgmmreg(
  X,
  Y,
  CX,
  CY,
  wx = NULL,
  wy = NULL,
  maxIter = 200,
  subsample = NULL,
  tol = 1e-08
)
```

**Arguments**

X	reference point set, a N x D matrix
Y	point set to transform, a M x D matrix,
CX	array of covariance matrices for each point in X
CY	array of covariance matrices for each point in Y
wx	(optional) vector of mixture weights for X.
wy	(optional) vector of mixture weights for Y.
maxIter	maximum number of iterations to perform (default: 200)
subsample	if set, use this randomly selected fraction of the points
tol	tolerance for determining convergence (default: 1e-8)

**Value**

a list of

- Y: transformed point set,
- R: rotation matrix,
- t: translation vector,
- c: final value of the cost function,
- converged: logical, whether the algorithm converged.

**Examples**

```
data.file1 <- system.file("test_data", "parasaurolophusA.txt", package = "LOMAR",
  mustWork = TRUE)
PS1 <- read.csv(data.file1, sep = '\t', header = FALSE)
data.file2 <- system.file("test_data", "parasaurolophusB.txt", package = "LOMAR",
  mustWork = TRUE)
C1 <- diag(0.1, ncol(PS1)) + jitter(0.01, amount = 0.01)
C1 <- replicate(nrow(PS1), C1)
PS2 <- read.csv(data.file2, sep = '\t', header = FALSE)
C2 <- diag(0.1, ncol(PS2)) + jitter(0.01, amount = 0.01)
```

```
C2 <- replicate(nrow(PS2),C2)
transformation <- wgmmreg(PS1, PS2, C1, C2, subsample = 0.1, maxIter = 30, tol = 1e-4)
## Not run:
# Visualize registration outcome
library(rgl)
plot3d(PS1, col = "blue")
points3d(PS2, col = "green")
points3d(transformation[['Y']], col = "magenta")

## End(Not run)
```

# Index

[apply\\_transformation](#), [2](#)  
[ary2ps](#), [3](#)

[circle\\_hough\\_transform](#), [3](#)  
[costWd](#), [4](#)  
[cpd](#), [5](#)  
[crop\\_point\\_set](#), [7](#)

[downsample](#), [7](#)

[find\\_elbow](#), [8](#)

[Gaussian\\_Wd](#), [8](#)  
[get\\_kernel\\_matrix](#), [9](#)  
[get\\_persistence\\_diagrams](#), [10](#)  
[GMM\\_Wd](#), [11](#)  
[gradientWd](#), [12](#)

[icp](#), [12](#)  
[idx2rowcol](#), [14](#)  
[img2ps](#), [14](#)

[jrmpc](#), [15](#)

[local\\_densities](#), [17](#)  
[locprec2cov](#), [18](#)  
[locs2ps](#), [18](#)  
[locs\\_from\\_csv](#), [19](#)

[point\\_sets\\_from\\_locs](#), [21](#)  
[point\\_sets\\_from\\_tiffs](#), [23](#)  
[points2img](#), [20](#)  
[points\\_from\\_roi](#), [21](#)  
[ps2ary](#), [24](#)  
[pssk](#), [24](#)

[q2dr](#), [25](#)  
[q2r](#), [25](#)

[restore\\_coordinates](#), [26](#)  
[rotx](#), [26](#)

[roty](#), [27](#)  
[rotz](#), [27](#)

[sliced\\_Wd](#), [28](#)  
[standardize\\_coordinates](#), [28](#)

[tr](#), [29](#)

[wgmmreg](#), [29](#)