

# Package ‘Arothron’

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**Title** Geometric Morphometrics Analyses

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**Description** Tools for geometric morphometric analysis. The package includes tools of virtual anthropology to align two not articulated parts belonging to the same specimen, to build virtual cavities as endocast (Profico et al, 2018 <doi:10.1002/ajpa.23493>), and functions to import and export the coordinates of landmarks and 3D paths into 'landmarkAscii' and 'am' format files.

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Arothron-package

*Geometric Morphometrics Analyses*


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## Description

Tools for geometric morphometric analysis. The package includes tools of virtual anthropology to align two not articulated parts belonging to the same specimen, to build virtual cavities as endocast, and functions to import and export the coordinates of landmarks and 3D paths into the 'landmarkAscii' and 'am' format files.

## Author(s)

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

aro.clo.points	<i>aro.clo.points</i>
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**Description**

Find the closest matches between a reference (2D or 3D matrix) and a target matrix (2D/3D) or mesh returning row indices and distances

**Usage**

```
aro.clo.points(target, reference)
```

**Arguments**

target	kxm matrix or object of class "mesh3d"
reference	numeric: a kxm matrix (coordinates)

**Value**

position numeric: a vector of the row indices  
distances numeric: a vector of the coordinates distances

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

**Examples**

```
#load an example: mesh, and L set
data(yoda_sur)
data(yoda_set)
sur<-yoda_sur
set<-yoda_set
ver_pos<-aro.clo.points(target=sur,reference=set)
```

---

bary.mesh	<i>bary.mesh</i>
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**Description**

This function calculates the barycenter of a matrix or a 3D mesh

**Usage**

```
bary.mesh(mesh)
```

**Arguments**

mesh                    matrix mesh vertex

**Value**

barycenter numeric: x,y,z coordinates of the barycenter of the mesh

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

**Examples**

```
#load an example: mesh, and L set
data(SCP1.mesh)
sur<-SCP1.mesh
bary<-bary.mesh(mesh=sur)
```

---

compare\_check.set            *compare\_check.set*

---

**Description**

This function applies the Digital Alignment Tool (DTA) on a disarticulated model using a reference landmark configuration

**Usage**

```
compare_check.set(RM_set_1, RM_set_2, DM_set_1, DM_set_2, DM_mesh_1, DM_mesh_2)
```

**Arguments**

RM_set_1	matrix: 3D landmark set of the first module acquired on the reference model
RM_set_2	matrix: 3D landmark set of the second module acquired on the reference model
DM_set_1	matrix: 3D landmark set of the first module acquired on the disarticulated model
DM_set_2	matrix: 3D landmark set of the second module acquired on the disarticulated model
DM_mesh_1	mesh3d: mesh of the disarticulated model (first module)
DM_mesh_2	mesh3d: mesh of the disarticulated model (second module)

**Value**

SF1 numeric: scale factor used to scale the reference set (first module)  
 SF2 numeric: scale factor used to scale the reference set (second module)  
 RM\_set\_1\_sc matrix: scaled 3D reference set (first module)  
 RM\_set\_2\_sc matrix: scaled 3D reference set (second module)  
 AM\_model list: output of the Morpho::rotmesh.onto function  
 dist\_from\_mesh numeric: mesh distance between the aligned model and the scaled reference set  
 eucl\_dist\_1 numeric: euclidean distance between the landmark configuration of the disarticulated and reference model (first module)  
 eucl\_dist\_2 numeric: euclidean distance between the landmark configuration of the disarticulated and reference model (second module)  
 procr\_dist numeric: procrustes distance between the landmark configuration of the aligned and reference model  
 procr\_dist\_1 numeric: procrustes distance between the landmark configuration of the disarticulated and reference model (first module)  
 procr\_dist\_2 numeric: procrustes distance between the landmark configuration of the disarticulated and reference model (second module)  
 eucl\_dist numeric: euclidean distance between the landmark configuration of the aligned and reference model  
 single\_1\_1 numeric: euclidean distance between the landmark configuration of the disarticulated and reference model (first module)  
 single\_1\_2 numeric: euclidean distance between the landmark configuration of the disarticulated and reference model (second module)

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

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 dec.curve

*dec.curve*


---

**Description**

This function computes the order of points on a open 3D curve and finds intermediate points

**Usage**

```
dec.curve(mat_input, mag, plot = TRUE)
```

**Arguments**

mat_input	numeric: a kx3 matrix
mag	numeric: how many times will be divided by the number of initial points
plot	logical: if TRUE will be plotted the starting and final point matrices

**Value**

matt numeric: a kx3 matrix with points coordinates

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

**Examples**

```
## Create and plot a 3D curve
require(compositions)
require(rgl)
curve_3D<-cbind(1:10,seq(1,5,length=10),rnorm(10,sd = 0.2))
plot3D(curve_3D,bbox=FALSE)
rgl.close()
## Create and plot the new 3D curve (with intermediate points)
dec_curve_3D<-dec.curve(curve_3D, 2, plot = TRUE)
```

---

DM\_base\_sur

*example dataset*

---

**Description**

3D mesh of the first part of the Homo sapiens disarticulated model

**Usage**

```
data(DM_base_sur)
```

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

DM\_face\_sur

*example dataset*

---

**Description**

3D mesh of the second part of the Homo sapiens disarticulated model

**Usage**

```
data(DM_face_sur)
```

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

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DM_set	<i>example dataset</i>
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---

**Description**

Landmark configurations of the two part of the disarticulated model

**Usage**

```
data(DM_set)
```

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

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dta	<i>dta</i>
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---

**Description**

This function applies the Digital Alignment Tool (DTA) on a disarticulated model using a reference sample

**Usage**

```
dta(RM_sample, mod_1, mod_2, pairs_1, pairs_2, DM_mesh_1, DM_mesh_2, DM_set_1,
    DM_set_2, method = c("euclidean"))
```

**Arguments**

RM_sample	3D array: 3D landmark configurations of the reference sample
mod_1	numeric vector: vector containing the position of which landmarks belong to the first module
mod_2	numeric vector: vector containing the position of which landmarks belong to the second module
pairs_1	matrix: a X x 2 matrix containing the indices of right and left landmarks of the first module
pairs_2	matrix: a X x 2 matrix containing the indices of right and left landmarks of the second module
DM_mesh_1	mesh3d: mesh of the disarticulated model (first module)
DM_mesh_2	mesh3d: mesh of the disarticulated model (second module)
DM_set_1	matrix: 3D landmark set of the first module acquired on the disarticulated model
DM_set_2	matrix: 3D landmark set of the second module acquired on the disarticulated model
method	character: specify method to be used to individuate the best DTA ("euclidean" or "procrustes")

**Value**

AM\_mesh mesh3d: mesh of the aligned model  
 AM\_set matrix: landmark configuration of the aligned model  
 AM\_id character: name of the item of the reference sample resulted as best DTA  
 AM\_SF\_1 numeric: scale factor used to scale the reference set (first module)  
 AM\_SF\_2 numeric: scale factor used to scale the reference set (second module)  
 distance numeric: distance between the landmark configuration of the aligned and the reference model  
 tot\_proc numeric vector: procrustes distances between aligned and reference models (all DTAs)  
 tot\_eucl numeric vector: euclidean distances between aligned and reference models (all DTAs)  
 setarray 3D array: landmark configurations of the disarticulated model aligned on each item of the reference sample

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

**Examples**

```
## Load and plot the disarticulated model of the Homo sapiens case study
library(compositions)
library(rgl)
data(DM_base_sur)
data(DM_face_sur)
open3d()
wire3d(DM_base_sur,col="white")
wire3d(DM_face_sur,col="white")
## Load the landmark configurations associated to the DM
data(DM_set)
## Load the reference sample
data(RMs_sets)
## Define the landmarks belonging to the first and second module
mod_1<-c(1:17) #cranial base
mod_2<-c(18:32) #facial complex
## Define the paired landmarks for each module (optional symmetrization process)
pairs_1<-cbind(c(4,6,8,10,12,14,16),c(5,7,9,11,13,15,17))
pairs_2<-cbind(c(23,25,27,29,31),c(24,26,28,30,32))
## Run DTA
ex.dta<-dta(RM_sample=RMs_sets, mod_1=mod_1, mod_2=mod_2, pairs_1=pairs_1, pairs_2=pairs_2,
DM_mesh_1=DM_base_sur,DM_mesh_2=DM_face_sur, DM_set_1= DM_set[mod_1,], DM_set_2=DM_set[mod_2,])
## Print the name of the best RM
ex.dta$AM_id
## Save the mesh and the landmark set of the AM
AM_mesh<-ex.dta$AM_mesh
AM_set<-ex.dta$AM_set
## Plot the aligned 3D model
library(compositions)
library(rgl)
```



```
open3d()
wire3d(AM_mesh,col="white")
plot3D(AM_set,bbox=FALSE,add=TRUE)
```

---

endo_set	<i>example dataset</i>
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### Description

POVs defined inside the endocranial cavity

### Usage

```
data(endo_set)
```

### Author(s)

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

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export_amira	<i>export_amira</i>
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### Description

This function exports a list of 3D landmark set in separate files (format landmarkAscii)

### Usage

```
export_amira(lista, path)
```

### Arguments

lista	list containing 3D landmark sets
path	character: path of the folder where saving the Amira landmark sets

### Author(s)

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

### Examples

```
x<-c(1:20)
y<-seq(1,3,length=20)
z<-rnorm(20,0.01)
vertices<-cbind(x,y,z)
set<-list(vertices)
example<-export_amira(set,path=tempdir())
```

export\_amira.path      *export\_amira.path*

---

### Description

Convert and save a 3D matrix into a AmiraMesh ASCII Lineset (.am) object

### Usage

```
export_amira.path(vertices, filename, Lines = c(1:(dim(vertices)[1] - 1) - 1,
-1), path)
```

### Arguments

vertices	numeric: a kx3 matrix
filename	character: name of the requested output
Lines	numeric: sequence of the vertices that defines the line
path	character: folder path

### Author(s)

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

### Examples

```
library(Arothron)
x<-c(1:20)
y<-seq(1,3,length=20)
z<-rnorm(20,0.01)
vertices<-cbind(x,y,z)
export_amira.path(vertices=vertices,filename="example_line",path=tempdir())
```

---

ext.int.mesh      *ext.int.mesh*

---

### Description

This function finds the vertices visible from a set of points of view

### Usage

```
ext.int.mesh(mesh, views = 20, dist.sphere = 3, param1 = 2.5,
param2 = 10, default = TRUE, import_pov, matrix_pov, expand = 1,
scale.factor, method = "ast3d", start.points = 250, num.cores = NULL)
```

**Arguments**

mesh	object of class mesh3d
views	numeric: number of points of view
dist.sphere	numeric: scale factor. This parameter the distance between the barycenter of the mesh and the radius of the sphere used to define set of points of view
param1	numeric: first parameter for spherical flipping (usually ranged from 0.5 to 5, try!)
param2	numeric second paramter for spherical flipping (don't change it!)
default	logical: if TRUE the points of views are defined automatically, if FALSE define the matrix_pov
import_pov	logical: if FALSE an interactive 3D plot for the definition of the points of view is returned
matrix_pov	matrix: external set of points of view
expand	numeric: scale factor for the grid for the interactive 3D plot
scale.factor	numeric: scale factor for
method	character: select "a" or "c"
start.points	numeric: number of POVs available
num.cores	numeric: number of cores

**Value**

position numeric: a vector with vertex number nearest the landmark set

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

ext.mesh.rai

*ext.mesh.rai*

---

**Description**

This function returns a 3D mesh with colours based on the vertices visibile from each point of view

**Usage**

```
ext.mesh.rai(scans, mesh)
```

**Arguments**

scans	an ext.int.mesh
mesh	matrix mesh vertex (the same of the ext.int.mesh object)

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

grid_pov	<i>grid_pov</i>
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---

**Description**

This function creates a grid for an interactive way to define the set of the points of view

**Usage**

```
grid_pov(mesh, expand = 1)
```

**Arguments**

mesh	object of class mesh3d
expand	numeric: scale factor for the grid for the interactive 3D plot

**Value**

matrice matrix: matrix with the x,y,z coordinates of the points of view

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

human_skull	<i>example dataset</i>
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---

**Description**

3D mesh of a human skull

**Usage**

```
data(human_skull)
```

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

krd1_tooth	<i>example dataset</i>
------------	------------------------

---

**Description**

3D mesh of a deciduous Neanderthal tooth

**Usage**

```
data(krd1_tooth)
```

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

landmark_frm2amira	<i>landmark_frm2amira</i>
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---

**Description**

This function converts the .frm files, from Evan Toolbox, stored in a folder into the format landmarkAscii

**Usage**

```
landmark_frm2amira(path_folder_frm, path_amira_folder)
```

**Arguments**

path\_folder\_frm

character: path of the folder where the .frm files are stored

path\_amira\_folder

character: path folder to store the landmarkAscii configurations

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

malleus\_bone            *example dataset*

---

**Description**

3D mesh of a human malleus

**Usage**

```
data(malleus_bone)
```

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

noise.mesh            *noise.mesh*

---

**Description**

This function adds noise to a mesh

**Usage**

```
noise.mesh(mesh, noise = 0.025, seed = 123)
```

**Arguments**

mesh	triangular mesh stored as object of class "mesh3d"
noise	sd deviation to define vertex noise
seed	seed for random number generator

**Value**

mesh\_n a 3D model of class "mesh3d" with noise

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

**Examples**

```
#load mesh
library(compositions)
library(rgl)
data("SCP1.mesh")
mesh<-SCP1.mesh
#add noise
noised<-noise.mesh(mesh,noise=0.05)
#plot original and mesh with noise added
open3d()
shade3d(mesh,col=3)
shade3d(noised,col=2,add=TRUE)
```

---

out.inn.mesh

*out.inn.mesh*


---

**Description**

This function separates a 3D mesh subjected to the ext.int.mesh into two 3D models: the visible mesh and the not visible one

**Usage**

```
out.inn.mesh(scans, mesh, plot = TRUE)
```

**Arguments**

scans	an ext.int.mesh
mesh	matrix mesh vertex (the same of the ext.int.mesh object)
plot	logical: if TRUE the wireframe of the mesh with the visible vertices is plotted

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

**Examples**

```
## Not run:
#CA-LSE tool on Neanderthal tooth
#load a mesh
data(krd1_tooth)
library(rgl)
library(Rvcg)
library(compositions)
ca_lse_krd1<-ext.int.mesh(mesh= krd1_tooth, views=50, param1=3, default=TRUE,
import_pov = NULL,expand=1, scale.factor=1,num.cores = NULL)
vis_inv_krd1<-out.inn.mesh(ca_lse_krd1, krd1_tooth, plot=TRUE)
inv_mesh<-vcgIsolated(vis_inv_krd1$invisible)
```

```

open3d()
shade3d(inv_mesh,col=2)
open3d()
shade3d(vis_inv_krd1$visible, col=3)
#CA-LSE tool on human malleus
#load a mesh
data(malleus_bone)
ca_lse_malleus<-ext.int.mesh(mesh= malleus_bone, views=50, param1=3,
default=TRUE, import_pov = NULL, expand=1, scale.factor=1)
vis_inv_malleus<-out.inn.mesh(ca_lse_malleus, malleus_bone, plot=TRUE)
inv_mesh<- vis_inv_malleus$invisible
inv_mesh<-ca_lse_malleus$invisible

#AST-3D tool
#load a mesh
data(human_skull)
data(endo_set)
ast3d_endocast<-ext.int.mesh(mesh=human_skull, views=50, param1=0.6, default=FALSE,
import_pov = TRUE,expand=1, matrix_pov =endo_set, scale.factor=1,num.cores = NULL)
vis_inv_endo<-out.inn.mesh(ast3d_endocast,human_skull,plot=TRUE)
vis_mesh<-vcgIsolated(vis_inv_endo$visible)
open3d()
shade3d(vis_mesh,col=3)

## End(Not run)

```

---

patches\_frm2amira

*patches\_frm2amira*

---

## Description

This function converts the .frm files, from Evan Toolbox, stored in a folder into the format landmarkAscii (semilandmark patches)

## Usage

```
patches_frm2amira(path_folder_frm, path_amira_folder)
```

## Arguments

path\_folder\_frm

character: path of the folder where the .frm files are stored

path\_amira\_folder

character: path folder to store the landmarkAscii configurations

## Author(s)

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia



---

pov\_selector                      *pov\_selector*

---

### Description

Internal function to define the points of view

### Usage

```
pov_selector(mesh, grid, start.points = 250, method = "ast3d")
```

### Arguments

mesh	object of class mesh3d
grid	matrix: a 3D grid
start.points	numeric: number of center to be found
method	character: select "a" or "c" for respectively AST-3D and CA-LSE method

### Value

selection numeric: positioning vector of the selected points of the grid

### Author(s)

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

read.amira.dir                      *read.amira.dir*

---

### Description

This function reads and stores in an array the coordinated allocated in a folder in separate files (format landmarkAscii)

### Usage

```
read.amira.dir(path.dir, nland)
```

### Arguments

path.dir	character: path of the folder
nland	numeric: number of landmark sampled in Amira

### Value

array.set numeric: a kx3xn array with landmark coordinates

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

`read.amira.set`      *read.amira.set*

---

**Description**

This function converts a landmarkAscii file set in a kx3x1 array

**Usage**

```
read.amira.set(name.file, nland)
```

**Arguments**

<code>name.file</code>	character: path of a landmarkAscii file
<code>nland</code>	numeric: number of landmark sampled in Amira, if is set on "auto" it will be automatically recognized

**Value**

array.set numeric: a kx3x1 array with landmark coordinates

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

`read.path.amira`      *read.path.amira*

---

**Description**

This function extracts and orders the coordinate matrix from a surface path file from Amira

**Usage**

```
read.path.amira(path.name)
```

**Arguments**

<code>path.name</code>	character: path of surface path .ascii extension file
------------------------	---

**Value**

data numeric: a kxd matrix with xyz coordinates

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

repmat	<i>repmat</i>
--------	---------------

---

**Description**

This function repeats copies of a matrix

**Usage**

```
repmat(X, m, n)
```

**Arguments**

X	numeric: a matrix
m	numeric: number of times to repeat the X matrix in row and column dimension
n	numeric: repetition factor for each dimension

**Value**

matrice: repeated matrix

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

RMs_sets	<i>example dataset</i>
----------	------------------------

---

**Description**

Array containing the landmark coordinates of the reference sample for Digital Alignment Tool example

**Usage**

```
data(RMs_sets)
```

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

SCP1.mesh

*example dataset*

---

**Description**

Mesh of the Saccopastore 1 Neanderthal skull

**Usage**

```
data(SCP1.mesh)
```

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

sinus\_set

*example dataset*

---

**Description**

POVs sampled inside the maxillary sinus cavity

**Usage**

```
data(sinus_set)
```

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

spherical.flipping

*spherical.flipping*

---

**Description**

Internal spherical flipping function

**Usage**

```
spherical.flipping(C, mesh, param1, param2)
```

**Arguments**

C	numeric: coordinates of the point of view
mesh	object of class mesh3d
param1	numeric: first parameter for spherical flipping (usually ranged from 0.1 to 3, try!)
param2	numeric second paramter for spherical flipping (don't change it!)

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

*trasf.mesh*                      *trasf.mesh*

---

**Description**

This function centers a mesh on the barycenter coordinates

**Usage**

`trasf.mesh(mesh, barycenter)`

**Arguments**

mesh	a 3D mesh of class "mesh3d"
barycenter	numeric: coordinates of the center

**Value**

mesh a 3D mesh of class "mesh3d"

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

yoda\_set

*example dataset*

---

**Description**

Landmark set on Yoda

**Usage**

```
data(yoda_set)
```

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

---

yoda\_sur

*example dataset*

---

**Description**

Mesh of Yoda

**Usage**

```
data(yoda_sur)
```

**Author(s)**

Antonio Profico, Alessio Veneziano, Marina Melchionna, Pasquale Raia

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