

# Package ‘JSDNE’

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**Title** Estimating the Age using Auricular Surface by DNE

**Version** 4.4.4

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**Description** The age is estimated by calculating the Dirichlet Normal Energy (DNE) on the whole auricular surface and the apex of the auricular surface. It involves three estimation methods: principal component discriminant analysis (PCQDA), principal component regression analysis (PCR), and principal component logistic regression analysis (PCLR) methods. The package is created with the data from the Louis Lopes Collection in Lisbon, the 21st Century Identified Human Remains Collection in Coimbra, and the CAL Milano Cemetery Skeletal Collection in Milan.

**License** GPL-3

**Encoding** UTF-8

**RoxygenNote** 7.3.1

**Depends** R (>= 2.10)

**LazyData** true

**Imports** dplyr, MASS, molaR, nnet, Rvcg

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

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## Contents

Apex . . . . .	2
PCLR_result . . . . .	2
PCLR_Test . . . . .	3
PCLR_Train . . . . .	3
PCQDA_result . . . . .	4
PCQDA_Test . . . . .	4

PCQDA_Train . . . . .	5
PCR_result . . . . .	5
PCR_Test . . . . .	6
PCR_Train . . . . .	6
RawData . . . . .	7
WholeSurface . . . . .	7

<b>Index</b>	<b>8</b>
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Apex	<i>Surface mesh of apex of auricular surface.</i>
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### Description

Surface mesh of apex of auricular surface.

### Usage

```
data(Apex)
```

### Format

An object of class mesh3d of length 4.

### Examples

```
PCQDA_output <- PCQDA_result(WholeSurface,Apex)
PCR_output <- PCR_result(WholeSurface,Apex)
PCLR_output <- PCLR_result(WholeSurface,Apex)
```

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PCLR_result	<i>Estimating the age using DNE_PCLR method</i>
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### Description

DNE\_PCLR method is the principal component logistic regression analysis (PCLR) method using the Dirichlet Normal Energy (DNE). This method involves 2 age groups to distinguish if the specimen is over 63 or under 67. The function automatically calculates the DNE on the auricular surface. It provides the estimated age group and age range of the estimated age group.

### Usage

```
PCLR_result(x, y)
```

### Arguments

x	the name of inputted ply file of the whole auricular surface
y	the name of inputted ply file of the apex of the auricular surface

**Value**

estimated result gets printed to the console

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PCLR\_Test

*PCLR\_Test*

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**Description**

PCLR\_Test is the test set of the PCR model. It consists of Age, Cluster1, MeanDNE.Apex, TotalDNE.TotalPolygonFaces, MedianDNE.Whole, IQRDNE.Whole and MeanDNE.Convex. The number of rows is 191.

**Usage**

PCLR\_Test

**Format**

An object of class data.frame with 191 rows and 7 columns.

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PCLR\_Train

*PCLR\_Train*

---

**Description**

PCLR\_Train is the train set of the PCR model. It consists of Age, Cluster1, MeanDNE.Apex, TotalDNE.TotalPolygonFaces, MedianDNE.Whole, IQRDNE.Whole and MeanDNE.Convex. The number of rows is 699.

**Usage**

PCLR\_Train

**Format**

An object of class data.frame with 699 rows and 7 columns.

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PCQDA_result	<i>Estimating the age using DNE_PCQDA method</i>
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### Description

DNE\_PCQDA method is the principal component quadratic discriminant analysis (PCQDA) method using the Dirichlet Normal Energy (DNE). This method involves 4 age groups. The function automatically calculates the DNE on the auricular surface. It provides the estimated age group and age range of the estimated age group.

### Usage

```
PCQDA_result(x, y)
```

### Arguments

x	the name of inputted ply file of the whole auricular surface
y	the name of inputted ply file of the apex of the auricular surface

### Value

estimated result gets printed to the console

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PCQDA_Test	<i>PCQDA_Test</i>
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### Description

PCQDA\_Test is the test set of the PCQDA model. It consists of Cluster2, Age, MeanDNE.Apex, TotalDNE.TotalPolygonFaces, Proportion.DNEunder0.0001, and Proportion.DNEover0.6. The number of rows is 186.

### Usage

```
PCQDA_Test
```

### Format

An object of class `data.frame` with 186 rows and 6 columns.

---

PCQDA\_Train

*PCQDA\_Train*


---

**Description**

PCQDA\_Train is the train set of the PCQDA model. It consists of Cluster2, Age, MeanDNE.Apex, TotalDNE.TotalPolygonFaces, Proportion.DNEunder0.0001, and Proportion.DNEover0.6. The number of rows is 704.

**Usage**

```
PCQDA_Train
```

**Format**

An object of class data.frame with 704 rows and 6 columns.

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PCR\_result

*Estimating the age using PCR method*


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**Description**

DNE\_PCR method is the principal component linear regression analysis (PCR) method using the Dirichlet Normal Energy (DNE). The function automatically calculates the DNE on the auricular surface. It provides the estimated age and standard errors (SE).

**Usage**

```
PCR_result(x, y)
```

**Arguments**

x                    the name of inputted ply file of the whole auricular surface  
y                    the name of inputted ply file of the apex of the auricular surface

**Value**

estimated result gets printed to the console

---

PCR\_Test

*PCR\_Test*

---

**Description**

PCR\_Test is the test set of the PCR model. It consists of Age, MeanDNE.Apex, IQRDNE.Apex, TotalDNE.TotalPolygonFaces, MeanDNE.Convex and Proportion.DNEunder0.0001. The number of rows is 188.

**Usage**

PCR\_Test

**Format**

An object of class data.frame with 188 rows and 6 columns.

---

PCR\_Train

*PCR\_Train*

---

**Description**

PCR\_Train is the train set of the PCR model. It consists of Age, MeanDNE.Apex, IQRDNE.Apex, TotalDNE.TotalPolygonFaces, MeanDNE.Convex and Proportion.DNEunder0.0001. The number of rows is 702.

**Usage**

PCR\_Train

**Format**

An object of class data.frame with 702 rows and 6 columns.

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RawData	<i>RawData</i>
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**Description**

RawData includes the raw information of DNE variables and biological information of auricular surfaces (age and sex) of 890 auricular surface. It consists of Age, Cluster1, Cluster2, Collection, Sex, MeanDNE.Apex, MedianDNE.Apex, IQRDNE.Apex, TotalDNE.TotalPolygonFaces, MedianDNE.Whole, IQRDNE.Whole, MeanDNE.Convex, MeanDNE.Concave, Proportion.DNEunder0.0001 and Proportion.DNEover0.6. Cluster1 and Cluster2 is the clustering information for PCLR and PCQDA, respectively.

**Usage**

```
RawData
```

**Format**

An object of class `data.frame` with 890 rows and 15 columns.

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WholeSurface	<i>Surface mesh of whole auricular surface.</i>
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**Description**

Surface mesh of whole auricular surface.

**Usage**

```
data(WholeSurface)
```

**Format**

An object of class `mesh3d` of length 4.

**Examples**

```
PCQDA_output <- PCQDA_result(WholeSurface,Apex)
PCR_output <- PCR_result(WholeSurface,Apex)
PCLR_output <- PCLR_result(WholeSurface,Apex)
```

# Index

## \* datasets

- Apex, [2](#)
- PCLR\_Test, [3](#)
- PCLR\_Train, [3](#)
- PCQDA\_Test, [4](#)
- PCQDA\_Train, [5](#)
- PCR\_Test, [6](#)
- PCR\_Train, [6](#)
- RawData, [7](#)
- WholeSurface, [7](#)

Apex, [2](#)

PCLR\_result, [2](#)  
PCLR\_Test, [3](#)  
PCLR\_Train, [3](#)  
PCQDA\_result, [4](#)  
PCQDA\_Test, [4](#)  
PCQDA\_Train, [5](#)  
PCR\_result, [5](#)  
PCR\_Test, [6](#)  
PCR\_Train, [6](#)

RawData, [7](#)

WholeSurface, [7](#)