Package ‘VectorCodeR’

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Type Package

Title Easily Analyze Your Gait Patterns Using Vector Coding Technique

Version 0.2.0

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Description Facilitate the analysis of inter-limb and intra-limb coordination in human movement. It provides functions for calculating the phase angle between two segments, enabling researchers and practitioners to quantify the coordination patterns within and between limbs during various motor tasks.
Needham, R., Naemi, R., & Chockalingam, N. (2014) <doi:10.1016/j.jbiomech.2013.12.032>.
Needham, R., Naemi, R., & Chockalingam, N. (2015) <doi:10.1016/j.jbiomech.2015.07.023>.
Tepavac, D., & Field-Fote, E. C. (2001) <doi:10.1123/jab.17.3.259>.
Park, J.H., Lee, H., Cho, Js. et al. (2021) <doi:10.1038/s41598-020-80237-w>.

License GPL-3

Depends R (>= 3.5.0), readxl, tidyverse, grDevices, graphics, stats, ggplot2, tidyr, dplyr

Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

NeedsCompilation no

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Contents

`ang_ang_plot` *ang_ang_plot*

Description

angle-angle plot

Usage

```
ang_ang_plot(ang1, ang2)
```

Arguments

`ang1`	Hip angle vector.
`ang2`	Knee angle vector.

Value

A angle_angle figure.

Examples

```
v1 <- sample$hip
v2 <- sample$knee
v3 <- sample$ankle
ang_ang_plot(v1, v2)
```

`area` *Area of cyclogram*

Description

The cyclogram area is representative of the conjoint range of joint movements

Usage

```
area(ang1, ang2, len)
```

Arguments

`ang1`	Any body segment joint angle vector.
`ang2`	Another body segment joint angle vector.
`len`	Length of the input vector

Details

area of cyclogram

Value

A numeric value of the area of cyclogram.

Examples

```
data(sample)
v1 <- sample$hip
v2 <- sample$knee
len <- length(v1)
area(v1, v2, len)
```

`CAV` *CAV*

Description

CAV plot

Usage

```
CAV(df)
```

Arguments

`df`	hip, ankle, knee dataframe

Value

A variability plot

Examples

```
data(sample)
v1 <- sample$hip
v2 <- sample$knee
v3 <- sample$ankle
df <- sample
CAV(df)
ts.plot(CAV(df))
```

`perimeter` *perimeter of the cyclogram*

Description

The cyclogram perimeter provides information on the average joint velocity

Usage

```
perimeter(ang1, ang2, len)
```

Arguments

`ang1`	Any body segment joint angle vector.
`ang2`	Another body segment joint angle vector.
`len`	Length of the input vector

Details

perimeter of the cyclogram

Value

A numeric value of the perimeter of cyclogram.

Examples

```
data(sample)
v1 <- sample$hip
v2 <- sample$knee
len <- length(v1)
perimeter(v1, v2, len)
```

`phase_angle` *phase_angle*

Description

waited to read the paper

Usage

```
phase_angle(ang1, ang2)
```

Arguments

`ang1`	Any body segment joint angle vector.
`ang2`	Another body segment joint angle vector.

Details

coupling angle plot

Value

A phase_angle figure.

Examples

```
data(sample)
v1 <- sample$hip
v2 <- sample$knee
v3 <- sample$ankle
phase_angle(v1, v2)
```

`phase_ratio` *phase_ratio*

Description

phase-ratio statistics

Usage

```
phase_ratio(pa)
```

Arguments

`pa`	phase-angle vector.

Value

A phase-ratio dataframe.

Examples

```
data(sample)
v1 <- sample$hip
v2 <- sample$knee
v3 <- sample$ankle
pa <- phase_angle(v1, v2)
phase_ratio(pa)
```

`sample` *sample dataset*

Description

sample dataset

Usage

```
data(sample)
```

Format

An object of class `"data.frame"`

knee time series data recoding knee joint angles

hip time series data recoding hip joint angles

ankle time series data recoding ankle joint angles

Examples

```
data(sample)
head(sample)
```

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