

# 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](https://doi.org/10.1016/j.jbiomech.2013.12.032)>.

Needham, R., Naemi, R., & Chockalingam, N. (2015) <[doi:10.1016/j.jbiomech.2015.07.023](https://doi.org/10.1016/j.jbiomech.2015.07.023)>.

Tepavac, D., & Field-Fote, E. C. (2001) <[doi:10.1123/jab.17.3.259](https://doi.org/10.1123/jab.17.3.259)>.

Park, J.H., Lee, H., Cho, Js. et al. (2021) <[doi:10.1038/s41598-020-80237-w](https://doi.org/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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**Repository** CRAN

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ang_ang_plot	<i>ang_ang_plot</i>
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## 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)
```

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area	<i>Area of cyclogram</i>
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**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	<i>CAV</i>
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---

**Description**

CAV plot

**Usage**

```
CAV(df)
```

**Arguments**

df	hip, ankle, knee dataframe
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**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)
```

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phase_angle	<i>phase_angle</i>
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**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	<i>phase_ratio</i>
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**Description**

phase-ratio statistics

**Usage**

```
phase_ratio(pa)
```

**Arguments**

pa	phase-angle vector.
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**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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