Package 'DescriptiveRepresentationCalculator'

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Title Descriptive Representation Calculator from 'The Composition of Descriptive Representation'

Version 2.0

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Description This package contains two main functions. The first computes the expected degree of representation for a given group in a political body under a random sampling model. The second computes the residual standard deviation in using the expected value as a prediction for observed values under the model.

Depends R (>= 3.3.3)

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Encoding UTF-8

LazyData true

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RoxygenNote 7.2.1

R topics documented:

`ExpectedRepresentation` *Compute the expected degree of representation for any group in a political body*

Description

Finds the degree of expected representation for any group in a political body under a random sampling model as described in Gerring, Jerzak and Oncel (2023+).

Usage

```
ExpectedRepresentation(PopShares, BodyN)
```

Arguments

PopShares	A numeric vector containing the group-level population proportions.
BodyN	A positive integer denoting the size of the political body in question.
a=-0.5, b=1	Parameters controlling the affine transformation for how the representation measure is summarized. That is, a and b control how the expected L1 deviation of the population shares from the body shares is re-weighted. The expected L1 deviation is the average value of the absolute deviation of the population from body shares under a random sampling model. This expected L1 deviation is multiplied by a; b is as an additive re-scaling term: a*E[L1]+b. By default, a=-0.5 and b=1 so that the expected Rose Index of Proportionality is returned.

Value

The expected degree of representation (a scalar).

Examples

```
ExpectedRep <- ExpectedRepresentation(PopShares = c(1/3, 2/3, 1/3),
                                      BodyN = 50)

print( ExpectedRep )
```

ObservedRepresentation

Compute the observed degree of representation for any group in a political body

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Description

Finds the degree of observed representation for any group in a political body.

Usage

```
ObservedRepresentation(BodyMemberCharacteristics, PopShares)
```

Arguments

BodyMemberCharacteristics	A vector specifying the characteristics for members of a political body.
PopShares	A numeric vector specifying population shares of identities specified in BodyMemberCharacteristic The names of the entries in PopShares should correspond to identities in BodyMemberCharacteristi (see Example).
BodyShares	(optional) A numeric vector with same structure as PopShares specifying group population shares of a given body. If specified, used by default instead of BodyMemberCharacteristics.

a=-0.5, b=1 Parameters controlling the affine transformation for how the representation measure is summarized. That is, a and b control how the L1 deviation of the population shares from the body shares is re-weighted. This expected L1 deviation is multiplied by a; b is as an additive re-scaling term: a*L1+b. By default, a=-0.5 and b=1 so that the Rose Index of Proportionality is returned.

Value

The observed degree of representation (a scalar). By default, this quantity is the Rose Index of Proportionality.

Examples

```
ObsRep <- ObservedRepresentation(
                        BodyMemberCharacteristics = c("A","A","C","A","C","A"),
                        PopShares = c("A"=1/3,"B"=2/3, "C"=1/3))

print( ObsRep ) # 0.833
```

SDRepresentation *Compute the amount of representation left unexplained by a random sampling model.*

Description

Finds the residual standard deviation when using the expected representation for any group in a political body to predict observed representation as described in Gerring, Jerzak and Oncel, 2023+.

Usage

```
SDRepresentation(PopShares, BodyN)
```

Arguments

PopShares A numeric vector containing the group-level population proportions.

BodyN A positive integer denoting the size of the political body in question.

a=-0.5, b=1 Parameters controlling the affine transformation for how the representation measure is summarized. That is, a and b control how the expected L1 deviation of the population shares from the body shares is re-weighted. The expected L1 deviation is the average value of the absolute deviation of the population from body shares under a random sampling model. This expected L1 deviation is multiplied by a; b is as an additive re-scaling term: a*E[L1]+b. By default, a=-0.5 and b=1 so that the expected Rose Index of Proportionality is used in the calculation.

Value

A scalar summary of the amount of representation not explained by a random sampling model. More precisely, this function returns the the residual standard deviation when using the expected degree of representation to predict observed representation under a random sampling model.

Examples

```
SDRep <- SDRepresentation(PopShares = c(1/3, 2/3, 1/3),
                                  BodyN = 50)

print( SDRep )
```

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