

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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LazyData true

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Imports stats

RoxygenNote 7.2.3

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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, a = -0.5, b = 1)
```

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, b	The a and b parameters control 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: $a \cdot E[L1] + b$. 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

Description

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

Usage

```
ObservedRepresentation(BodyMemberCharacteristics, PopShares, BodyShares, a = -0.5, b = 1)
```

Arguments

BodyMemberCharacteristics	A vector specifying the characteristics for members of a political body.
PopShares	A numeric vector specifying population shares of identities specified in BodyMemberCharacteristics. The names of the entries in PopShares should correspond to identities in BodyMemberCharacteristics (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, b 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: $a \cdot L1 + b$. 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 )
```

SDRepresentation	<i>Compute the amount of representation left unexplained by a random sampling model.</i>
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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, a = -0.5, b = 1, nMonte = 10000)
```

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, b	Parameters controlling the affine transformation for how the representation measure is summarized. That is, <i>a</i> and <i>b</i> 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 <i>a</i> ; <i>b</i> is as an additive re-scaling term: $a \cdot E[L1] + b$. By default, $a = -0.5$ and $b = 1$ so that the expected Rose Index of Proportionality is used in the calculation.
nMonte	A positive integer denoting number of Monte Carlo iterations used to approximate the variance of representation under a random sampling model.

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.

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