

# 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:

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ExpectedRepresentation

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

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## 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: $a \cdot E[L1] + b$ . 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 )
```

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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 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.

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

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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)
```

### 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**

```
ResidualRep <- ResidualRepresentation(PopShares = c(1/3, 2/3, 1/3),  
                                     BodyN = 50)  
  
print( ResidualRep )
```

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