

Package 'DescriptiveRepresentationCalculator'

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Title Characterizing Observed and Expected Representation

Version 1.1.0

Description A system for analyzing descriptive representation, especially for comparing the composition of a political body to the population it represents. Users can compute the expected degree of representation for a body under a random sampling model, the expected degree of representation variability, as well as representation scores from observed political bodies. The package is based on Gerring, Jerzak, and Oncel (2024) <[doi:10.1017/S0003055423000680](https://doi.org/10.1017/S0003055423000680)>.

URL <https://github.com/cjerzak/DescriptiveRepresentationCalculator-software/>

BugReports <https://github.com/cjerzak/DescriptiveRepresentationCalculator-software/issues>

Depends R (>= 3.3.3)

License GPL-3

Encoding UTF-8

Imports stats

Suggests knitr

VignetteBuilder knitr

RoxygenNote 7.3.2

NeedsCompilation no

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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 (2024).

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).

References

- John Gerring, Connor T. Jerzak, Erzen Oncel. (2024), The Composition of Descriptive Representation, *American Political Science Review*, 118(2): 784-801. doi:10.1017/S0003055423000680

See Also

- [ObservedRepresentation](#) for calculating representation scores from observed data.
- [SDRepresentation](#) for calculating representation unexplained under the random sampling model.

Examples

```
ExpectedRep <- ExpectedRepresentation(PopShares = c(1/4, 2/4, 1/4),
                                     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 the body-member characteristics input. The names of the entries in PopShares should correspond to identities in that body-member characteristics input (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: $a \times L1 + b$. 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.

See Also

- [ExpectedRepresentation](#) for calculating expected representation scores under random sampling.
- [SDRepresentation](#) for calculating representation unexplained under the random sampling model.

Examples

```
ObsRep <- ObservedRepresentation(
  BodyMemberCharacteristics = c("A", "A", "C", "A", "C", "A"),
  PopShares = c("A"=1/4, "B"=2/4, "C"=1/4))

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 (2024).

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, 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 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.

References

- John Gerring, Connor T. Jerzak, Erzen Oncel. (2024), The Composition of Descriptive Representation, *American Political Science Review*, 118(2): 784-801. doi:[10.1017/S0003055423000680](https://doi.org/10.1017/S0003055423000680)

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