

# Z\_validity\_test: A Test for Instrument Validity

In CarrThomas/TestforInstrumentValidity: A Test for Instrument Validity

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## Description

`Z_validity_test` performs the test for instrument validity described in Kitagawa (2015) in the case of a binary treatment, an instrument that can take many values, and no conditioning covariates.

## Usage

```
1 Z_validity_test(Y, D, Z, Z_order, xis, B = 500, alpha = c(0.1, 0.05, 0.01))
```

## Arguments

Y	A vector containing observations of the outcome variable.
D	A vector containing observations of the treatment variable.
Z	A vector containing observations of the instrument variable.
Z_order	A vector containing the unique values of the instrument variable ordered so that the propensity score is increasing with the value of the instrument. For example, if the instrument takes values 1, 2, 3 and we belive that $P(D=1 Z=1) < P(D=1 Z=2) < P(D=1 Z=3)$ , then <code>Z_order</code> would be <code>c(1, 2, 3)</code> .
xis	A vector containing values of the trimming constant. Individual entries should be $>0$ . For example, <code>c(0.05, 0.1, 0.3, 0.5)</code> .
B	The number of bootstrap iterations when constructing standard errors. Defaults to 500.
alpha	A vector of significance levels for which critical values will be calculated. Each entry should be between 0 and 1. By default, critical values are returned for the 10%, 5% and 1% levels of significance.

## Details

a

## Value

teststat	A vector with <code>length(xis)</code> entries containing the value of the test statistic corresponding to each value of the trimming constant.
pvals	A vector of with <code>length(xis)</code> containing the p-value corresponding to each value of the trimming constant.
cvs	A matrix with <code>length(alpha)</code> rows and <code>length(xis)</code> columns. Entry $(i,j)$ is the critical value for significance level <code>alpha[i]</code> when the trimming constant is <code>xis[j]</code> .

## Examples

```
1  ## Example where the null is valid
2
3
4  set.seed(1234);
5  Z <- c(rep(1, 1000), rep(0, 1000));
6  D <- rbinom(2000, 1, 1 / 2);
7  Y <- D + rnorm(2000);
8
9  xis <- c(sqrt(0.005 * (1 - 0.005)), sqrt(0.05 * (1 - 0.05)), sqrt(0.1 * (1 - 0.1)), 1);
10 Z_validity_test(Y, D, Z, c(0, 1), xis)
11
12 # Returns
13 $teststat
14 [1] 3.1702131 2.1545545 1.5652476 0.4695743
15
16 $pvals
17 [1] 0.710 0.912 0.978 0.984
18
19 $cvs
20      [,1]      [,2]      [,3]      [,4]
21 90% 3.855944 3.449081 3.218573 1.274559
22 95% 4.036757 3.693522 3.532302 1.408723
23 99% 4.245746 4.039350 3.953901 1.677051
24
25 ## Example where the null is not valid
26
27 set.seed(5678);
28 Z <- c(rep(1, 1000), rep(0, 1000));
29 D <- rbinom(2000, 1, 0.55 * Z + 0.45 * (1 - Z));
30 Y <- (1 - D * (1 - Z)) * rnorm(2000) + D * (1 - Z) * rnorm(2000, -0.7, 1);
31
32 xis <- c(sqrt(0.005 * (1 - 0.005)), sqrt(0.05 * (1 - 0.05)), sqrt(0.1 * (1 - 0.1)), 1);
33 Z_validity_test(Y, D, Z, c(0, 1), xis)
34
35 # Returns
36 $teststat
37 [1] 7.261042 7.261042 7.261042 2.593839
38
39 $pvals
40 [1] 0 0 0 0
```

43	90%	3.868514	3.466813	3.282482	1.299155
44	95%	4.059778	3.718391	3.624888	1.431084
45	99%	4.331277	4.254834	4.018666	1.744133

Run this example

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