

Quantitative bias analysis

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Quantitative bias analysis

Objective: To quantify the magnitude and direction of systematic error (bias)

Quantitative bias analysis

Quantify bias from systematic error

- Confounding
- Selection bias
- Misclassification

Quantitative bias analysis

Quantify bias from systematic error

- Confounding
- Selection bias
- Misclassification

Reviewer #2

'The authors failed to take into account confounding by _____

Quantitative bias analysis

1. Given confounding by an unmeasured variable, what effect estimate would remain if we were able to adjust for this confounder?

Point estimate with bias →

Point estimate taking into account bias

Quantitative bias analysis

1. Given confounding by an unmeasured variable, what effect estimate would remain if we were able to adjust for this confounder?

Quantitative bias analysis

1. Given confounding by an unmeasured variable, what effect estimate would remain if we were able to adjust for this confounder?
2. How strong would an unknown confounder have to be to fully explain the observed effect?

Quantitative bias analysis

1. Simple bias analysis
2. Probabilistic bias analysis

Quantitative bias analysis

- 1. Simple bias analysis**
2. Probabilistic bias analysis

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2. How strong would an unknown confounder have to be to fully explain the observed effect?

$$ARR = RR \times \frac{P_{C1}(RR_{CD} - 1) + 1}{P_{C0}(RR_{CD} - 1) + 1}$$

P_{C1} : Prevalence of confounder among exposed

P_{C0} : Prevalence of confounder among unexposed

RR_{CD} : Relative risk of confounder associated with outcome

Schneeweiss S. Sensitivity analysis and external adjustment for unmeasured confounders in epidemiologic database studies of therapeutics. *Pharmacoepidemiology & Drug Safety* 2006 May. 15(5):291-303. (.pdf format)

$$RR = \frac{ARR}{\left[\frac{P_{C1}(RR_{CD}-1)+1}{P_{C0}(RR_{CD}-1)+1} \right]}$$

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P_{C1}
 P_{C0}
 RR_{CD}

Bias parameters

Example

Does male circumcision protect against HIV infection?

Possible confounder: Being Muslim

RR not adjusted for religion: 0.35 (95% CI 0.28 to 0.44)

Tyndall et al., 1996

$$RR = \frac{ARR}{\left[\frac{P_{C1}(RR_{CD}-1)+1}{P_{C0}(RR_{CD}-1)+1} \right]}$$

P_{C1}
 P_{C0}
 RR_{CD}

Bias parameters



Ethiopia

Uganda

Kenya

Somalia

Rwanda

●
Nairobi

Burundi

Tanzania

$$RR = \frac{ARR}{\left[\frac{P_{C1}(RR_{CD}-1)+1}{P_{C0}(RR_{CD}-1)+1} \right]}$$

$$P_{C1} \quad \mathbf{0.8}$$

$$P_{C0} \quad \mathbf{0.1}$$

$$RR_{CD} \quad \mathbf{0.65}$$

$$RR = \frac{0.35}{\frac{0.8(0.65-1)+1}{0.1(0.65-1)+1}} = 0.47$$

<http://www.drugepi.org/dope-downloads>

Sensitivity Analysis

- Sensitivity Analysis of Confounding 2018 (.xls format)
- Schneeweiss S. Sensitivity analysis and external adjustment for unmeasured confounders in epidemiologic database studies of therapeutics. *Pharmacoepidemiology & Drug Safety* 2006 May. 15(5):291-303. (.pdf format)

File Home SDU Insert Page Layout Formulas Data Review View Developer Help Tell me what you want to do

Templafy Paste Copy Format Painter

Arial 10 Wrap Text

General

Normal Bad Good Neutral

Check Cell Explanatory... Followed Hyp... Hyperlink

Templafy Clipboard Font Alignment Number Styles

V30

A B C D E F G H I J K L M N O P Q R S T U

2. Array approach

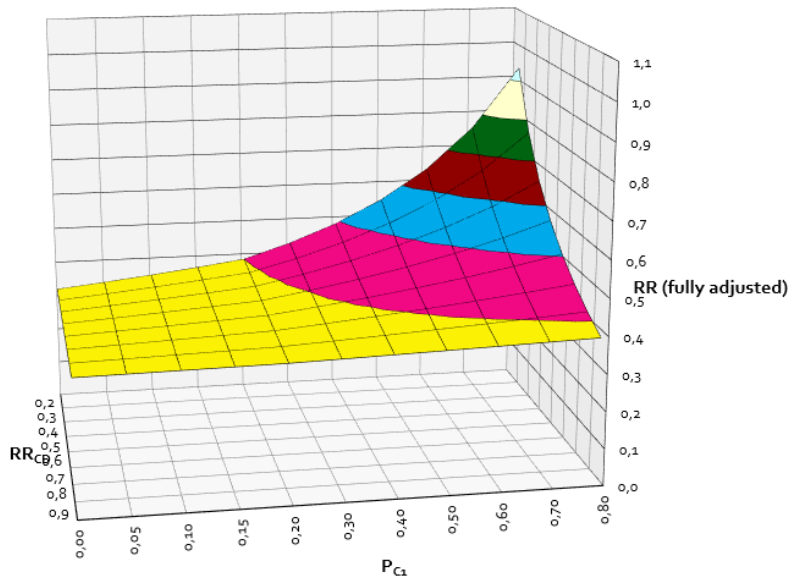
Example: HIV infection and religion

$$RR_{adj} = \frac{ARR}{\frac{P_{C1}(RR_{CD}-1)+1}{P_{C0}(RR_{CD}-1)+1}}$$

% Bias = [(ARR-RRadj.) / RRadj.] * 100

fx	X	Y	fx	Z2	Z1
ARR	RR _{CD}	P _{C1}	P _{C0}	RR _{adjusted}	% Bias
0.35	0.2	0.00	0.050	0.34	4.17
0.35	0.3	0.00	0.050	0.34	3.63
0.35	0.4	0.00	0.050	0.34	3.09
0.35	0.5	0.00	0.050	0.34	2.56
0.35	0.6	0.00	0.050	0.34	2.04
0.35	0.7	0.00	0.050	0.34	1.52
0.35	0.8	0.00	0.050	0.35	1.01
0.35	0.9	0.00	0.050	0.35	0.50
0.35	1.0	0.00	0.050	0.35	0.00
0.35	1.1	0.00	0.050	0.35	-0.50
0.35	0.2	0.05	0.050	0.35	0.00
0.35	0.3	0.05	0.050	0.35	0.00
0.35	0.4	0.05	0.050	0.35	0.00
0.35	0.5	0.05	0.050	0.35	0.00
0.35	0.6	0.05	0.050	0.35	0.00
0.35	0.7	0.05	0.050	0.35	0.00
0.35	0.8	0.05	0.050	0.35	0.00
0.35	0.9	0.05	0.050	0.35	0.00
0.35	1.0	0.05	0.050	0.35	0.00
0.35	1.1	0.05	0.050	0.35	0.00
0.35	0.2	0.10	0.050	0.37	-4.17
0.35	0.3	0.10	0.050	0.36	-3.63
0.35	0.4	0.10	0.050	0.36	-3.09
0.35	0.5	0.10	0.050	0.36	-2.56
0.35	0.6	0.10	0.050	0.36	-2.04
0.35	0.7	0.10	0.050	0.36	-1.52
0.35	0.8	0.10	0.050	0.35	-1.01
0.35	0.9	0.10	0.050	0.35	-0.50
0.35	1.0	0.10	0.050	0.35	0.00
0.35	1.1	0.10	0.050	0.35	0.50
0.35	0.2	0.15	0.050	0.38	-8.33
0.35	0.3	0.15	0.050	0.38	-7.25
0.35	0.4	0.15	0.050	0.37	-6.19
0.35	0.5	0.15	0.050	0.37	-5.13
0.35	0.6	0.15	0.050	0.36	-4.08
0.35	0.7	0.15	0.050	0.36	-3.05
0.35	0.8	0.15	0.050	0.36	-2.02
0.35	0.9	0.15	0.050	0.35	-1.01
0.35	1.0	0.15	0.050	0.35	0.00
0.35	1.1	0.15	0.050	0.35	1.00

ARR = 0.35
P_{C0} = 0.05



ARR = 0.35



2. Array approach

Example: HIV infection and religion

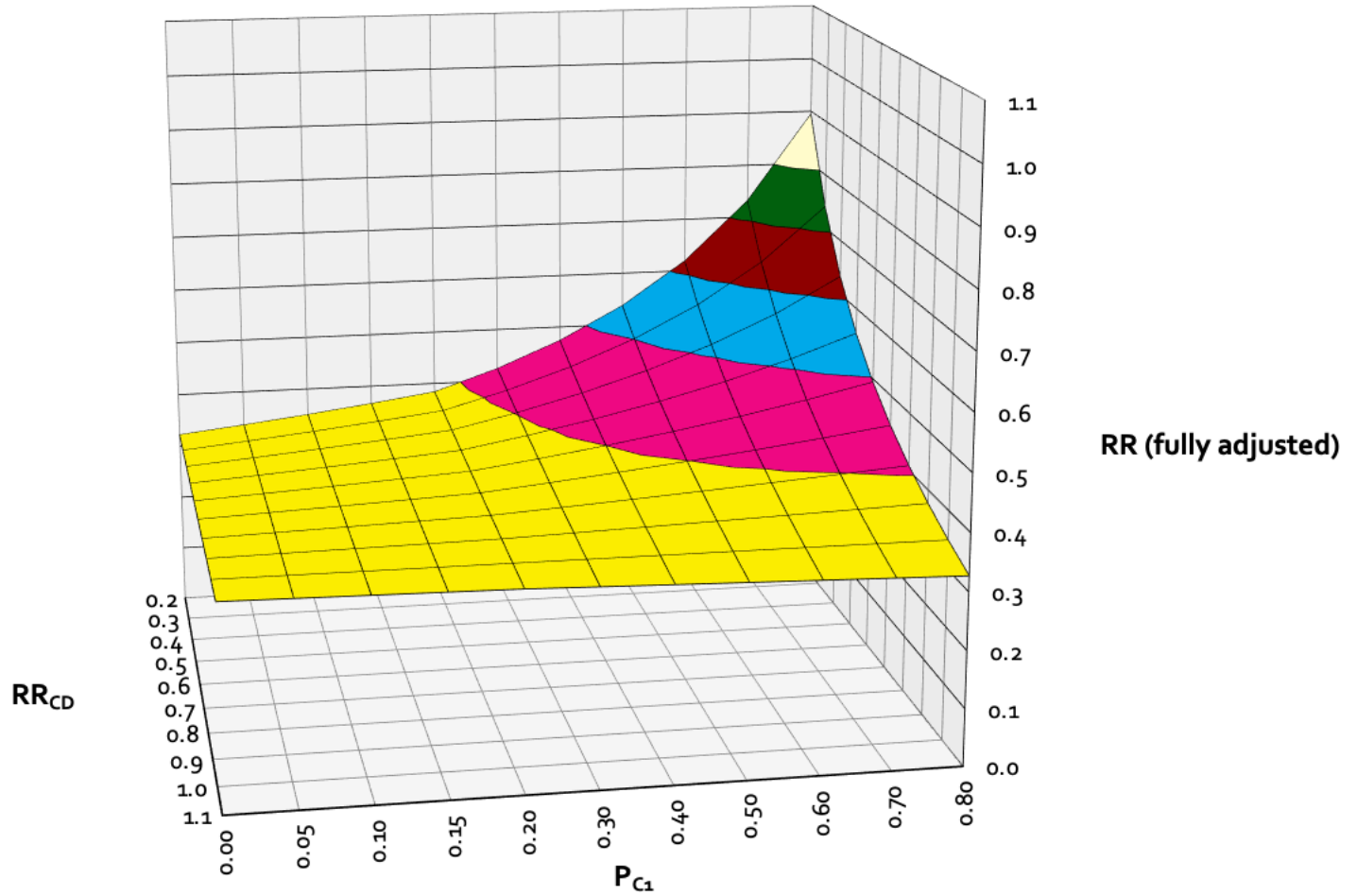
$$RR_{adj.} = \frac{ARR}{\left[\frac{P_{C1}(RR_{CD} - 1) + 1}{P_{C0}(RR_{CD} - 1) + 1} \right]}$$

	fix	X	Y	fix	Z2	Z1
	ARR	RR _{CD}	P _{C1}	P _{C0}	RR _{adjusted}	% Bias
6	0.35	0.2	0.00	0.100	0.32	8.70
7	0.35	0.3	0.00	0.100	0.33	7.53
8	0.35	0.4	0.00	0.100	0.33	6.38
9	0.35	0.5	0.00	0.100	0.33	5.26
10	0.35	0.6	0.00	0.100	0.34	4.17
11	0.35	0.7	0.00	0.100	0.34	3.09
12	0.35	0.8	0.00	0.100	0.34	2.04
13	0.35	0.9	0.00	0.100	0.35	1.01
14	0.35	1.0	0.00	0.100	0.35	0.00
15	0.35	1.1	0.00	0.100	0.35	-0.99
16	0.35	0.2	0.05	0.100	0.34	4.35
17	0.35	0.3	0.05	0.100	0.34	3.76
18	0.35	0.4	0.05	0.100	0.34	3.19
19	0.35	0.5	0.05	0.100	0.34	2.63
20	0.35	0.6	0.05	0.100	0.34	2.08
21	0.35	0.7	0.05	0.100	0.34	1.55
22	0.35	0.8	0.05	0.100	0.35	1.02
23	0.35	0.9	0.05	0.100	0.35	0.51
24	0.35	1.0	0.05	0.100	0.35	0.00
25	0.35	1.1	0.05	0.100	0.35	-0.50
26	0.35	0.2	0.10	0.100	0.35	0.00

% Bias = [(ARR-RRadj.)/RRadj.]*100

ARR = 0.35
P_{C0} = 0.1

ARR = 0.35
P_{Co} = 0.1



Diagramdesign Formater

Formellinje

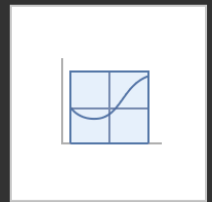
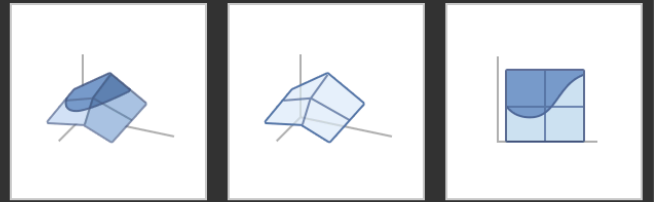
Ombyt række/kolonne

K L M N O P Q

- Søjle
- Kurve
- Cirkel
- Hierarki
- Statistisk
- X Y (punkt)
- Vandfald**
- Kombination
- Kort
- Gem som skabelon...
- Administrer skabeloner...



Grundflade



Radar



RR (fully adjusted)

ut; CCB Rule Out; Zolpidem

+

ARR = 0.35

$P_{C_0} = 0.1$

RR

0.8-0.9

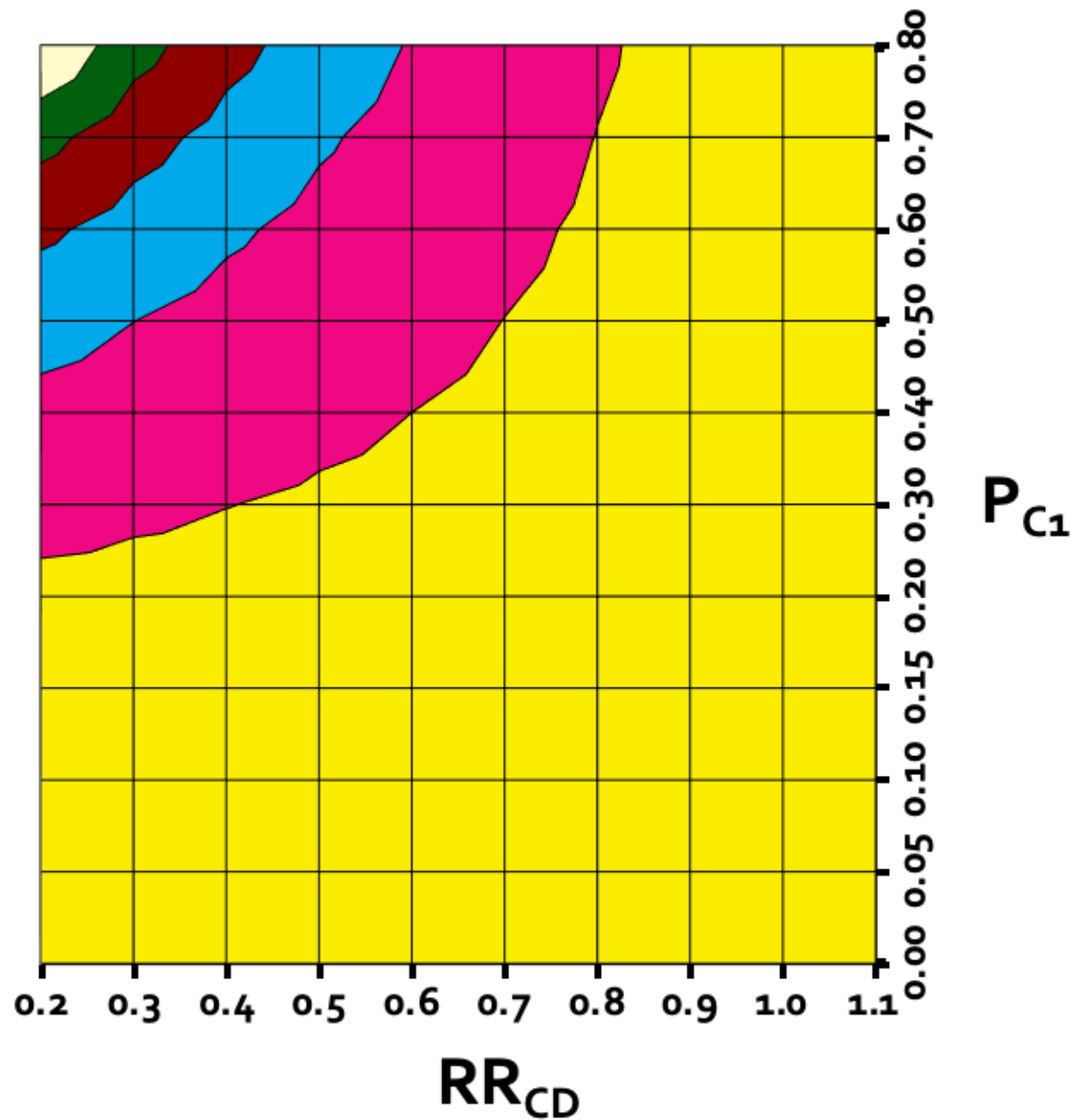
0.7-0.8

0.6-0.7

0.5-0.6

0.4-0.5

0.3-0.4



1. Given confounding by an unmeasured variable, what effect estimate would remain if we were able to adjust for this confounder?

2. How strong would an unknown confounder have to be to fully explain the observed effect?

2. How strong would an unknown confounder have to be in order to fully explain the observed effect?

RR_{CD}

RR_{EC}

Bias parameters

Example

How strong would confounding be to explain the effect of smoking on lung cancer?

RR 10.73, 95% CI 8.02 to 14.36

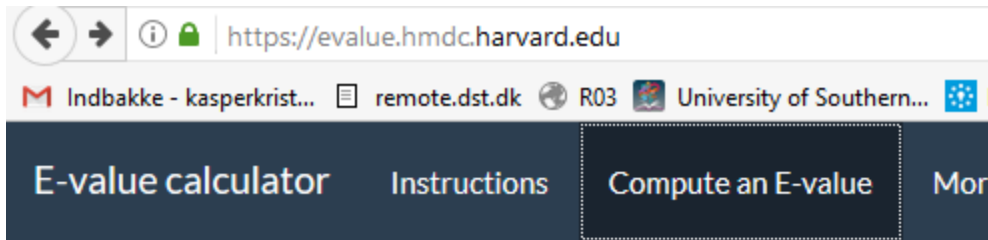
The E-value is the minimum strength of association on the relative risk scale that a confounder would need to have with both the treatment and outcome to explain away the observed association

E-value calculations are straightforward. For an observed risk ratio of RR :

$$\text{E-value} = RR + \sqrt{RR \times (RR - 1)}.$$

The proof appears elsewhere (37). The formula applies to a risk ratio greater than 1; for a risk ratio less than 1, one first takes the inverse of the observed risk ratio and then applies the formula.

<https://evaluate.hmdc.harvard.edu/>



Outcome type

Relative risk / rate ratio ▼

Point estimate

▲ ▼

Confidence interval lower limit

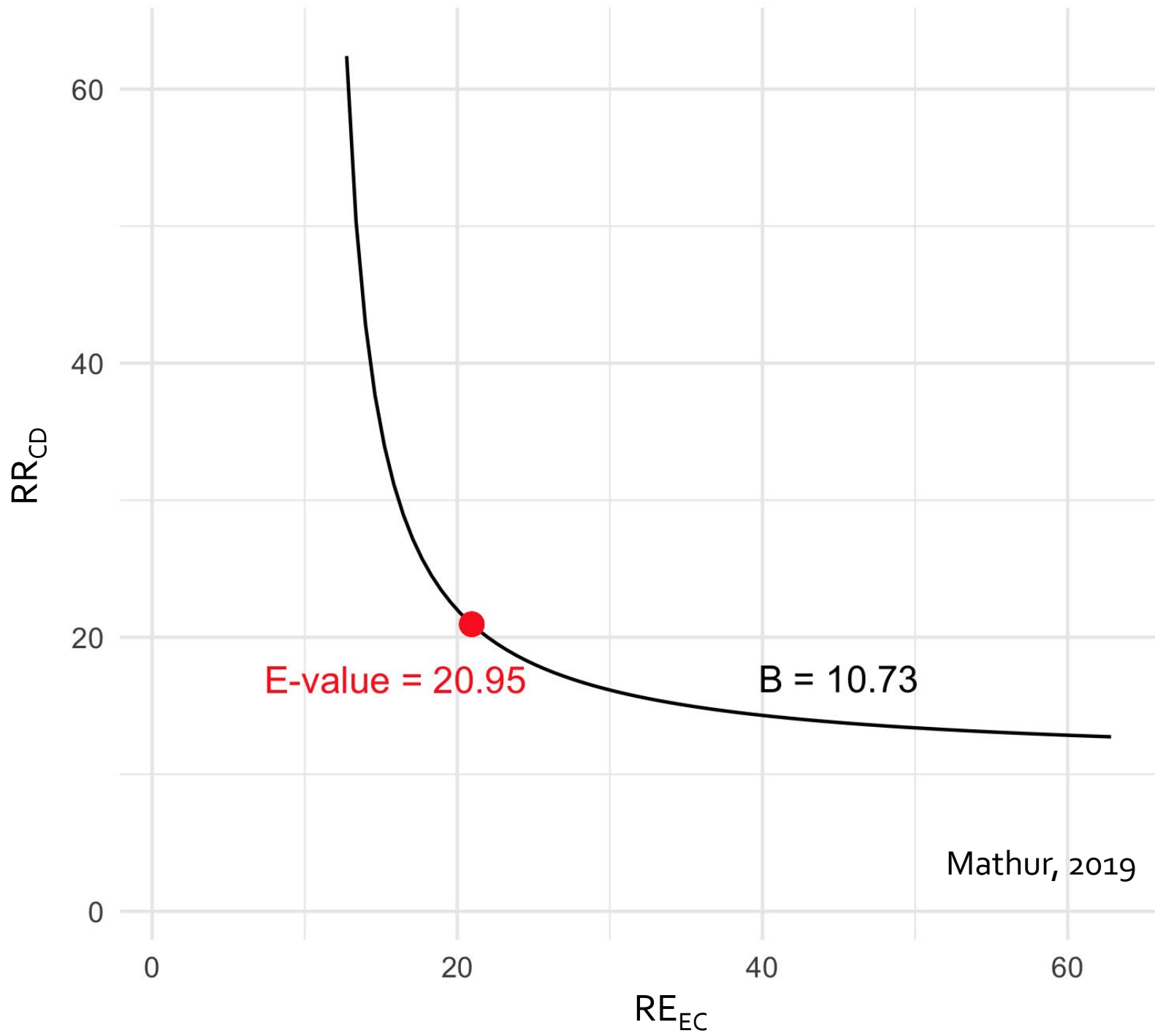
▲ ▼

Confidence interval upper limit

▲ ▼

**True causal effect to which to shift estimate
(default: null)**

1 ▲ ▼



Hydrochlorothiazide use and risk of nonmelanoma skin cancer: A nationwide case-control study from Denmark



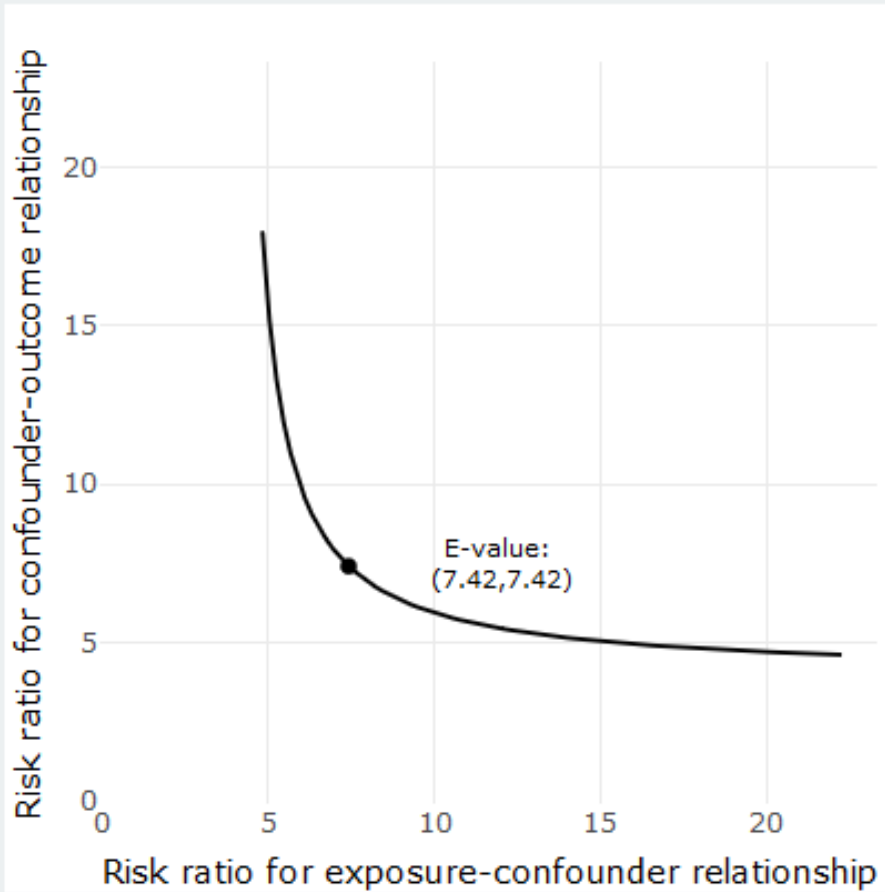
Sidsel Arnsfang Pedersen, MD,^{a,b,c} David Gaist, PhD,^{a,b} Sigrun Alba Johannesdottir Schmidt, PhD,^d
Lisbet Rosenkrantz Hölmich, DMSc,^e Søren Friis, MD,^{d,f,g} and Anton Pottegård, PhD^c
Odense, Aarhus, Herlev, and Copenhagen, Denmark

Background: Hydrochlorothiazide, one of the most frequently used diuretic and antihypertensive drugs in the United States and Western Europe, is photosensitizing and has previously been linked to lip cancer.

Objective: To examine the association between hydrochlorothiazide use and the risk of basal cell carcinoma (BCC) and squamous cell carcinoma (SCC).

Methods: From the Danish Cancer Registry, we identified patients (cases) with nonmelanoma skin cancer (NMSC) during 2004-2012. Controls were matched 1:20 by age and sex. Cumulative hydrochlorothiazide use (in 1995-2012) was assessed from the Danish Prescription Registry. Using conditional logistic regression, we calculated **odds ratios (ORs)** for BCC and SCC associated with hydrochlorothiazide use.

Results: High use of hydrochlorothiazide ($\geq 50,000$ mg) was associated with ORs of 1.29 (95% confidence interval [CI], 1.23-1.35) for BCC and **3.98 (95% CI, 3.68-4.31)** for SCC. We found clear dose-response relationships between hydrochlorothiazide use and both BCC and SCC; the highest cumulative dose category ($\geq 200,000$ mg of HCTZ) had ORs of 1.54 (95% CI, 1.38-1.71) and 7.38 (95% CI, 6.32-8.60) for BCC and SCC, respectively. Use of other diuretics and antihypertensives was not associated with NMSC.



E-value for point estimate: 7.4
E-value for lower limit of CI: 6.8

'The observed risk ratio could be explained away by an unmeasured confounder that was associated with both hydrochlorothiazide and skin cancer by a risk ratio of 7.4-fold each.

The confidence interval could be moved to the null by an unmeasured confounder associated with both hydrochlorothiazide and skin cancer by a risk-ratio of 6.8-fold'

Quantitative bias analysis

1. Simple bias analysis
- 2. Probabilistic bias analysis**

1. Given confounding by an unmeasured variable, what effect estimate would remain if we were able to adjust for this confounder?
2. How strong would an unknown confounder have to be to fully explain the observed effect?

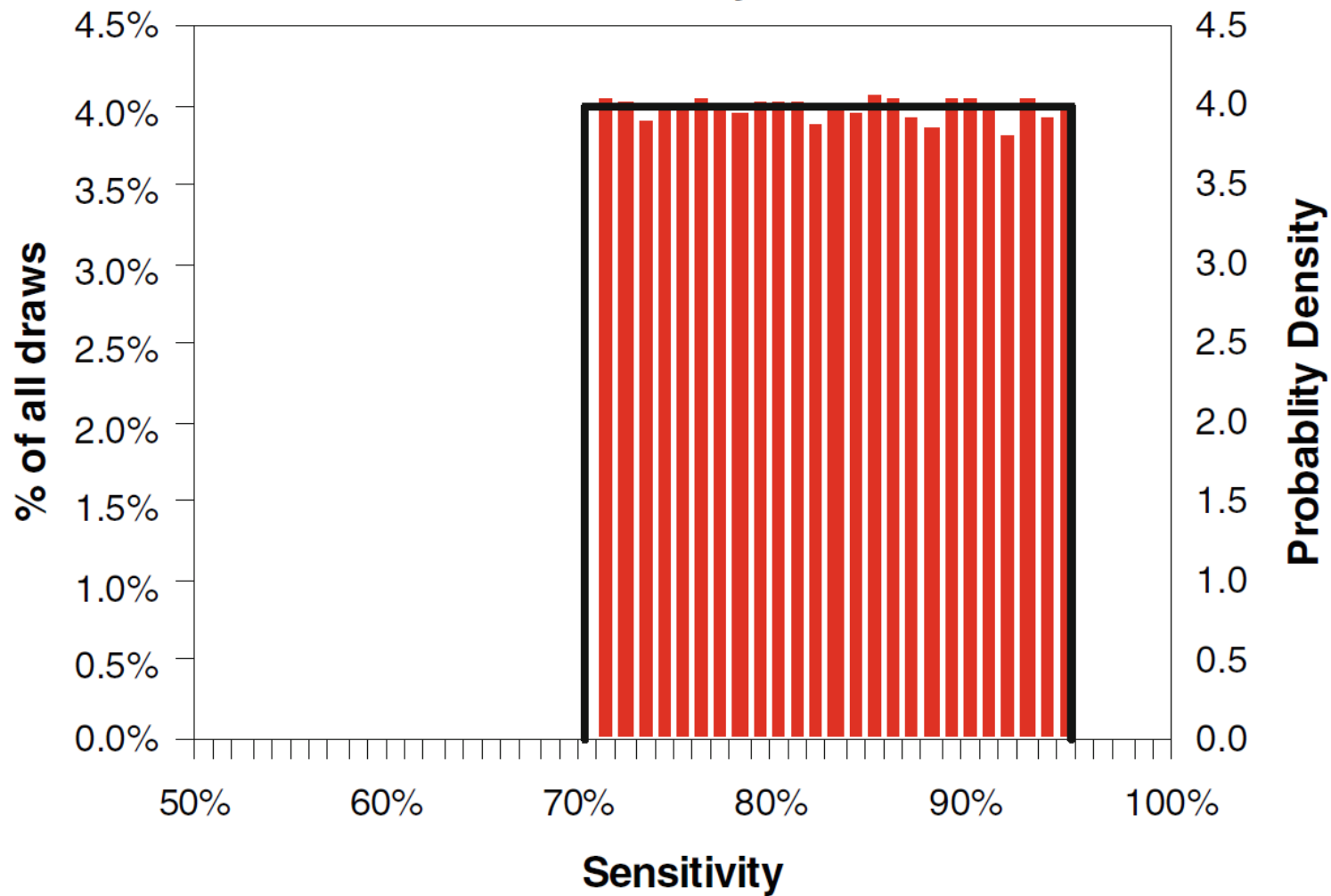
~~**Bias parameters**~~



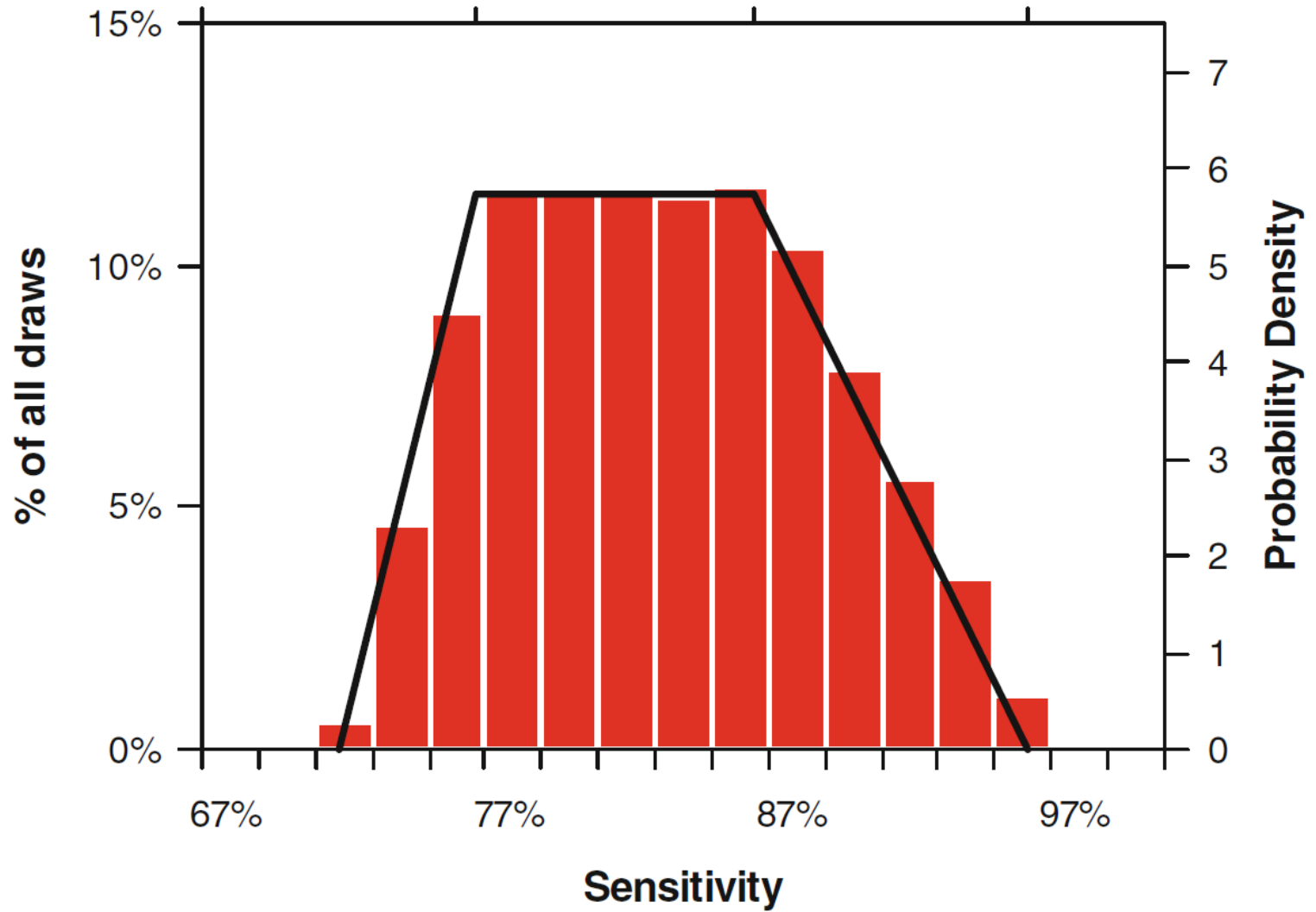
**Probability distribution
of bias parameters**

1. Assign probability distributions to each bias parameter
2. Randomly sample from the bias parameter distributions
3. Use simple bias analysis to correct for the bias
4. Resample, save, and summarize

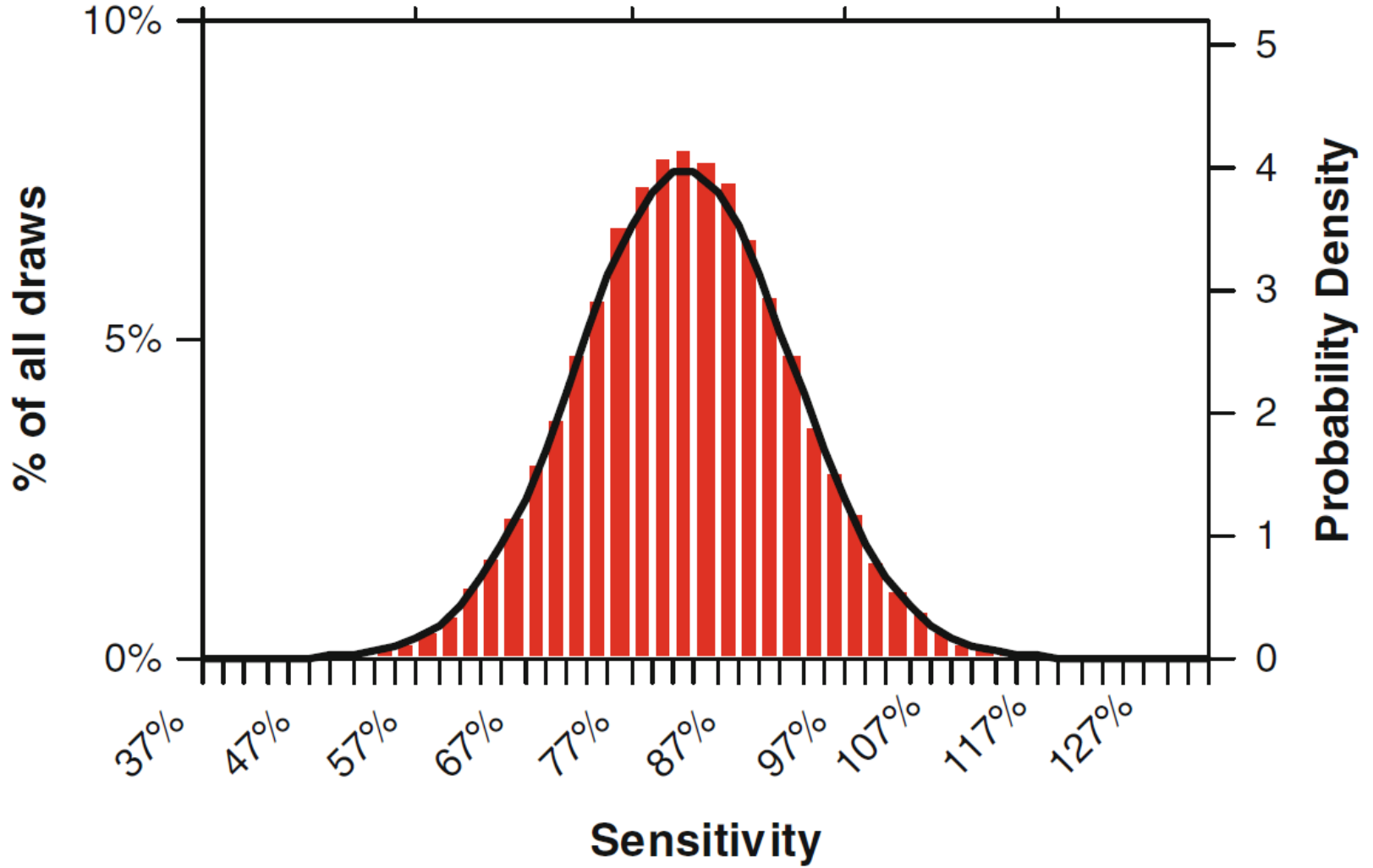
Uniform Probability Distribution



Trapezoidal Probability Distribution



Normal Probability Distribution



Ressoruces for
probabilistic bias
analysis in Excel and
SAS:

[https://sites.google.com
/site/biasanalysis/](https://sites.google.com/site/biasanalysis/)

Timothy L. Lash
Matthew P. Fox
Aliza K. Fink

Applying Quantitative Bias Analysis to Epidemiologic Data

A tool for deterministic and probabilistic sensitivity analysis of epidemiologic studies

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Milano, Italy

Matteo Bottai

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Arnold School of Public Health
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Columbia, SC

Alicja Wolk

Division of Nutritional Epidemiology
Institute of Environmental Medicine
Karolinska Institutet
Stockholm, Sweden

Sander Greenland

Departments of Epidemiology and Statistics
University of California, Los Angeles
Los Angeles, CA

Abstract. Classification errors, selection bias, and uncontrolled confounders are likely to be present in most epidemiologic studies, but the uncertainty introduced by these types of biases is seldom quantified. The authors present a simple yet easy-to-use Stata command to adjust the relative risk for exposure misclassification, selection bias, and an unmeasured confounder. This command implements both deterministic and probabilistic sensitivity analysis. It allows the user to specify a variety of probability distributions for the bias parameters, which are used to simulate distributions for the bias-adjusted exposure–disease relative risk. We illustrate the command by applying it to a case–control study of occupational resin exposure and lung-cancer deaths. By using plausible probability distributions

Example

Does circumcision protect against HIV infection?

Possible confounder: being muslim

Table 8.8 Observed data on the association between male circumcision (E) and HIV (D) (Tyndall et al, 1996)

	Total	
D_+	E_1 105	E_0 85
D_-	527	93
Total	632	178
	RR	0.35

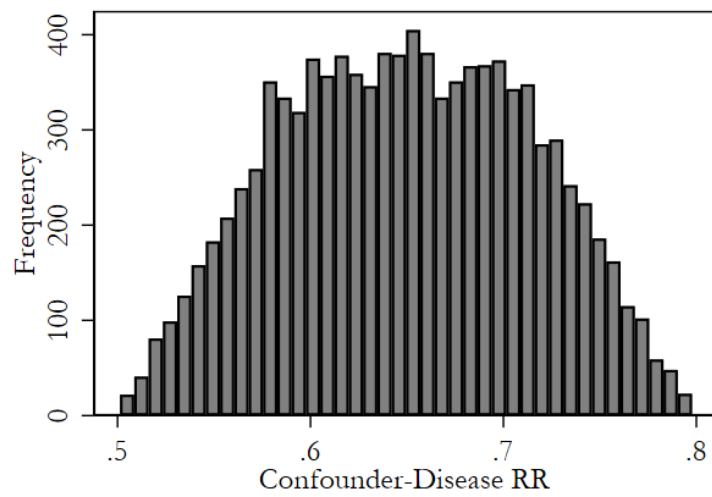
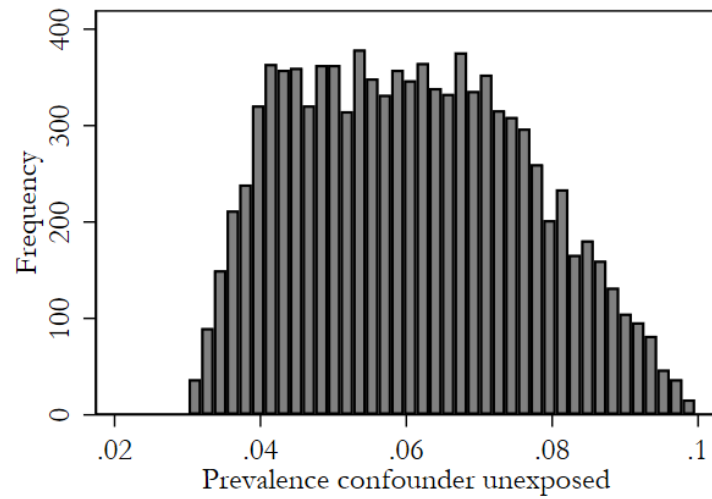
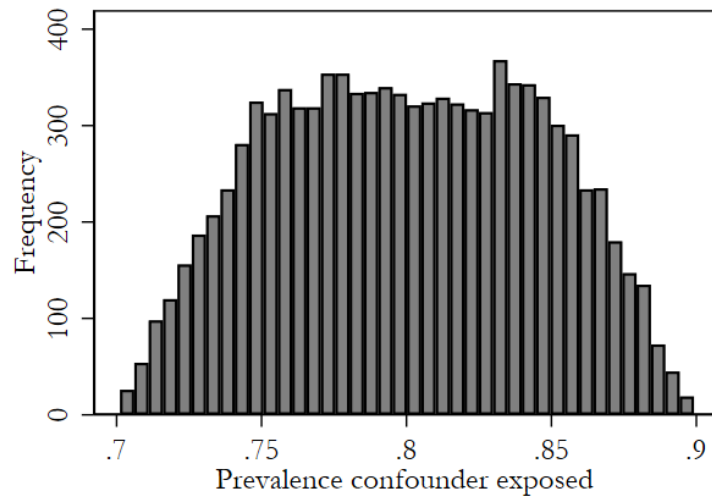
RR not adjusted for religion: 0.35 (95% CI 0.28 to 0.44)

Example

1. Assign probability distributions to each bias parameter
2. Randomly sample from the bias parameter distributions
3. Use simple bias analysis to correct for the bias
4. Resample, save, and summarize

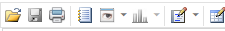
Table 8.9 Bias parameter distributions for a probabilistic bias analysis of the relationship between male circumcision and HIV stratified by an unmeasured confounder (religion)

Bias parameter	Description	Min	Mod _{low}	Mod _{up}	Max
p_1 (%)	Prevalence of being Muslim among circumcised	70	75	85	90
p_0 (%)	Prevalence of being Muslim among uncircumcised	3	4	7	10
RR _{CD}	Association between being Muslim and HIV acquisition	0.5	0.6	0.7	0.8



Example

1. Assign probability distributions to each bias parameter
2. Randomly sample from the bias parameter distributions
3. Use simple bias analysis to correct for the bias
4. Resample, save, and summarize



Review

Filter commands here

Command

findit episens

```
(R)
-----
Statistics/Data Analysis 15.1 Copyright 1985-2017 StataCorp LLC
                               StataCorp
                               4905 Lakeway Drive
                               College Station, Texas 77845 USA
                               800-STATA-PC      http://www.stata.com
                               979-696-4600     stata@stata.com
                               979-696-4601 (fax)

Unlimited-user Stata network license expires 31 Jul 2019:
  Serial number: 301509002998
  Licensed to:   IT service
                SDU

Notes:
  1. Unicode is supported; see help unicode\_advice.

. findit episens
.
.
```

Command

findit episens

Variables

Filter variables here

Name	Label
------	-------

There are no items to show.

Name	Label
------	-------

Properties

Variables

Name	Label
------	-------

Data

Filename	Label
Variables	0
Observations	0
Size	0
Memory	32M
Sorted by	

Viewer - search episens, all

File Edit History Help

net sj 8-1 st0138 search episens, all x

search for **episens** (manual: [R] search)

Search of official help files, FAQs, Examples, SJs, and STBs

SJ-8-1 [st0138](#) Deterministic and probabilistic sensitivity analysis
. N. Orsini, R. Bellocco, M. Bottai, A. Wolk, and S. Greenland
(help [episens](#), [episensi](#) if installed)
Q1/08 [SJ 8\(1\):29--48](#)
A tool for deterministic and probabilistic sensitivity
analysis of epidemiologic studies that adjusts the
relative risk for exposure misclassification, selection
bias, and an unmeasured confounder

Web resources from Stata and other users

(contacting <http://www.stata.com>)

3 packages found (Stata Journal and STB listed first)

[st0138](#) from <http://www.stata-journal.com/software/sj8-1>
SJ8-1 st0138. Deterministic and probabilistic sensitivity... /
Deterministic and probabilistic sensitivity analysis of / epidemiological
results / by N.Orsini and Alicja Wolk, Division of Nutritional
Epidemiology / Karolinska Institutet, Stockholm, Sweden / Rino Bellocco,

[episens](#) from <http://fmwww.bc.edu/RePEc/bocode/e>
'EPISENS': module for basic sensitivity analysis of epidemiological
results / episens provides basic sensitivity analysis of the observed /
relative risks adjusting for unmeasured confounding and /
misclassification of the exposure. episensi is the / immediate form of

[episensrri](#) from <http://fmwww.bc.edu/RePEc/bocode/e>
'EPISENSRRI': module for basic sensitivity analysis for unmeasured
confounders / episensrri provides basic sensitivity analysis of the
apparent or / observed relative risks according to specified plausible /

Viewer - net sj 8-1 st0138

File Edit History Help

net sj 8-1 st0138

net sj 8-1 st0138 x

Dialog* Also see* Jump to*

package **st0138** from <http://www.stata-journal.com/software/sj8-1>

TITLE

SJ8-1 st0138. Deterministic and probabilistic sensitivity...

DESCRIPTION/AUTHOR(S)

Deterministic and probabilistic sensitivity analysis of
epidemiological results
by N.Orsini and Alicja Wolk, Division of Nutritional Epidemiology
Karolinska Institutet, Stockholm, Sweden
Rino Bellocco, Department of Statistics
University of Milano-Bicocca, Milano, Italy
Matteo Bottai, Department of Epidemiology and Biostatistics
University of South Carolina
Sander Greenland, Departments of Epidemiology and Statistics
University of California, Los Angeles
Support: nicola.orsini@ki.se
After installation, type help **episens**

INSTALLATION FILES [\(click here to install\)](#)

- [st0138/episens.ado](#)
- [st0138/episensi.ado](#)
- [st0138/episens.hlp](#)
- [st0138/episensi.hlp](#)
- [st0138/episens_mcsa_unc.ado](#)
- [st0138/episens_mcsa_mie.ado](#)
- [st0138/episens_mcsa_sel.ado](#)
- [st0138/episens_mcsa_all.ado](#)

ANCILLARY FILES [\(click here to get\)](#)

- [st0138/sj_paper_examples.do](#)

[\(click here to return to the previous screen\)](#)

```
episensi 105 85 527 93, st(cs) reps(10000)
dpunexp(trapezoidal(0.03 0.04 0.07 0.10))
dpexp(trapezoidal(0.7 0.75 0.85 0.9))
drrcd(trapezoidal(0.5 0.6 0.7 0.8))
grarrtot grprior nodot
```

```
episensi 105 85 527 93, st(cs) reps(10000)
dpunexp(trapezoidal(0.03 0.04 0.07 0.10))
dpexp(trapezoidal(0.7 0.75 0.85 0.9))
drrcd(trapezoidal(0.5 0.6 0.7 0.8))
grarrtot grprior nodot
```

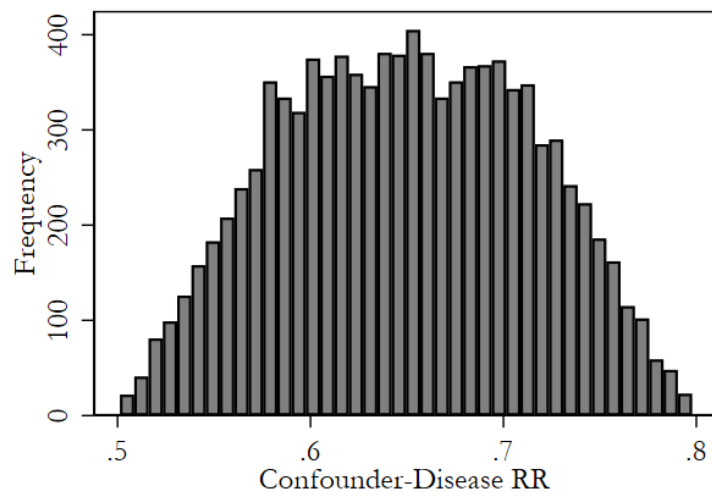
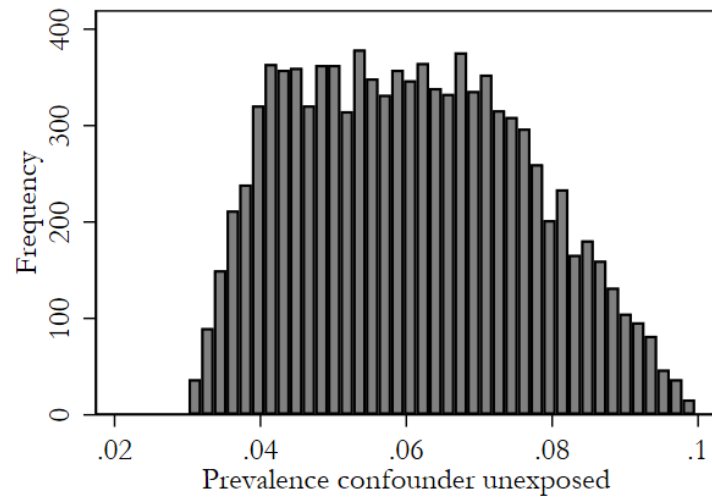
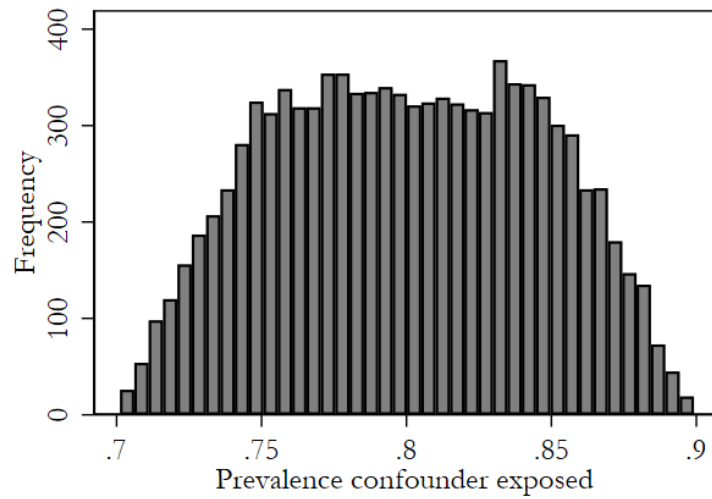
```
episensi 105 85 527 93, st(cs) reps(10000)  
dpunexp(trapezoidal(0.03 0.04 0.07 0.10))  
dpexp(trapezoidal(0.7 0.75 0.85 0.9))  
drrcd(trapezoidal(0.5 0.6 0.7 0.8))  
grarrtot grprior nodot
```

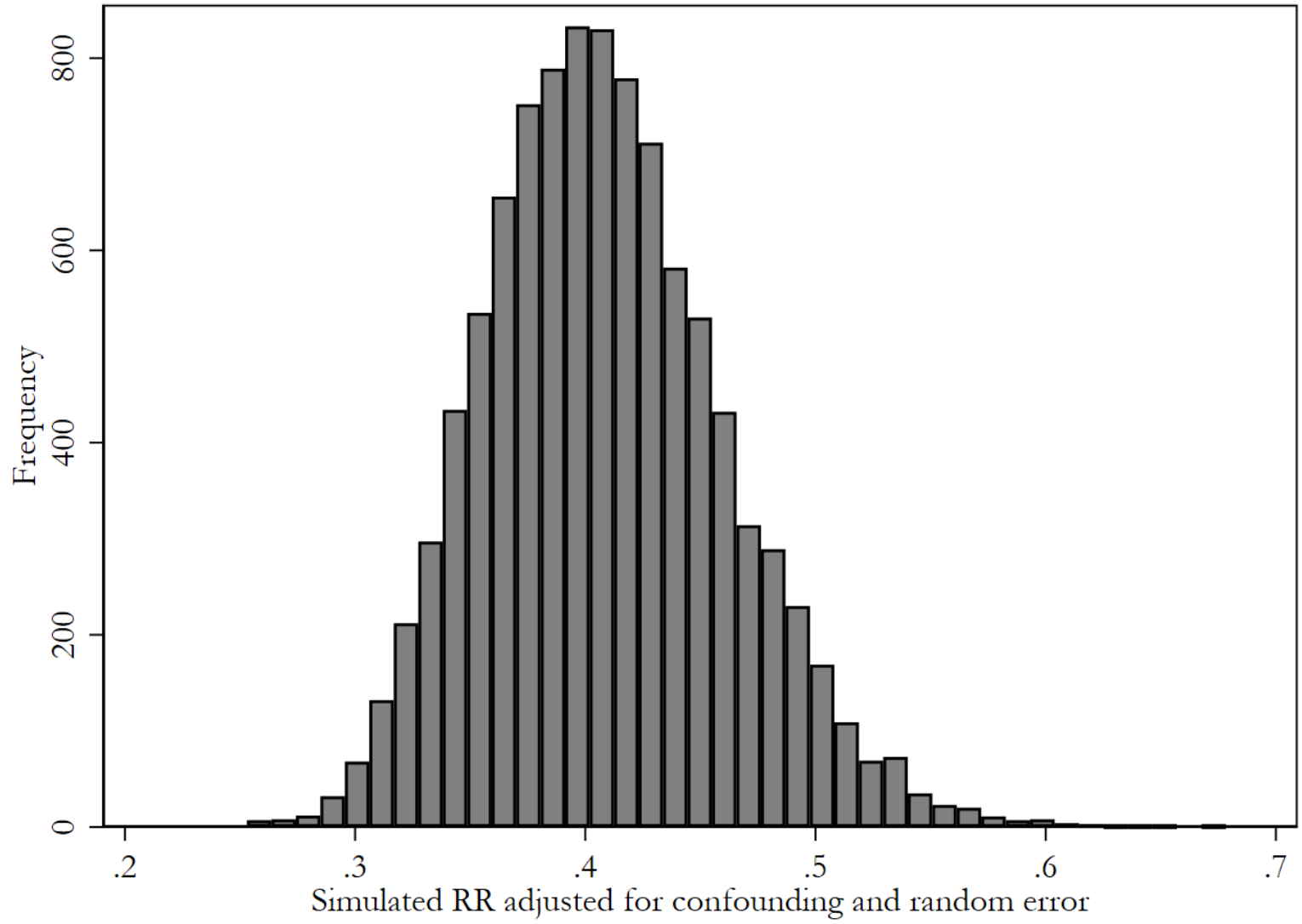
```
episensi 105 85 527 93, st(cs) reps(10000)
dpunexp(trapezoidal(0.03 0.04 0.07 0.10))
dpexp(trapezoidal(0.7 0.75 0.85 0.9))
drrcd(trapezoidal(0.5 0.6 0.7 0.8))
grarrtot grprior nodot
```



```
episensi 105 85 527 93, st(cs) reps(10000)
dpunexp(trapezoidal(0.03 0.04 0.07 0.10))
dpexp(trapezoidal(0.7 0.75 0.85 0.9))
drrcd(trapezoidal(0.5 0.6 0.7 0.8))
grarrtot grprior nodot
```

```
episensi 105 85 527 93, st(cs) reps(10000)
dpunexp(trapezoidal(0.03 0.04 0.07 0.10))
dpexp(trapezoidal(0.7 0.75 0.85 0.9))
drrcd(trapezoidal(0.5 0.6 0.7 0.8))
grarrtot grprior nodot
```





```
. episensi 105 85 527 93, st(cs) reps(1000) dpunexp(trapezoidal(0.03 0.04 0
> 5 0.85 0.9)) drrcd(trapezoidal(0.5 0.6 0.7 0.8)) grarrtot grprior nodot
```

```
Pr(c=1|e=1): Trapezoidal(.7, .75, .85, .9)
```

```
Pr(c=1|e=0): Trapezoidal(.03, .04, .07, .1)
```

Probabilistic sensitivity analysis for unmeasured confounding

		Percentiles		Ratio
	2.5	50	97.5	97.5/2.5

Conventional	0.28	0.35	0.44	1.59
Systematic error	0.38	0.40	0.44	1.17
Systematic and random error	0.31	0.40	0.51	1.65

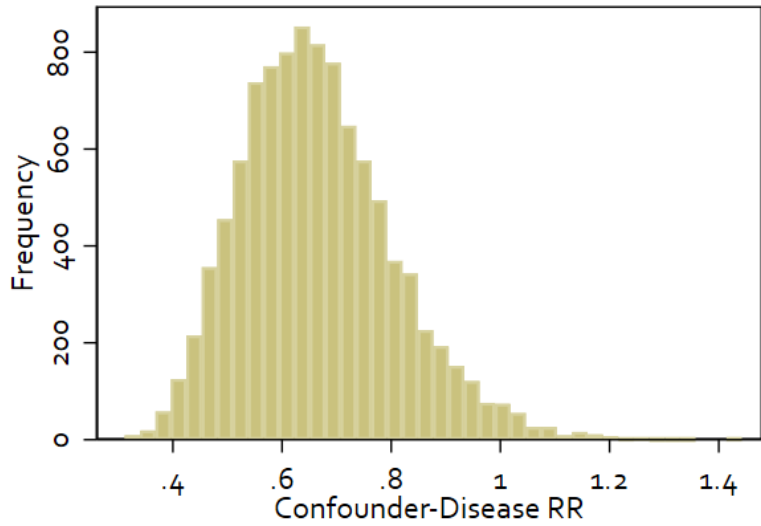
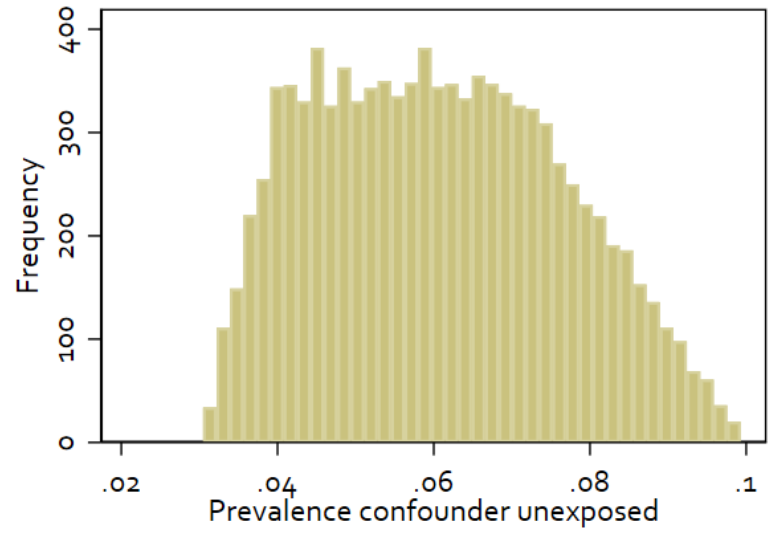
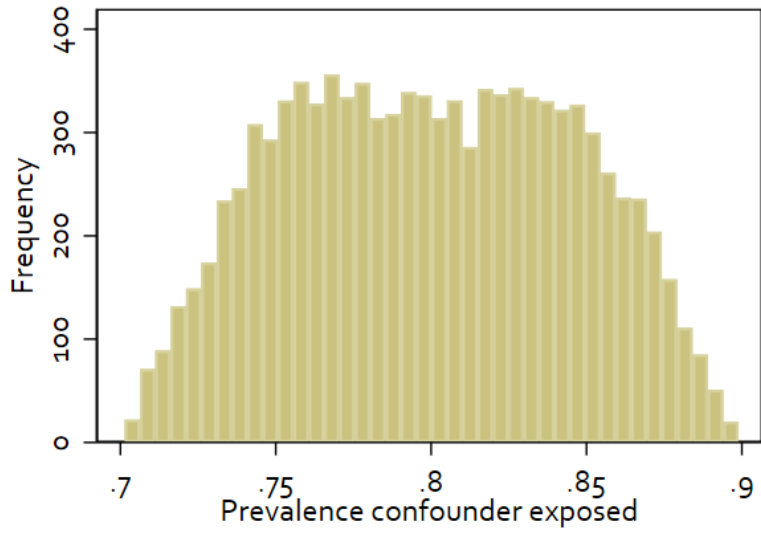
.

$RR_{CD}: 0.65 \quad (0.4-0.9)$

```
episensi 105 85 527 93, st(cc) reps(1000)
dpunexp(trapezoidal(0.03 0.04 0.07 0.10))
dpexp(trapezoidal(0.7 0.75 0.85 0.9))
drrcd(log-n(-0.43 0.21))
grarrtot grprior nodot
```

$RR_{cd}: \ln(0.65) = -0.43$

$SD: (\ln(0.9) - \ln(0.4)) / (2 * 1.96) = 0.21$



```
. episensi 105 85 527 93, st(cc) reps(10000) dpunexp(trapezoidal(0.03 0.04
> 0.85 0.9)) drrcd(log-n(-0.43 0.21)) grarrtot gprior nodot
```

```
Pr(c=1|e=1): Trapezoidal(.7,.75,.85,.9)
```

```
Pr(c=1|e=0): Trapezoidal(.03,.04,.07,.1)
```

```
RR_cd      : Log-Normal(-0.43,0.21)
```

Probabilistic sensitivity analysis for unmeasured confounding

	Percentiles			Ratio
	2.5	50	97.5	97.5/2.5

Conventional	0.15	0.22	0.31	2.06
Systematic error	0.22	0.30	0.39	1.77
Systematic and random error	0.19	0.30	0.47	2.52

ORIGINAL REPORT

Methods to apply probabilistic bias analysis to summary estimates of association[†]

Timothy L. Lash DSc, MPH^{1,2*}, Morten Schmidt MB¹,
Annette Østergaard Jensen MD, PhD¹ and Malene Cramer Engebjerg MSc¹

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Quantitative bias analysis

1. Simple bias analysis
2. Probabilistic bias analysis
 - Confounding
 - Selection bias
 - Misclassification

Probabilistic bias analysis

- Confounding
- Selection bias
- Misclassification

Accounting for several biases at the same time: Multiple bias modeling

PHARMACOEPIDEMIOLOGY AND DRUG SAFETY 2006; **15**: 291–303

Published online 31 January 2006 in Wiley InterScience (www.interscience.wiley.com). DOI: 10.1002/pds.1200

ORIGINAL REPORT

Sensitivity analysis and external adjustment for unmeasured confounders in epidemiologic database studies of therapeutics[†]

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<http://www.drugepi.org/dope-downloads>

Sensitivity Analysis in Observational Research: Introducing the E-Value

Tyler J. VanderWeele, PhD, and Peng Ding, PhD

Sensitivity analysis is useful in assessing how robust an association is to potential unmeasured or uncontrolled confounding. This article introduces a new measure called the “E-value,” which is related to the evidence for causality in observational studies that are potentially subject to confounding. The E-value is defined as the minimum strength of association, on the risk ratio scale, that an unmeasured confounder would need to have with both the treatment and the outcome to fully explain away a specific treatment-outcome association, conditional on the measured covariates. A large E-value implies that considerable unmeasured confounding would be needed to explain away an effect estimate. A small E-value implies little unmeasured confounding would be needed to explain away an effect estimate.

The authors propose that in all observational studies intended to produce evidence for causality, the E-value be reported or some other sensitivity analysis be used. They suggest calculating the E-value for both the observed association estimate (after adjustments for measured confounders) and the limit of the confidence interval closest to the null. If this were to become standard practice, the ability of the scientific community to assess evidence from observational studies would improve considerably, and ultimately, science would be strengthened.

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<https://evalue.hmdc.harvard.edu/>

Statistics for Biology and Health

Timothy L. Lash
Matthew P. Fox
Aliza K. Fink

Applying Quantitative Bias Analysis to Epidemiologic Data

 Springer

ORIGINAL REPORT

Methods to apply probabilistic bias analysis to summary estimates of association[†]

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Education Corner

Good practices for quantitative bias analysis

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George Maldonado,⁴ Lawrence C McCandless⁵ and Sander Greenland⁶**

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