

Epidemiology is a data science – if only epidemiologists knew

Success stories of modernizing data science practice and education in epidemiology

Konrad H. Stopsack, BIPS

Travis A. Gerke, cStructure

Emily Riederer, Capital One

Malcolm Barrett, Stanford University

Wednesday, June 11, 2025

Data Science

Medicine

Epidemiology

Informatics

Biostatistics

...

Health Science

Population Science

Computer Science

Data Science

... Science

Data Science

Medicine

Health Science

Epidemiology

Population Science

Informatics

Computer Science

Biostatistics

Data Science

...

... Science

Epidemiologic data science

Caring for our data before we put it into a model or into a paper.

Epidemiologists care about their data



Epidemiologists care about their data



Eur J Epidemiol (2017) 32:863–865
DOI 10.1007/s10654-017-0314-3

ESSAY

The growing rift between epidemiologists and their data

Kenneth J. Rothman^{1,2}

Cutter Lecture, Harvard School of Public Health, December 2014

Welcome to this SER session!



Konrad Stopsack (BIPS)
Epidemiologic research

Table creation

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Epidemiologic research
Table creation



Travis Gerke (PCCTC/cStructure)
Clinical trials/Startup
DAG/LLM-based causal workflows

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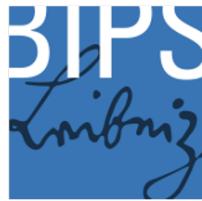


Travis Gerke (PCCTC/cStructure)
Clinical trials/Startup
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Emily Riederer (Capital One)
Finance
Project organization and workflows

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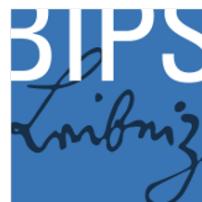


Emily Riederer (Capital One)
Finance
Project organization and workflows



Malcolm Barrett (Stanford)
Research/programming
Code review

Questions?



Please submit your questions using the Whova App as we go along.

A screenshot of the Whova mobile application interface. At the top, there's a blue header bar with the time "10:41", signal strength, "5G", and battery level "100%". Below the header, the word "Details" is centered above a list of items. A red rectangular box highlights the "0 Questions Asked" item in the list.

10:41 5G 100%

< Home Details

Symposia

Epidemiology is a data science – if only epidemiologists knew: Success stories of modernizing data science practice and education in epidemiology

Wed, Jun 11
10:15 AM - 11:45 AM

Location: Commonwealth >

122 Attending >

0 Session Polls >

3 Likes >

0 Comments >

0 Questions Asked > 0 Questions Asked

Overview

Chair(s): Konrad Stopsack Presenters: · Konrad Stopsack - Use Case 1: No more hand-typed numbers – Epidemiologic results tables in 20... [See more](#)

Speaker

 Konrad Stopsack

Questions?

Please submit your questions using the Whova App as we go along.

10:41 5G 100%

< Home Details ⌂

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See more

Speaker

Konrad Stopsack

10:42 5G 100%

< Questions for Epidemiology is a d... ⌂

Sort: Votes Filter: All

Ask a Question

View as Attendee

No more hand-typed numbers – Epidemiologic results tables in 2025

Konrad H. Stopsack

Professor and Chair, Department of Epidemiologic Methods and Etiologic Research
Leibniz Institute for Prevention Research and Epidemiology – BIPS
Bremen, Germany

I have no relevant financial relationships to disclose.

How do our analyses produce results?

1. Write code in a text editor

```
1 data work.cribriiform;
2   merge work.cases cribri.cribriiform_final;
3   by id;
4   if missing(cribriiform) then delete;
5   label cribriiform ='Morphology';
6   run;
7
8 proc phreg data=work.cribriiform;
9   class gleason (ref='2') cribriiform(ref='0');
10  model lethalfu*eventlethal(0)=cribriiform gleason / ties=efron;
11  hazardratio cribriiform / at(gleason=ref) diff=ref;
12  output out=phres wtresschoen=crib_res;
13 run;
```

How do our analyses produce results?

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2. Submit code to a server that houses the data

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How do our analyses produce results?

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2. Submit code to a server that houses the data
3. Receive a log file containing the results

```
1 data work.cribriform;
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12  output out=phres wtresschoen=crib_res;
13 run;
```

Analysis of Maximum Likelihood Estimates						
Parameter	DF	Parameter Estimate	Standard Error	Chi-Square	Pr > ChiSq	Hazard Ratio
cribriform	1	0.97671	0.21231	21.1646	<.0001	2.656 Morphology

Hazard Ratios for Morphology				
Description	Point Estimate	Confidence Limits	95% Wald	
cribriform Unit=1	2.656	1.752	4.026	

How do our analyses produce results?

1. Write code in a text editor

2. Submit code to a server that houses the data

3. Receive a log file containing the results

4. Type the results into Word



Table 3. Lethal disease associated with invasive cribriform 4 (NC4) in the prospective prostate cancer cohorts with and the Physicians' Health Study.

	Total	Lethal	HR ^a	95% CI ^a
Overall	218	43		
Unadjusted			2.66	1.75 to 4.03
Model 1: + Gleason			1.62	1.05 to 2.49
Model 2: + Age, BMI			1.67	1.08 to 2.59
Model 3: + cTNM			1.45	0.92 to 2.27

```

1 data work.cribriform;
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3 by id;
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Wish list for epidemiologic results tables, 2025

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Wish list for epidemiologic results tables, 2025

1. Descriptive and inferential results should go hand-in-hand

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Wish list for epidemiologic results tables, 2025

1. Descriptive and inferential results should go hand-in-hand
2. Code should produce a publication-ready table
3. Sensitivity analyses should be easy and quick

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Wish list for epidemiologic results tables, 2025

1. Descriptive and inferential results should go hand-in-hand
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Let us make creating epidemiologic results tables easy, reproducible, and fun!

Example data built into R

```
data(flchain, package = "survival")
```

Monoclonal gammopathy of unclear significance (MGUS) and mortality, Olmsted County, MN, 1995–2003

age	sex	sample_yr	creatinine	MGUS status	futime	death
97	F	1997	1.7	No MGUS	0.23	1
92	F	2000	0.9	No MGUS	3.51	1
94	F	1997	1.4	No MGUS	0.19	1
92	F	1996	1.0	No MGUS	0.31	1
93	F	1996	1.1	No MGUS	2.84	1
90	F	1997	1.0	No MGUS	3.71	1
90	F	1996	0.8	No MGUS	7.81	1
90	F	1999	1.2	No MGUS	1.02	1
93	F	1996	1.2	No MGUS	9.06	1
91	F	1996	0.8	No MGUS	3.63	1

... plus 7864 additional observations.

Kyle R *et al.* Prevalence of monoclonal gammopathy of undetermined significance. *N Engl J Med.* 2006.

Dispenzieri A *et al.* Use of nonclonal serum immunoglobulin free light chains to predict overall survival in the general population. *Mayo Clin Proc.* 2012.

Creating epidemiologic results tables, 2025

```
1 library(rifftable)
2
3 tribble(
4   ~type,           ~label,
5   "total",        "Participants",
6   "events/time",  "Deaths/person-years",
7   "cuminc",       "10-year risk",
8   "cumincratio", "10-year risk ratio (95% CI)",
9   "hr",           "Hazard ratio (95% CI)"
10 ) |>
11   mutate(
12     exposure = "mgus_factor",
13     event = "death",
14     time = "futime",
15     arguments = list(list(timepoint = 10)))
16 ) |>
17   rifftable(data = flchain) |>
18   rt_gt()
```

Creating epidemiologic results tables, 2025

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```

MGUS status	No MGUS	MGUS
Participants	7759	115
Deaths/person-years	2153/77632	16/1292
10-year risk	0.24	0.11
10-year risk ratio (95% CI)	1 (reference)	0.45 (0.30, 1.01)
Hazard ratio (95% CI)	1 (reference)	0.44 (0.27, 0.73)

Sensitivity analyses made easy

```
1 tribble(
2   ~type,           ~label,
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4   "hr",           "Hazard ratio (95% CI)"
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```

```

1 tribble(
2   ~type,      ~label,          ~confounders,
3   "events/total", "Deaths/participants",    """",
4   "hr",        "Hazard ratio (95% CI)",      """",
5   "hr",        " Creatinine-adjusted",        "+ creatinine",
6   "hr",        " Creatinine/age-adjusted",    "+ creatinine + age",
7 ) |>
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Creatinine/age-adjusted	1 (reference)	0.89 (0.54, 1.45)

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```

```

1 tribble(
2   ~type,      ~label,      ~ci,
3   "events/total", "Deaths/participants", NA,
4   "",           "Hazard ratio",  NA,
5   "hr",        "  with 95% CI", NA,
6   "hr",        "  with 80% CI",  0.8,
7   "hr",        "  with 99.5% CI", 0.995
8 ) |>
9   mutate(
10  exposure = "mgus_factor",
11  event = "death",
12  time = "futime",
13  confounders = "+ creatinine"
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3   "events/total", "Deaths/participants",    """",
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```

```

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4   "",           "Hazard ratio",  NA,
5   "hr",        "  with 95% CI", NA,
6   "hr",        "  with 80% CI",  0.8,
7   "hr",        "  with 99.5% CI", 0.995
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MGUS status	No MGUS	MGUS
Deaths/participants	2153/7759	16/115
Hazard ratio		
with 95% CI	1 (reference)	0.52 (0.32, 0.84)
with 80% CI	1 (reference)	0.52 (0.37, 0.71)
with 99.5% CI	1 (reference)	0.52 (0.26, 1.04)

Stratified and regression analyses at once

```
1 tribble(
2   ~type,           ~label,           ~stratum,
3   "events/total", "Deaths/participants",  "",
4   "hr",            "Hazard ratio (95% CI)", c("F", "M"),
5   "",              "*Female*",        "F",
6   "events/total", " Deaths/participants", "F",
7   "hr",            " Hazard ratio (95% CI)", "F",
8   "",              "*Male*",          "M",
9   "events/total", " Deaths/participants", "M",
10  "hr",            " Hazard ratio (95% CI)", "M",
11 ) |>
12 mutate(
13   exposure = "mgus_factor",
14   event = "death",
15   time = "futime",
16   effect_modifier = "sex"
17 ) |>
18 riftable(data = flchain) |>
19 rt_gt()
```

Stratified and regression analyses at once

```

1 tribble(
2   ~type,      ~label,      ~stratum,
3   "events/total", "Deaths/participants",    "",
4   "hr",        "Hazard ratio (95% CI)",    c("F", "M"),
5   "",          "*Female*",                 "F",
6   "events/total", " Deaths/participants",   "F",
7   "hr",        " Hazard ratio (95% CI)",   "F",
8   "",          "*Male*",                   "M",
9   "events/total", " Deaths/participants",   "M",
10  "hr",        " Hazard ratio (95% CI)",   "M",
11 ) |>
12 mutate(
13   exposure = "mgus_factor",
14   event = "death",
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Deaths/participants	2153/7759	16/115	
Hazard ratio (95% CI)	1 (reference)	0.44 (0.27, 0.73)	
<i>Female</i>			
Deaths/participants	1154/4282	11/68	
Hazard ratio (95% CI)	1 (reference)	0.55 (0.30, 0.99)	
<i>Male</i>			
Deaths/participants	999/3477	5/47	
Hazard ratio (95% CI)	1 (reference)	0.32 (0.13, 0.76)	

Different exposure? No problem

```

1 tribble(
2   ~type,      ~label,          ~stratum,
3   "events/total", "Deaths/participants",  "", 
4   "hr",       "Hazard ratio (95% CI)",  c("F", "M"),
5   "",         "*Female*",        "F",
6   "events/total", "Deaths/participants",  "F",
7   "hr",       "Hazard ratio (95% CI)",  "F",
8   "",         "*Male*",          "M",
9   "events/total", "Deaths/participants",  "M",
10  "hr",      "Hazard ratio (95% CI)",  "M",
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7   "hr",       "Hazard ratio (95% CI)",  "F",
8   "",         "*Male*",          "F",
9   "events/total", "Deaths/participants",  "M",
10  "hr",      "Hazard ratio (95% CI)",  "M",
11 ) |>
12 mutate(
13   exposure = "age_group",
14   event = "death",
15   time = "futime",
16   effect_modifier = "sex"
17 ) |>
18 riftable(data = flchain) |>
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	MGUS status	No MGUS	MGUS
Deaths/participants	2153/7759	16/115	
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<i>Male</i>			
Deaths/participants	999/3477	5/47	
Hazard ratio (95% CI)	1 (reference)	0.32 (0.13, 0.76)	

	Age at inclusion, years	50-<65	65-80	80+
Deaths/participants	443/4373	1088/2736	638/765	
Hazard ratio (95% CI)	1 (reference)	4.4 (4.0, 5.0)	17 (15, 19)	
<i>Female</i>				
Deaths/participants	193/2272	528/1538	444/540	
Hazard ratio (95% CI)	1 (reference)	4.5 (3.8, 5.3)	20 (17, 24)	
<i>Male</i>				
Deaths/participants	250/2101	560/1198	194/225	
Hazard ratio (95% CI)	1 (reference)	4.6 (4.0, 5.3)	16 (13, 19)	

Different exposure? No problem

```

1 tribble(
2   ~type,      ~label,          ~stratum,
3   "events/total", "Deaths/participants",  "", 
4   "hr",       "Hazard ratio (95% CI)",  c("F", "M"),
5   "",         "*Female*",        "F",
6   "events/total", "Deaths/participants",  "F",
7   "hr",       "Hazard ratio (95% CI)",  "F",
8   "",         "*Male*",          "M",
9   "events/total", "Deaths/participants",  "M",
10  "hr",      "Hazard ratio (95% CI)",  "M",
11 ) |>
12 mutate(
13   exposure = "mgus_factor",
14   event = "death",
15   time = "futime",
16   effect_modifier = "sex"
17 ) |>
18 riftable(data = flchain) |>
19 rt_gt()

```

```

1 tribble(
2   ~type,      ~label,          ~stratum,
3   "events/total", "Deaths/participants",  "", 
4   "hr",       "Hazard ratio (95% CI)",  c("F", "M"),
5   "",         "*Female*",        "F",
6   "events/total", "Deaths/participants",  "F",
7   "hr",       "Hazard ratio (95% CI)",  "F",
8   "",         "*Male*",          "F",
9   "events/total", "Deaths/participants",  "M",
10  "hr",      "Hazard ratio (95% CI)",  "M",
11 ) |>
12 mutate(
13   exposure = "age_group",
14   event = "death",
15   time = "futime",
16   effect_modifier = "sex"
17 ) |>
18 riftable(data = flchain) |>
19 rt_gt()

```

	MGUS status	No MGUS	MGUS
Deaths/participants	2153/7759	16/115	
Hazard ratio (95% CI)	1 (reference)	0.44 (0.27, 0.73)	
<i>Female</i>			
Deaths/participants	1154/4282	11/68	
Hazard ratio (95% CI)	1 (reference)	0.55 (0.30, 0.99)	
<i>Male</i>			
Deaths/participants	999/3477	5/47	
Hazard ratio (95% CI)	1 (reference)	0.32 (0.13, 0.76)	

	Age at inclusion, years	50-<65	65-80	80+
Deaths/participants	443/4373	1088/2736	638/765	
Hazard ratio (95% CI)	1 (reference)	4.4 (4.0, 5.0)	17 (15, 19)	
<i>Female</i>				
Deaths/participants	193/2272	528/1538	444/540	
Hazard ratio (95% CI)	1 (reference)	4.5 (3.8, 5.3)	20 (17, 24)	
<i>Male</i>				
Deaths/participants	250/2101	560/1198	194/225	
Hazard ratio (95% CI)	1 (reference)	4.6 (4.0, 5.3)	16 (13, 19)	

Different exposure? No problem

```

1 tribble(
2   ~type,      ~label,           ~stratum,
3   "events/total", "Deaths/participants",  "", 
4   "hr",        "Hazard ratio (95% CI)",  c("F", "M"),
5   "",          "*Female*",           "F",
6   "events/total", "Deaths/participants", "F",
7   "hr",        "Hazard ratio (95% CI)", "F",
8   "",          "*Male*",            "M",
9   "events/total", "Deaths/participants", "M",
10  "hr",       "Hazard ratio (95% CI)", "M",
11 ) |>
12 mutate(
13   exposure = "mgus_factor",
14   event = "death",
15   time = "futime",
16   effect_modifier = "sex"
17 ) |>
18 rifttable(data = flchain) |>
19 rt_gt()

```

```

1 tribble(
2   ~type,      ~label,
3   "events/total", "Deaths/participant",
4   "hr",        "Hazard ratio (95% CI)",
5   "",          "*Female*",           "F",
6   "events/total", "Deaths/participant",
7   "hr",        "Hazard ratio (95% CI)",
8   "",          "*Male*",            "M",
9   "events/total", "Deaths/participant",
10  "hr",       "Hazard ratio (95% CI)",
11 ) |>
12 mutate(
13   exposure = "age_group",
14   event = "death",
15   time = "futime",
16   effect_modifier = "sex"
17 ) |>
18 rifttable(data = flchain) |>
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```



	MGUS status	No MGUS	MGUS
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Deaths/participants	999/3477	5/47	
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	Age at inclusion, years	50-<65	65-80	80+
Deaths/participants	443/4373	1088/2736	638/765	
Hazard ratio (95% CI)	1 (reference)	4.4 (4.0, 5.0)	17 (15, 19)	
<i>Female</i>				
Deaths/participants	193/2272	528/1538	444/540	
Hazard ratio (95% CI)	1 (reference)	4.5 (3.8, 5.3)	20 (17, 24)	
<i>Male</i>				
Deaths/participants	250/2101	560/1198	194/225	
Hazard ratio (95% CI)	1 (reference)	4.6 (4.0, 5.3)	16 (13, 19)	

riftable's data model

The design

```

1 design <- tribble(
2   ~type,           ~label,
3   "total",        "Participants",
4   "events/time", "Deaths/person-years",
5   "cuminc",       "10-year risk",
6   "cumincratio", "10-year risk ratio (95% CI)",
7   "hr",           "Hazard ratio (95% CI)"
8 ) |>
9   mutate(
10   exposure = "mgus_factor",
11   event = "death",
12   time = "futime",
13   arguments = list(list(timepoint = 10))
14 )

```

The data

```

# A tibble: 7,874 × 7
  age sex sample_yr creatinine mgus_factor futime death
  <dbl> <fct>    <dbl>      <dbl> <fct>      <dbl> <dbl>
1 97 F     1997      1.7 No MGUS  0.233     1
2 92 F     2000      0.9 No MGUS  3.51      1
3 94 F     1997      1.4 No MGUS  0.189     1
4 92 F     1996      1   No MGUS  0.315     1
5 93 F     1996      1.1 No MGUS  2.84      1
6 90 F     1997      1   No MGUS  3.71      1
7 90 F     1996      0.8 No MGUS  7.81      1
8 90 F     1999      1.2 No MGUS  1.02      1
9 93 F     1996      1.2 No MGUS  9.06      1
10 91 F    1996      0.8 No MGUS  3.63      1
# i 7,864 more rows

```

riftable's data model

The design

```
# A tibble: 5 × 6
  type      label            exposure event time   arguments
  <chr>     <chr>           <chr>    <chr> <chr> <list>
1 total     Participants    mgus_fa... death futi... <named list>
2 events/time Deaths/person-years mgus_fa... death futi... <named list>
3 cuminc    10-year risk    mgus_fa... death futi... <named list>
4 cumincratio 10-year risk ratio (9... mgus_fa... death futi... <named list>
5 hr        Hazard ratio (95% CI) mgus_fa... death futi... <named list>
```

The data

```
# A tibble: 7,874 × 7
  age sex   sample_yr creatinine mgus_factor futime death
  <dbl> <fct>    <dbl>       <dbl> <fct>      <dbl> <dbl>
1 97   F        1997       1.7  No MGUS    0.233    1
2 92   F        2000       0.9  No MGUS    3.51     1
3 94   F        1997       1.4  No MGUS    0.189    1
4 92   F        1996       1    No MGUS    0.315    1
5 93   F        1996       1.1  No MGUS    2.84     1
6 90   F        1997       1    No MGUS    3.71     1
7 90   F        1996       0.8  No MGUS    7.81     1
8 90   F        1999       1.2  No MGUS    1.02     1
9 93   F        1996       1.2  No MGUS    9.06     1
10 91  F        1996       0.8  No MGUS    3.63     1
# i 7,864 more rows
```

rifftable's data model

The design

```
# A tibble: 5 × 6
  type      label            exposure event time   arguments
  <chr>     <chr>          <chr>    <chr> <chr> <list>
1 total     Participants    mgus_fa... death futi... <named list>
2 events/time Deaths/person-years mgus_fa... death futi... <named list>
3 cuminc    10-year risk    mgus_fa... death futi... <named list>
4 cumincrato 10-year risk ratio (9... mgus_fa... death futi... <named list>
5 hr        Hazard ratio (95% CI) mgus_fa... death futi... <named list>
```

The data

```
# A tibble: 7,874 × 7
  age sex  sample_yr creatinine mgus_factor futime death
  <dbl> <fct> <dbl>       <dbl> <fct>       <dbl> <dbl>
1 97   F      1997       1.7 No MGUS  0.233   1
2 92   F      2000       0.9 No MGUS  3.51    1
3 94   F      1997       1.4 No MGUS  0.189   1
4 92   F      1996       1   No MGUS  0.315   1
5 93   F      1996       1.1 No MGUS  2.84    1
6 90   F      1997       1   No MGUS  3.71    1
7 90   F      1996       0.8 No MGUS  7.81    1
8 90   F      1999       1.2 No MGUS  1.02    1
9 93   F      1996       1.2 No MGUS  9.06    1
10 91   F     1996       0.8 No MGUS  3.63    1
# i 7,864 more rows
```

The table produced by `rifftable()`

```
1 rifftable(
2   design = design,
3   data = flchain
4 )
```



```
# A tibble: 5 × 3
`MGUS status` `No MGUS` MGUS
<chr>          <chr>    <chr>
1 Participants  7759    115
2 Deaths/person-years 2153/77632 16/1292
3 10-year risk 0.24    0.11
4 10-year risk ratio (95% CI) 1 (reference) 0.45 (0.30, 1.01)
5 Hazard ratio (95% CI) 1 (reference) 0.44 (0.27, 0.73)
```

rifftable's data model

The design

```
# A tibble: 5 × 6
  type      label            exposure event time  arguments
  <chr>     <chr>           <chr>    <chr> <chr> <list>
1 total     Participants    mgus_fa... death futi... <named list>
2 events/time Deaths/person-years mgus_fa... death futi... <named list>
3 cuminc    10-year risk    mgus_fa... death futi... <named list>
4 cumincrato 10-year risk ratio (9... mgus_fa... death futi... <named list>
5 hr        Hazard ratio (95% CI) mgus_fa... death futi... <named list>
```

The data

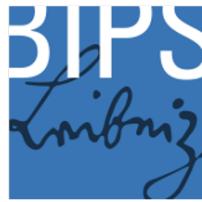
```
# A tibble: 7,874 × 7
  age sex   sample_yr creatinine mgus_factor futime death
  <dbl> <fct>    <dbl>       <dbl> <fct>      <dbl> <dbl>
1 97 F      1997       1.7 No MGUS  0.233  1
2 92 F      2000       0.9 No MGUS  3.51   1
3 94 F      1997       1.4 No MGUS  0.189   1
4 92 F      1996       1  No MGUS  0.315   1
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9 93 F      1996       1.2 No MGUS  9.06   1
10 91 F     1996       0.8 No MGUS  3.63   1
# i 7,864 more rows
```

The table produced by `rifftable()`

```
1 rifftable(
2   design = design,
3   data = flchain
4 ) |>
5   rt_gt()
```

MGUS status	No MGUS	MGUS
Participants	7759	115
Deaths/person-years	2153/77632	16/1292
10-year risk	0.24	0.11
10-year risk ratio (95% CI)	1 (reference)	0.45 (0.30, 1.01)
Hazard ratio (95% CI)	1 (reference)	0.44 (0.27, 0.73)

Great software for analyses and tables exists

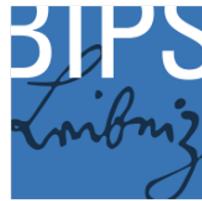


- Excel calculator **Episheet**
by Kenneth Rothman
- R package **gtsummary**
by Daniel Sjoberg
- Many others, of varying scope and quality

Great software for analyses and tables exists

Why rfttable

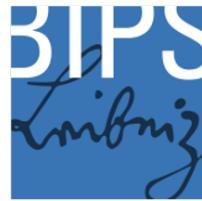
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Why rifttable

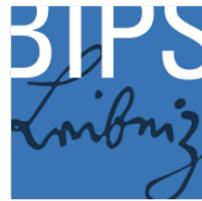


- Integrates into real data analysis

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Why rifttable



- Integrates into real data analysis
- Shows descriptive and inferential statistics side-by-side

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Why rifttable

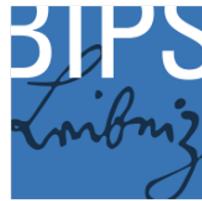


- Integrates into real data analysis
- Shows descriptive and inferential statistics side-by-side
- Makes stratified analyses easy
(and table 2 fallacies hard)

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Why rifttable



- Integrates into real data analysis
- Shows descriptive and inferential statistics side-by-side
- Makes stratified analyses easy
(and table 2 fallacies hard)
- Rounds estimates well

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- Many others, of varying scope and quality

Why rifttable



- Integrates into real data analysis
- Shows descriptive and inferential statistics side-by-side
- Makes stratified analyses easy
(and table 2 fallacies hard)
- Rounds estimates well
- Facilitates sensitivity analyses

Great software for analyses and tables exists

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Why rifttable

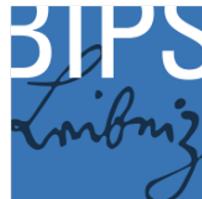


- Integrates into real data analysis
- Shows descriptive and inferential statistics side-by-side
- Makes stratified analyses easy
(and table 2 fallacies hard)
- Rounds estimates well
- Facilitates sensitivity analyses
- Extends with custom estimators

Great software for analyses and tables exists

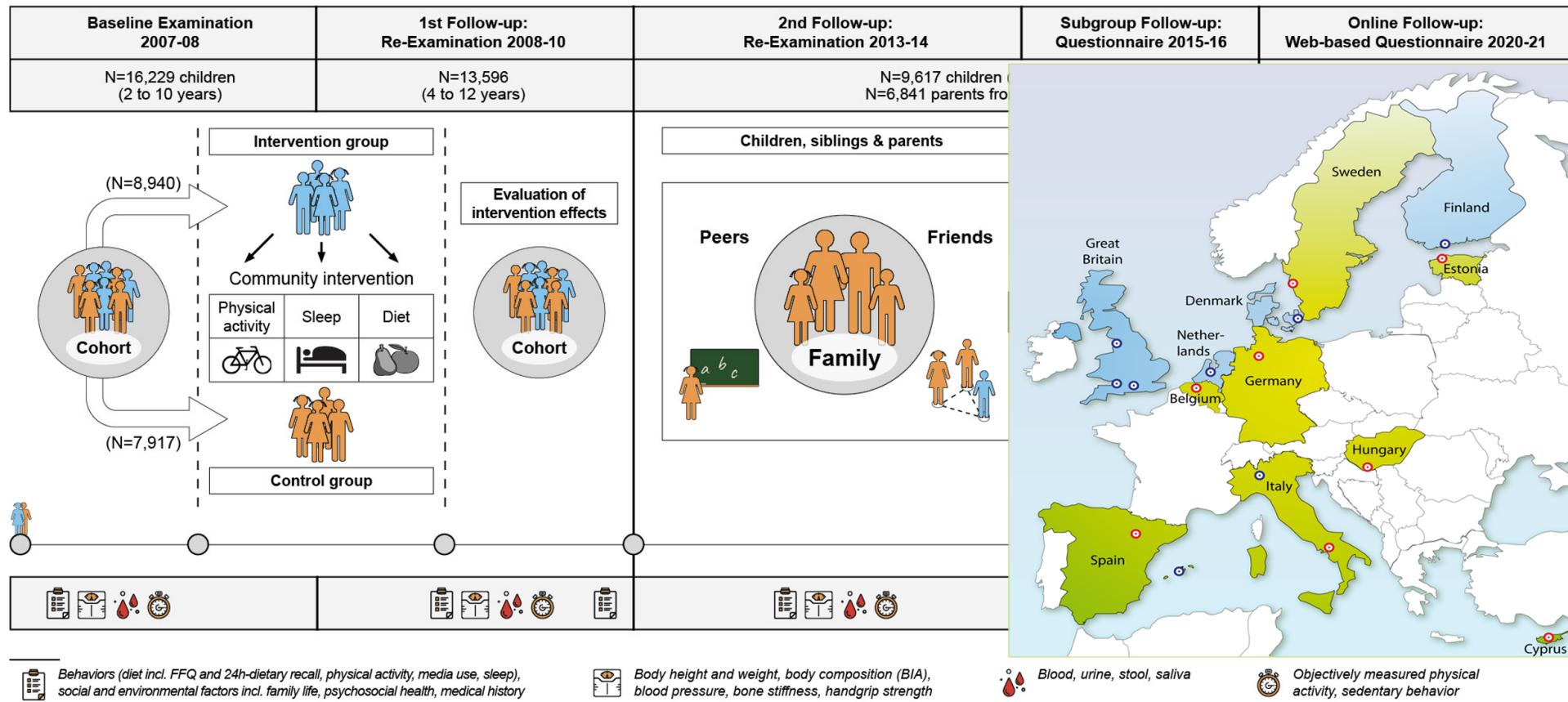
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Why rifttable



- Integrates into real data analysis
- Shows descriptive and inferential statistics side-by-side
- Makes stratified analyses easy
(and table 2 fallacies hard)
- Rounds estimates well
- Facilitates sensitivity analyses
- Extends with custom estimators
- Has a website with copy-paste examples

The IDEFICS/I.Family cohort



Ahrens W et al. The IDEFICS cohort: design, characteristics and participation in the baseline survey. *Int J Obes.* 2011;35:S3-S15.

Ahrens W et al. Cohort profile: The transition from childhood to adolescence in European children – How I.Family extends the IDEFICS cohort. *Int J Epidemiol.* 2017;46:1394-1395.

The IDEFICS/I.Family cohort: Table 1

```
idefics |>
  filter(survey == 0) |> # Baseline only
  table1_design(
    age, country, migrant,
    bmi_score_cole_12, bmi_m, bmi_f, one_parent,
    birth_w,
    energy,
    by = gender
  ) |>
  mutate(
    digits = if_else(
      outcome %in% c("energy", "birth_w"),
      true = 0,
      false = NA
    )
  ) |>
  rifftable(diff_digits = 1) |>
  rt_gt() |>
  gt::tab_footnote(footnote = "Statistics shown in
```

Ahrens W *et al.* The IDEFICS cohort: design, characteristics and participation in the baseline survey. *Int J Obes.* 2011;35:S3-S15.

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  table1_design(
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    bmi_score_cole_12, bmi_m, bmi_f, one_parent,
    birth_w,
    energy,
    by = gender
  ) |>
  mutate(
    digits = if_else(
      outcome %in% c("energy", "birth_w"),
      true = 0,
      false = NA
    )
  ) |>
  rifftable(diff_digits = 1) |>
  rt_gt() |>
  gt::tab_footnote(footnote = "Statistics shown are count (percent) or median (interquartile range).")
```

Characteristic	Boys	Girls
N	8251	7979
Age at enrollment, years	6.2 (4.4, 7.5)	6.3 (4.5, 7.6)
Country		
Italy	1167 (14%)	1083 (14%)
Estonia	849 (10%)	870 (11%)
Cyprus	1222 (15%)	1161 (15%)
Belgium	980 (12%)	945 (12%)
Sweden	927 (11%)	882 (11%)
Germany	1053 (13%)	1013 (13%)
Hungary	1284 (16%)	1284 (16%)
Spain	769 (9%)	741 (9%)
Parent(s) with migration history	1251 (16%)	1253 (16%)
Unknown	378	353
z-score of BMI by Cole (2012)	0.2 (-0.5, 1.0)	0.3 (-0.4, 1.1)
Maternal BMI, kg/m ²	23.0 (20.9, 25.9)	22.9 (20.9, 25.8)
Unknown	536	519
Paternal BMI, kg/m ²	26.0 (24.1, 28.4)	26.0 (24.0, 28.4)
Unknown	1294	1291
Single-parent family	1148 (15%)	1061 (14%)
Unknown	633	594
Birth weight, g	3415 (3060, 3760)	3280 (2970, 3600)
Unknown	490	467
Usual energy intake, kcal/day	1563 (1388, 1728)	1431 (1304, 1546)
Unknown	3101	2935

Statistics shown are count (percent) or median (interquartile range).

Ahrens W *et al.* The IDEFICS cohort: design, characteristics and participation in the baseline survey. *Int J Obes.* 2011;35:S3-S15.

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riftable, v0.7.1

https://stopsack.github.io/riftable/ 80% Search

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Automated, Reproducible Generation of Results Tables: Bridging the Rift Between Epidemiologists and Their Data

Tables are the key format in which epidemiologists present their results. Many results tables in applied studies merely show point estimates and confidence intervals, or even p-values, from regression models: a “growing rift between epidemiologists and their data” (Rothman 2017). “Actual,” descriptive data, such as counts stratified by exposure and a main confounder or effect modifier, are often lacking.

riftable creates presentation-ready results tables for epidemiologists in an automated, reproducible fashion. The user provides the final analytical dataset and specifies the design of the table, with rows and/or columns defined by exposure(s), effect modifier(s), and estimands as desired, allowing to show descriptors and inferential estimates in one table – bridging the rift between epidemiologists and their data, one table at a time.

Installation

The riftable package can be installed from CRAN:

```
install.packages("riftable")
```

Development versions can be installed from [GitHub](#) using:

```
remotes::install_github("stopsack/riftable")
```

The latter installation procedure requires the remotes package, obtainable via
`install.packages("remotes")`.

Example

```
library(riftable)

example_design <- tibble::tribble(
  ~label, ~type, ~stratum,
  "Overall", "", "",
  "- Deaths/N", "outcomes/total", c("Low", "High"),
  ...)
```

<https://stopsack.github.io/riftable>



riftable, v0.7.1



https://stopsack.github.io/riftable/

riftable 0.7.1 Get started FAQ Example Tables More ▾

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Example

```
library(riftable)

example_design <- tibble::tribble(
  ~label, ~type, ~stratum,
  "Overall", "", ""),
  "- Deaths/N", "outcomes/total",
  ...)
```

Links
[View on CRAN](#)
[Browse source code](#)

License
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GPL (>= 3)

Citation
[Citing riftable](#)

Developers
Konrad H. Stopsack
Author, maintainer, copyri

Dev status



Also...

- Quantiles and quantile regression
- Ratios of continuous outcomes
- Competing events
- Clustering
- Trends (slopes)
- Stratified and joint models
- Inverse probability-weighted estimates
- Regression-based risk ratios and risk differences for binary outcomes

<https://stopsack.github.io/riftable>



riftable, v0.7.1



https://stopsack.github.io/riftable/

80% Search

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Automated, Reproducible Generation of Results Tables: Bridging the Rift Between Epidemiologists and Their Data

Tables are the key format in which epidemiologists present their results. Many results tables in applied studies merely show point estimates and confidence intervals, or even p-values, from regression models: a “growing rift between epidemiologists and their data” (Rothman 2017). “Actual,” descriptive data, such as counts stratified by exposure and a main confounder or effect modifier, are often lacking.

riftable creates presentation-ready results tables for epidemiologists in an automated, reproducible fashion. The user provides the final analytical dataset and specifies the design of the table, with rows and/or columns defined by exposure(s), effect modifier(s), and estimands as desired, allowing to show descriptors and inferential estimates in one table – bridging the rift between epidemiologists and their data, one table at a time.

Installation

The riftable package can be installed from CRAN:

```
install.packages("riftable")
```

Development versions can be installed from [GitHub](#) using:

```
remotes::install_github("stopsack/riftable")
```

The latter installation procedure requires the remotes package, obtainable via
`install.packages("remotes")`.

Example

```
library(riftable)

example_design <- tibble::tribble(
  ~label, ~type, ~stratum,
  "Overall", "", ""),
  "- Deaths/N", "outcomes/total",
  ...)
```

Links
[View on CRAN](#)
[Browse source code](#)

License
[Full license](#)
GPL (>= 3)

Citation
[Citing riftable](#)

Developers
Konrad H. Stopsack
Author, maintainer, copyri

Dev status
 R-CMD-check passing
 codecov 99%

Also...

- Quantiles and quantile regression
- Ratios of continuous outcomes
- Competing events
- Clustering
- Trends (slopes)
- Stratified and joint models
- Inverse probability-weighted estimates
- **Regression-based risk ratios and risk differences for binary outcomes**

<https://stopsack.github.io/riftable>



Regression models for risk ratios and risk differences

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Exposure	Unexposed	Exposed
Total	1000	1000
Cases/non-cases	20/980	40/960
Risk	2%	4%
Risk ratio	1 (reference)	2.00 (1.18, 3.4)
Odds ratio	1 (reference)	2.04 (1.20, 3.6)

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Exposure	Unexposed	Exposed
Total	1000	1000
Cases/non-cases	960/40	980/20
Risk	96%	98%
Risk ratio	1 (reference)	1.02 (1.01, 1.04)
Odds ratio	1 (reference)	2.04 (1.20, 3.6)

Why are we still reporting odds ratios in cross-sectional and cohort studies?

1. Log-binomial models do not converge

```
1 data(breastcancer, package = "risks")
2 glm(
3   formula = death ~ stage + receptor,
4   data = breastcancer,
5   family = binomial(link = "log")
6 )
```

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4. And there is Miettinen’s case-duplication approach

We no longer need to report odds ratios in cross-sectional and cohort studies

```
1 library(risks)
2 summary(
3   riskratio(
4     formula = death ~ stage + receptor,
5     data = breastcancer
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```
Risk ratio model, fitted via marginal standardization of a logistic model
with delta method (margstd_delta).
Call:
stats::glm(formula = death ~ stage + receptor, family = binomial(link =
"logit"),
           start = "(no starting values)")

Coefficients: (3 not defined because of singularities)
              Estimate Std. Error z value Pr(>|z|)
stageStage I    0.0000    0.0000    NaN    NaN
stageStage II   0.8989    0.3875   2.320   0.0203 *
stageStage III  1.8087    0.3783   4.781 1.75e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 228.15  on 191  degrees of freedom
Residual deviance: 185.88  on 188  degrees of freedom
AIC: 193.88

Number of Fisher Scoring iterations: 4

Confidence intervals for coefficients: (delta method)
                                2.5 % 97.5 %
stageStage I  0.0000000 0.000000
```

Estimating and reporting adjusted risk ratios and risk differences made easy

```
1 tribble(
2   ~type,           ~label,
3   "outcomes/total", "Deaths/total",
4   "risk",          "Risk",
5   "rr",            "Risk ratio (95% CI)",
6   "rd",            "Risk difference (95% CI)",
7 ) |>
8   mutate(
9     outcome = "death",
10    exposure = "stage",
11    confounders = "+ receptor"
12  ) |>
13  rifftable(data = breastcancer) |>
14  rt_gt() |>
15  gt::tab_footnote(footnote = "Adjusted for hormone receptor status.")
```

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Stage	Stage I	Stage II	Stage III
Deaths/total	7/67	26/96	21/29
Risk	0.10	0.27	0.72
Risk ratio (95% CI)	1 (reference)	2.46 (1.15, 5.3)	6.1 (2.91, 13)
Risk difference (95% CI)	0 (reference)	0.16 (0.05, 0.28)	0.57 (0.38, 0.77)
Adjusted for hormone receptor status.			

Compare methods if you like. In practice, simply use *g*-computation for RRs and RDs

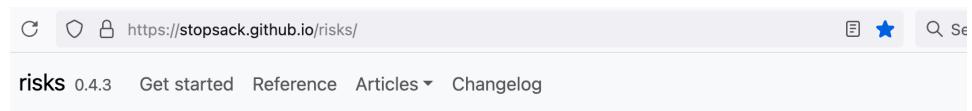
```

1 tribble(
2   ~type,           ~label,           ~arguments,
3   "outcomes/total", "Deaths/total", NA,
4   "risk",          "Risk",          NA,
5   "",              "Risk ratio (95% CI)", NA,
6   "rr",            "  *g*-computation, delta method CI", list(approach = "margstd_delta"),
7   "rr",            "  *g*-computation, bootstrap CI", list(approach = "margstd_boot"),
8   "rr",            " Poisson model, robust CI", list(approach = "robpoisson"),
9   "rr",            " Case-duplication approach", list(approach = "duplicate"),
10  "rd",            "Risk difference (95% CI)", NA,
11 ) |>
12 mutate(
13   outcome = "death",
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```

Stage	Stage I	Stage II	Stage III
Deaths/total	7/67	26/96	21/29
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Risk ratio (95% CI)			
g-computation, delta method CI	1 (reference)	2.46 (1.15, 5.3)	6.1 (2.91, 13)
g-computation, bootstrap CI	1 (reference)	2.46 (1.09, 5.9)	6.1 (3.0, 15)
Poisson model, robust CI	1 (reference)	2.52 (1.17, 5.4)	5.9 (2.78, 13)
Case-duplication approach	1 (reference)	2.52 (1.16, 5.5)	5.9 (2.79, 13)
Risk difference (95% CI)	0 (reference)	0.16 (0.05, 0.28)	0.57 (0.38, 0.77)
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risks, v0.4.3



The screenshot shows the top navigation bar of the GitHub page for the `risks` package. It includes links for "Get started", "Reference", "Articles", and "Changelog".

risks: Estimating risk ratios and risk differences using regression



Installation

The `risks` package can be installed from CRAN:

```
install.packages("risks")
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Development versions can be installed from [GitHub](#) using:

```
remotes::install_github("stopsack/risks")
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Summary

The `risks` package fits regression models for risk ratios (RR) and risk differences (RD). The package refers to "risk," but "prevalence" can be substituted throughout.

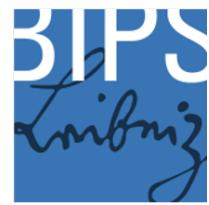
What is the association between an exposure (smoker/nonsmoker, age in years, or underweight/lean/overweight/obese) and the risk of a binary outcome (dead/alive, disease/healthy), perhaps adjusting for confounders (men/women, years of education)? For such questions, many studies default to reporting odds ratios, which may exaggerate associations when the outcome is common. Odds ratios are often used because they are easily obtained from logistic regression models. Obtaining risk ratios or risk differences, especially adjusting for confounders, has typically required more advanced biostatistics and programming skills, including in R.

The `risks` package makes estimating adjusted risk ratios and risk differences as simple as fitting a logistic regression model. No advanced programming or biostatistics skills are required. Risk ratios or risk differences are returned whenever the data would allow for fitting a logistic model.

<https://stopsack.github.io/risks>



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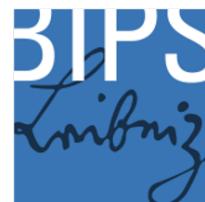
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Thank you for your attention – Please reach out

stopsack@leibniz-bips.de

We are hiring!



The [Leibniz Institute for Prevention Research and Epidemiology – BIPS](#) is one of Germany's largest and oldest research institutes focused on epidemiology.

Applications are open now for our PhD Program in Epidemiology, Statistics, and Prevention and Implementation Science, with an October start date.



[https://tinyurl.com/
bips-phd-program](https://tinyurl.com/bips-phd-program)

Reach out about this opportunity and others
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