Code

Analyses For the Manuscript: Association between Risk Literacy and Variations in Real-World Prescriptions of Potentially Hazardous Drugs Among General Physicians in England

2023-11-13

1 Get packages

Hide

```
library(tidyverse)  # for compiling data frame
library(DescTools)  # for proportion CIs and effect size
library(ggplot2)  # for graphical representation
library(psych)  # for reliability analysis/ some descriptive statistics
library(car)  #for leveneTests
library(expss)  #for Labeling
library("ggpubr")  #for combining figures
library("ggsignif")  #for adding p-values
```

2 Data input

Hide

```
varicare <- read.csv("VariCare_clean_2.csv")
varicare <- as_tibble(varicare)
varicare$starab <- as.numeric(varicare$starab)
val_lab(varicare$Years_Profession) = num_lab("
     1 <10 years
     2 10 -19 years
     3 20 - 29 years
     4 30 - 39 years
     5 ≥40 years
     ")
val_lab(varicare$s5_Range_number_physician_practice) = num_lab("
     1 1
     22-3
     3 4-5
     4 6-10
     5 ≥10
     ")
```

3 Recoding of Variables for Analyses

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```
Reliability analysis
Call: alpha(x = cbind(varicare$R1, varicare$R3, varicare$R4, varicare$R6,
    varicare$R7, varicare$R8, varicare$R9))

  raw_alpha std.alpha G6(smc) average_r S/N   ase mean   sd median_r
      0.56      0.56    0.55      0.15 1.3 0.038 0.57 0.24     0.17

    95% confidence boundaries
         lower alpha upper
Feldt     0.48  0.56  0.63
Duhachek  0.48  0.56  0.63

 Reliability if an item is dropped:
   raw_alpha std.alpha G6(smc) average_r  S/N alpha se  var.r med.r
V1      0.60      0.60    0.58      0.20 1.52    0.035 0.0076 0.192
V2      0.50      0.51    0.48      0.15 1.02    0.044 0.0117 0.139
V3      0.48      0.48    0.47      0.13 0.93    0.045 0.0146 0.098
V4      0.49      0.50    0.47      0.14 0.98    0.045 0.0102 0.139
V5      0.50      0.50    0.48      0.14 0.99    0.044 0.0140 0.111
V6      0.48      0.48    0.46      0.13 0.92    0.046 0.0105 0.139
V7      0.56      0.56    0.54      0.18 1.28    0.039 0.0145 0.192

 Item statistics
     n raw.r std.r r.cor r.drop mean   sd
V1 304  0.32  0.32 0.073   0.05 0.31 0.46
V2 304  0.57  0.56 0.443   0.33 0.64 0.48
V3 304  0.60  0.60 0.504   0.38 0.72 0.45
V4 304  0.59  0.58 0.478   0.35 0.59 0.49
V5 304  0.56  0.57 0.458   0.34 0.74 0.44
V6 304  0.60  0.61 0.523   0.38 0.69 0.46
V7 304  0.43  0.43 0.233   0.17 0.29 0.45

Non missing response frequency for each item
        0    1 miss
[1,] 0.69 0.31    0
[2,] 0.36 0.64    0
[3,] 0.28 0.72    0
[4,] 0.41 0.59    0
[5,] 0.26 0.74    0
[6,] 0.31 0.69    0
[7,] 0.71 0.29    0

Reliability analysis
Call: alpha(x = cbind(varicare$coi1, varicare$coi2, varicare$coi3,
    varicare$coi4, varicare$coi5))

  raw_alpha std.alpha G6(smc) average_r S/N   ase mean   sd median_r
      0.61      0.61    0.57      0.24 1.5 0.032 0.26 0.25     0.22

    95% confidence boundaries
```

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```
         lower alpha upper
Feldt     0.54  0.61  0.68
Duhachek  0.55  0.61  0.67

 Reliability if an item is dropped:
   raw_alpha std.alpha G6(smc) average_r  S/N alpha se  var.r med.r
V1      0.48      0.49    0.44      0.19 0.96    0.043 0.0115  0.17
V2      0.53      0.55    0.49      0.23 1.20    0.040 0.0054  0.22
V3      0.51      0.52    0.48      0.21 1.09    0.041 0.0127  0.22
V4      0.62      0.61    0.55      0.28 1.55    0.033 0.0133  0.30
V5      0.60      0.58    0.53      0.26 1.40    0.033 0.0178  0.28

 Item statistics
     n raw.r std.r r.cor r.drop  mean   sd
V1 304  0.73  0.70  0.61   0.49 0.237 0.43
V2 304  0.72  0.63  0.50   0.42 0.549 0.50
V3 304  0.73  0.66  0.54   0.45 0.359 0.48
V4 304  0.39  0.54  0.33   0.23 0.049 0.22
V5 304  0.47  0.58  0.39   0.27 0.086 0.28

Non missing response frequency for each item
        0    1 miss
[1,] 0.76 0.24    0
[2,] 0.45 0.55    0
[3,] 0.64 0.36    0
[4,] 0.95 0.05    0
[5,] 0.91 0.09    0

Reliability analysis
Call: alpha(x = cbind(varicare$BenzoH_bin, varicare$AntibioH_bin, varicare$Opioi
dH_bin))

  raw_alpha std.alpha G6(smc) average_r S/N   ase mean   sd median_r
      0.53      0.52    0.45      0.27 1.1 0.046 0.52 0.32     0.17

    95% confidence boundaries
         lower alpha upper
Feldt     0.43  0.53  0.62
Duhachek  0.44  0.53  0.62

 Reliability if an item is dropped:
   raw_alpha std.alpha G6(smc) average_r  S/N alpha se var.r med.r
V1      0.29      0.30    0.17      0.17 0.42    0.080    NA  0.17
V2      0.63      0.63    0.46      0.46 1.72    0.042    NA  0.46
V3      0.28      0.28    0.16      0.16 0.39    0.082    NA  0.16

 Item statistics
     n raw.r std.r r.cor r.drop mean   sd
V1 304  0.77  0.76  0.59   0.42 0.71 0.45
V2 304  0.58  0.62  0.26   0.20 0.21 0.41
V3 304  0.79  0.76  0.60   0.43 0.63 0.48
```


Wegwarth O, *et al. BMJ Qual Saf* 2024;0:1–8. doi: 10.1136/bmjqs-2023-016979

```
Non missing response frequency for each item
        0    1 miss
[1,] 0.29 0.71    0
[2,] 0.79 0.21    0
[3,] 0.37 0.63    0
```

4 Demographics

4.1 Years in Profession

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```
use_labels(varicare, table(Years_Profession))
DescTools::MultinomCI(as.vector(xtabs(~Years_Profession, data = varicare)), con
        f.level = 0.95,
    method = "goodman")
```

```
Years_Profession
    <10 years  10 -19 years 20 - 29 years 30 - 39 years     ≥40 years
           63           116            75            40            10
            est     lwr.ci     upr.ci
[1,] 0.20723684 0.15392332 0.27305671
[2,] 0.38157895 0.31306852 0.45514812
[3,] 0.24671053 0.18888492 0.31535622
[4,] 0.13157895 0.08942265 0.18947357
[5,] 0.03289474 0.01496057 0.07078284
```

4.2 Size of Practice

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```
use_labels(varicare, table(s5_Range_number_physician_practice))
DescTools::MultinomCI(as.vector(xtabs(~s5_Range_number_physician_practice, data
        = varicare)),
    conf.level = 0.95, method = "goodman")
```

```
s5_Range_number_physician_practice
   1    2  4-5 6-10  ≥10
   3   17   80  119   85
            est      lwr.ci     upr.ci
[1,] 0.009868421 0.002496345 0.03817808
[2,] 0.055921053 0.030512068 0.10030033
[3,] 0.263157895 0.203662369 0.33277091
[4,] 0.391447368 0.322397385 0.46513454
[5,] 0.279605263 0.218552148 0.35007327
```

4.3 Recorded Patient List Size

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```
mean(varicare$Patient_lsize)
sd(varicare$Patient_lsize)
```

```
[1] 13215.57
[1] 9971.924
```

4.4 Risk Literacy in Medical Teatment

Correctly answered risk questions regarding treatments.

Hide

```
xtabs(~R, data = varicare)
DescTools::MultinomCI(as.vector(xtabs(~R, data = varicare)), conf.level = 0.95,
        method = "goodman")
mean(varicare$R)
sd(varicare$R)
median(varicare$R)
ftable(varicare$Rsplit)
DescTools::MultinomCI(as.vector(xtabs(~Rsplit, data = varicare)))
```

```
R
 0  1  2  3  4  5  6  7
 9 16 37 54 56 75 41 16
           est     lwr.ci     upr.ci
[1,] 0.02960526 0.01231159 0.06948190
[2,] 0.05263158 0.02714590 0.09959477
[3,] 0.12171053 0.07932806 0.18225411
[4,] 0.17763158 0.12565054 0.24508906
[5,] 0.18421053 0.13125364 0.25232801
[6,] 0.24671053 0.18572322 0.31985789
[7,] 0.13486842 0.08998975 0.19727652
[8,] 0.05263158 0.02714590 0.09959477
[1] 3.976974
[1] 1.69725
[1] 4
   0   1

 116 188
          est    lwr.ci    upr.ci
[1,] 0.3815789 0.3289474 0.4403677
[2,] 0.6184211 0.5657895 0.6772099
```

4.5 Conflict of Interests

Total number of agreement to potential conflict of interest questions at least frequently.

Hide

```
xtabs(~coi, data = varicare)
DescTools::MultinomCI(as.vector(xtabs(~coi, data = varicare)), conf.level = 0.9
        5,
    method = "goodman")
mean(varicare$coi)
sd(varicare$coi)
median(varicare$coi)
ftable(varicare$coisplit)
DescTools::MultinomCI(as.vector(xtabs(~coisplit, data = varicare)))
```

```
coi
  0   1   2   3   4   5
103  88  58  39  12   4
           est      lwr.ci     upr.ci
[1,] 0.33881579 0.271519685 0.41332765
[2,] 0.28947368 0.226171108 0.36220092
[3,] 0.19078947 0.138518850 0.25690256
[4,] 0.12828947 0.085890764 0.18732859
[5,] 0.03947368 0.018879742 0.08068407
[6,] 0.01315789 0.003821629 0.04428868
[1] 1.279605
[1] 1.239122
[1] 1
   0   1

 249  55
          est    lwr.ci    upr.ci
[1,] 0.8190789 0.7796053 0.8636191
[2,] 0.1809211 0.1414474 0.2254612
```

4.5.1 For single COI Items

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```
xtabs(~coi1, data = varicare)
DescTools::MultinomCI(as.vector(xtabs(~coi1, data = varicare)))
xtabs(~coi2, data = varicare)
DescTools::MultinomCI(as.vector(xtabs(~coi2, data = varicare)))
xtabs(~coi3, data = varicare)
DescTools::MultinomCI(as.vector(xtabs(~coi3, data = varicare)))
xtabs(~coi4, data = varicare)
DescTools::MultinomCI(as.vector(xtabs(~coi4, data = varicare)))
xtabs(~coi5, data = varicare)
DescTools::MultinomCI(as.vector(xtabs(~coi5, data = varicare)))
```

```
coi1
  0   1
232  72
          est    lwr.ci    upr.ci
[1,] 0.7631579 0.7171053 0.8116204
[2,] 0.2368421 0.1907895 0.2853046
coi2
  0   1
137 167
          est    lwr.ci    upr.ci
[1,] 0.4506579 0.3947368 0.5098330
[2,] 0.5493421 0.4934211 0.6085172
coi3
  0   1
195 109
          est    lwr.ci    upr.ci
[1,] 0.6414474 0.5888158 0.6985206
[2,] 0.3585526 0.3059211 0.4156258
coi4
  0   1
289  15
           est     lwr.ci     upr.ci
[1,] 0.95065789 0.93092105 0.97497907
[2,] 0.04934211 0.02960526 0.07366328
coi5
  0   1
278  26
           est     lwr.ci    upr.ci
[1,] 0.91447368 0.88815789 0.9465798
[2,] 0.08552632 0.05921053 0.1176324
```

4.6 Harm and Benefit Perception of Low-value Prescriptions

Number out of 3 potential harms detected.

Hide

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```
xtabs(~BHR, data = varicare)
DescTools::MultinomCI(as.vector(xtabs(~BHR, data = varicare)), conf.level = 0.9
        5,
    method = "goodman")
mean(varicare$BHR)
ftable(varicare$BHRsplit)
DescTools::MultinomCI(as.vector(xtabs(~BHRsplit, data = varicare)))
```

```
BHR
  0   1   2   3
 58  67 133  46
           est    lwr.ci    upr.ci
[1,] 0.1907895 0.1409427 0.2530719
[2,] 0.2203947 0.1669687 0.2850658
[3,] 0.4375000 0.3683989 0.5091147
[4,] 0.1513158 0.1070290 0.2096258
[1] 1.549342
   0   1

 125 179
           est    lwr.ci    upr.ci
[1,] 0.4111842 0.3552632 0.4686376
[2,] 0.5888158 0.5328947 0.6462691
```

4.6.1 For Single Low-value Prescriptions

Hide

```
xtabs(~AntibioH_bin, data = varicare)
DescTools::MultinomCI(as.vector(xtabs(~AntibioH_bin, data = varicare)))
xtabs(~OpioidH_bin, data = varicare)
DescTools::MultinomCI(as.vector(xtabs(~OpioidH_bin, data = varicare)))
xtabs(~BenzoH_bin, data = varicare)
DescTools::MultinomCI(as.vector(xtabs(~BenzoH_bin, data = varicare)))
```


Wegwarth O, *et al. BMJ Qual Saf* 2024;0:1–8. doi: 10.1136/bmjqs-2023-016979

```
AntibioH_bin
  0   1
241  63
           est    lwr.ci    upr.ci
[1,] 0.7927632 0.7500000 0.8393007
[2,] 0.2072368 0.1644737 0.2537744
OpioidH_bin
  0   1
113 191
           est    lwr.ci    upr.ci
[1,] 0.3717105 0.3190789 0.4298129
[2,] 0.6282895 0.5756579 0.6863919
BenzoH_bin
  0   1
 87 217
           est    lwr.ci    upr.ci
[1,] 0.2861842 0.2368421 0.3386871
[2,] 0.7138158 0.6644737 0.7663186
```

5 Associations with Prescribing Behavior

5.1 Risk Literacy

5.1.1 Antibiotics

Hide

```
describeBy(varicare$Antibio_1000_Prop, varicare$Rsplit, mat = T)
leveneTest(varicare$Antibio_1000_Prop, varicare$Rsplit)
t.test(Antibio_1000_Prop ~ Rsplit, data = varicare, var.equal = T)
t.test(Antibio_1000_Prop ~ Rsplit, data = varicare, var.equal = F)
effectsize::cohens_d(Antibio_1000_Prop ~ Rsplit, data = varicare)

wilcox.test(Antibio_1000_Prop ~ Rsplit, data = varicare)
cor.test(varicare$Antibio_1000_Prop, varicare$R, method = "kendall")
```

	ite...	group1	vars	n	mean	sd	median	trimmed	mad
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
X11	1	0	1	116	48.83752	44.14682	36.05565	39.58796	17.01335
X12	2	1	1	188	40.60581	29.33674	32.98312	35.69655	13.93117

2 rows | 1-10 of 16 columns

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	3.522814	0.06149358
	302	NA	NA

2 rows

```
    Two Sample t-test

data:  Antibio_1000_Prop by Rsplit
t = 1.9525, df = 302, p-value = 0.0518
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 -0.06463324 16.52804942
sample estimates:
mean in group 0 mean in group 1
       48.83752        40.60581


    Welch Two Sample t-test

data:  Antibio_1000_Prop by Rsplit
t = 1.7803, df = 178.08, p-value = 0.07673
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 -0.8926968 17.3561130
sample estimates:
mean in group 0 mean in group 1
       48.83752        40.60581
```

Cohens_d	CI	CI_low	CI_high
<dbl>	<dbl>	<dbl>	<dbl>
0.2305283	0.95	-0.001797099	0.4624745

1 row

```
    Wilcoxon rank sum test with continuity correction

data:  Antibio_1000_Prop by Rsplit
W = 11944, p-value = 0.1624
alternative hypothesis: true location shift is not equal to 0


    Kendall's rank correlation tau

data:  varicare$Antibio_1000_Prop and varicare$R
z = -1.371, p-value = 0.1704
alternative hypothesis: true tau is not equal to 0
sample estimates:
        tau
-0.05670288
```

5.1.1.1 Control Analysis with STAR-PU adjusted Antibiotics prescription

Hide

```
describeBy(varicare$starab, varicare$Rsplit, mat = T)
leveneTest(varicare$starab, varicare$Rsplit)

t.test(starab ~ Rsplit, data = varicare, var.equal = F)
effectsize::cohens_d(starab ~ Rsplit, data = varicare)

wilcox.test(starab ~ Rsplit, data = varicare)
cor.test(varicare$starab, varicare$R, method = "kendall")
```

	ite...	group1	vars	n	mean	sd	median	trimmed	mad
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
X11	1	0	1	116	88.05565	82.88951	65.10826	70.40163	31.38469
X12	2	1	1	188	71.71148	52.55974	58.45645	62.89349	25.66570

2 rows | 1-10 of 16 columns

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	4.195324	0.04140001
	302	NA	NA

2 rows

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```
    Welch Two Sample t-test

data:  starab by Rsplit
t = 1.9009, df = 172.61, p-value = 0.05898
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 -0.6264322 33.3147654
sample estimates:
mean in group 0 mean in group 1
       88.05565        71.71148
```

Cohens_d	CI	CI_low	CI_high
<dbl>	<dbl>	<dbl>	<dbl>
0.2484706	0.95	0.01601301	0.4805199

1 row

```
    Wilcoxon rank sum test with continuity correction

data:  starab by Rsplit
W = 11976, p-value = 0.1499
alternative hypothesis: true location shift is not equal to 0


    Kendall's rank correlation tau

data:  varicare$starab and varicare$R
z = -1.5099, p-value = 0.1311
alternative hypothesis: true tau is not equal to 0
sample estimates:
        tau
-0.06244675
```

5.1.2 Opioids

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```
describeBy(varicare$Opioids_1000_Prop, varicare$Rsplit, mat = T)
leveneTest(varicare$Opioids_1000_Prop, varicare$Rsplit)
t.test(Opioids_1000_Prop ~ Rsplit, data = varicare, var.equal = T)
t.test(Opioids_1000_Prop ~ Rsplit, data = varicare, var.equal = F)
effectsize::cohens_d(Opioids_1000_Prop ~ Rsplit, data = varicare)

wilcox.test(Opioids_1000_Prop ~ Rsplit, data = varicare)
cor.test(varicare$Opioids_1000_Prop, varicare$R, method = "kendall")
```

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	ite...	group1	vars	n	mean	sd	median	trimmed	mad
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
X11	1	0	1	116	60.60229	63.48287	42.83695	49.13427	29.21174
X12	2	1	1	188	43.87658	48.02684	32.20906	34.51772	20.34062

2 rows | 1-10 of 16 columns

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	2.745265	0.0985814
	302	NA	NA

2 rows

```
    Two Sample t-test

data:  Opioids_1000_Prop by Rsplit
t = 2.6025, df = 302, p-value = 0.00971
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
  4.078992 29.372418
sample estimates:
mean in group 0 mean in group 1
       60.60229        43.87658


    Welch Two Sample t-test

data:  Opioids_1000_Prop by Rsplit
t = 2.4394, df = 195.57, p-value = 0.0156
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
  3.20361 30.24780
sample estimates:
mean in group 0 mean in group 1
       60.60229        43.87658
```

Cohens_d	CI	CI_low	CI_high
<dbl>	<dbl>	<dbl>	<dbl>
0.3072753	0.95	0.07432367	0.5397238

1 row

```
    Wilcoxon rank sum test with continuity correction

data:  Opioids_1000_Prop by Rsplit
W = 13720, p-value = 0.0001558
alternative hypothesis: true location shift is not equal to 0


    Kendall's rank correlation tau

data:  varicare$Opioids_1000_Prop and varicare$R
z = -3.32, p-value = 0.0009003
alternative hypothesis: true tau is not equal to 0
sample estimates:
       tau
-0.1373069
```

5.1.3 Gabapentin

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```
describeBy(varicare$Gaba_1000_Prop, varicare$Rsplit, mat = T)
leveneTest(varicare$Gaba_1000_Prop, varicare$Rsplit)
t.test(Gaba_1000_Prop ~ Rsplit, data = varicare, var.equal = T)
effectsize::cohens_d(Gaba_1000_Prop ~ Rsplit, data = varicare)

wilcox.test(Gaba_1000_Prop ~ Rsplit, data = varicare)
cor.test(varicare$Gaba_1000_Prop, varicare$R, method = "kendall")
```

	it...	group1	vars	n	mean	sd	median	trimmed	mad
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
X11	1	0	1	116	23.84103	22.83370	17.68269	19.90712	11.619689
X12	2	1	1	188	18.33588	18.83253	13.12066	14.69162	8.707433

2 rows | 1-10 of 16 columns

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	1.1286	0.2889229
	302	NA	NA

2 rows

```
    Two Sample t-test

data:  Gaba_1000_Prop by Rsplit
t = 2.2802, df = 302, p-value = 0.02329
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
  0.7541478 10.2561664
sample estimates:
mean in group 0 mean in group 1
       23.84103        18.33588
```

Cohens_d <dbl>	CI <dbl>	CI_low <dbl>	CI_high <dbl>
0.2692184	0.95	0.0365971	0.5013978

1 row

```
    Wilcoxon rank sum test with continuity correction

data:  Gaba_1000_Prop by Rsplit
W = 13504, p-value = 0.0004814
alternative hypothesis: true location shift is not equal to 0


    Kendall's rank correlation tau

data:  varicare$Gaba_1000_Prop and varicare$R
z = -2.6123, p-value = 0.008992
alternative hypothesis: true tau is not equal to 0
sample estimates:
       tau
-0.1080393
```

5.1.4 Benzodiazepines

Hide

```
describeBy(varicare$Benzo_1000_Prop, varicare$Rsplit, mat = T)
leveneTest(varicare$Benzo_1000_Prop, varicare$Rsplit)
t.test(Benzo_1000_Prop ~ Rsplit, data = varicare, var.equal = T)
effectsize::cohens_d(Benzo_1000_Prop ~ Rsplit, data = varicare)

wilcox.test(Benzo_1000_Prop ~ Rsplit, data = varicare)
cor.test(varicare$Benzo_1000_Prop, varicare$R, method = "kendall")
```

Analyses For the Manuscript: Association between Risk Literacy and Va...

	it... <chr>	group1 <chr>	vars <dbl>	n <dbl>	mean <dbl>	sd <dbl>	median <dbl>	trimmed <dbl>	mad <dbl>
X11	1	0	1	116	17.23183	15.64378	14.010500	14.79333	8.836798
X12	2	1	1	188	13.57629	14.22355	9.755144	10.70254	6.330182

2 rows | 1-10 of 16 columns

	Df <int>	F value <dbl>	Pr(>F) <dbl>
group	1	0.1426819	0.7058946
	302	NA	NA

2 rows

```
    Two Sample t-test

data:  Benzo_1000_Prop by Rsplit
t = 2.0948, df = 302, p-value = 0.03703
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 0.221473 7.089611
sample estimates:
mean in group 0 mean in group 1
       17.23183        13.57629
```

Cohens_d <dbl>	CI <dbl>	CI_low <dbl>	CI_high <dbl>
0.2473225	0.95	0.01487368	0.4793649

1 row

```
    Wilcoxon rank sum test with continuity correction

data:  Benzo_1000_Prop by Rsplit
W = 14022, p-value = 2.822e-05
alternative hypothesis: true location shift is not equal to 0


    Kendall's rank correlation tau

data:  varicare$Benzo_1000_Prop and varicare$R
z = -3.3601, p-value = 0.0007791
alternative hypothesis: true tau is not equal to 0
sample estimates:
       tau
-0.1389653
```

5.2 Conflict of Interests

5.2.1 Antibiotics

Hide

```
describeBy(varicare$Antibio_1000_Prop, varicare$coisplit, mat = T)
leveneTest(varicare$Antibio_1000_Prop, varicare$coisplit)
t.test(Antibio_1000_Prop ~ coisplit, data = varicare, var.equal = T)
effectsize::cohens_d(Antibio_1000_Prop ~ coisplit, data = varicare)

wilcox.test(Antibio_1000_Prop ~ coisplit, data = varicare)
cor.test(varicare$Antibio_1000_Prop, varicare$coi, method = "kendall")
```

	ite...	group1	vars	n	mean	sd	median	trimmed	mad
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
X11	1	0	1	249	44.41720	37.48313	32.97582	37.18098	15.33985
X12	2	1	1	55	40.71202	27.51261	36.61815	37.20101	13.25276

2 rows | 1-10 of 16 columns

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	1.57118	0.2110053
	302	NA	NA

2 rows

Analyses For the Manuscript: Association between Risk Literacy and Va...

```
    Two Sample t-test

data:  Antibio_1000_Prop by coisplit
t = 0.69264, df = 302, p-value = 0.4891
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 -6.821535 14.231895
sample estimates:
mean in group 0 mean in group 1
       44.41720        40.71202
```

Cohens_d	CI	CI_low	CI_high
<dbl>	<dbl>	<dbl>	<dbl>
0.1031963	0.95	-0.189019	0.395241

1 row

```
    Wilcoxon rank sum test with continuity correction

data:  Antibio_1000_Prop by coisplit
W = 6511.5, p-value = 0.5696
alternative hypothesis: true location shift is not equal to 0


    Kendall's rank correlation tau

data:  varicare$Antibio_1000_Prop and varicare$coi
z = -0.54365, p-value = 0.5867
alternative hypothesis: true tau is not equal to 0
sample estimates:
        tau
-0.02325431
```

5.2.1.1 Control Analysis with STAR-PU adjusted Antibiotics prescription

Hide

```
describeBy(varicare$starab, varicare$coisplit, mat = T)
leveneTest(varicare$starab, varicare$coisplit)

t.test(starab ~ coisplit, data = varicare, var.equal = T)
effectsize::cohens_d(starab ~ coisplit, data = varicare)

wilcox.test(starab ~ coisplit, data = varicare)
cor.test(varicare$starab, varicare$coi, method = "kendall")
```

Analyses For the Manuscript: Association between Risk Literacy and Va...

	ite...	group1	vars	n	mean	sd	median	trimmed	mad
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
X11	1	0	1	249	79.0319	69.07622	57.95848	65.38663	26.12845
X12	2	1	1	55	73.0413	51.08596	67.12335	66.10016	21.91684

2 rows | 1-10 of 16 columns

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	1.426743	0.233234
	302	NA	NA

2 rows

```
    Two Sample t-test

data:  starab by coisplit
t = 0.6072, df = 302, p-value = 0.5442
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 -13.42416  25.40535
sample estimates:
mean in group 0 mean in group 1
        79.0319         73.0413
```

	Cohens_d	CI	CI_low	CI_high
	<dbl>	<dbl>	<dbl>	<dbl>
	0.09046607	0.95	-0.2017119	0.3824944

1 row

```
    Wilcoxon rank sum test with continuity correction

data:  starab by coisplit
W = 6473.5, p-value = 0.5267
alternative hypothesis: true location shift is not equal to 0


    Kendall's rank correlation tau

data:  varicare$starab and varicare$coi
z = -0.45334, p-value = 0.6503
alternative hypothesis: true tau is not equal to 0
sample estimates:
        tau
-0.01939113
```

5.2.2 Opioids

Hide

```
describeBy(varicare$Opioids_1000_Prop, varicare$coisplit, mat = T)
leveneTest(varicare$Opioids_1000_Prop, varicare$coisplit)
t.test(Opioids_1000_Prop ~ coisplit, data = varicare, var.equal = T)
effectsize::cohens_d(Opioids_1000_Prop ~ coisplit, data = varicare)

wilcox.test(Opioids_1000_Prop ~ coisplit, data = varicare)
cor.test(varicare$Opioids_1000_Prop, varicare$coi, method = "kendall")
```

	ite...	group1	vars	n	mean	sd	median	trimmed	mad
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
X11	1	0	1	249	50.49688	57.72687	35.33221	39.32958	20.72413
X12	2	1	1	55	49.18071	40.44792	37.25119	42.81299	27.99762

2 rows | 1-10 of 16 columns

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	0.02927691	0.8642558
	302	*NA*	*NA*

2 rows

```
    Two Sample t-test

data:  Opioids_1000_Prop by coisplit
t = 0.16051, df = 302, p-value = 0.8726
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 -14.82007  17.45241
sample estimates:
mean in group 0 mean in group 1
       50.49688        49.18071
```

Cohens_d	CI	CI_low	CI_high
<dbl>	<dbl>	<dbl>	<dbl>
0.0239143	0.95	-0.268126	0.3159147

1 row

```
    Wilcoxon rank sum test with continuity correction

data:  Opioids_1000_Prop by coisplit
W = 6579, p-value = 0.6496
alternative hypothesis: true location shift is not equal to 0


    Kendall's rank correlation tau

data:  varicare$Opioids_1000_Prop and varicare$coi
z = -0.23752, p-value = 0.8123
alternative hypothesis: true tau is not equal to 0
sample estimates:
        tau
-0.01015965
```

5.2.3 Gabapentenin

Hide

```
describeBy(varicare$Gaba_1000_Prop, varicare$coisplit, mat = T)
leveneTest(varicare$Gaba_1000_Prop, varicare$coisplit)
t.test(Gaba_1000_Prop ~ coisplit, data = varicare, var.equal = T)
effectsize::cohens_d(Gaba_1000_Prop ~ coisplit, data = varicare)

wilcox.test(Gaba_1000_Prop ~ coisplit, data = varicare)
cor.test(varicare$Gaba_1000_Prop, varicare$coi, method = "kendall")
```

Analyses For the Manuscript: Association between Risk Literacy and Va...

	ite...	group1	vars	n	mean	sd	median	trimmed	mad
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
X11	1	0	1	249	20.47674	20.23470	15.23158	16.73635	9.796892
X12	2	1	1	55	20.25448	22.32364	14.20221	16.84897	9.850438

2 rows | 1-10 of 16 columns

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	0.02080541	0.8854065
	302	NA	NA

2 rows

```
    Two Sample t-test

data:  Gaba_1000_Prop by coisplit
t = 0.072334, df = 302, p-value = 0.9424
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 -5.824399  6.268926
sample estimates:
mean in group 0 mean in group 1
       20.47674        20.25448
```

	Cohens_d	CI	CI_low	CI_high
	<dbl>	<dbl>	<dbl>	<dbl>
	0.01077705	0.95	-0.2812471	0.3027836

1 row

```
    Wilcoxon rank sum test with continuity correction

data:  Gaba_1000_Prop by coisplit
W = 6867.5, p-value = 0.9736
alternative hypothesis: true location shift is not equal to 0


    Kendall's rank correlation tau

data:  varicare$Gaba_1000_Prop and varicare$coi
z = -0.28795, p-value = 0.7734
alternative hypothesis: true tau is not equal to 0
sample estimates:
        tau
-0.01231674
```

5.2.4 Benzodiazepines

Hide

```
describeBy(varicare$Benzo_1000_Prop, varicare$coisplit, mat = T)
leveneTest(varicare$Benzo_1000_Prop, varicare$coisplit)
t.test(Benzo_1000_Prop ~ coisplit, data = varicare, var.equal = T)
effectsize::cohens_d(Benzo_1000_Prop ~ coisplit, data = varicare)

wilcox.test(Benzo_1000_Prop ~ coisplit, data = varicare)
cor.test(varicare$Benzo_1000_Prop, varicare$coi, method = "kendall")
```

	it...	group1	vars	n	mean	sd	median	trimmed	mad
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
X11	1	0	1	249	15.48868	15.834607	11.94459	12.51316	8.225837
X12	2	1	1	55	12.62826	9.009621	10.13206	11.38810	6.289732

2 rows | 1-10 of 16 columns

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	1.938772	0.1648263
	302	*NA*	*NA*

2 rows

```
    Two Sample t-test

data:  Benzo_1000_Prop by coisplit
t = 1.2932, df = 302, p-value = 0.1969
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 -1.492385  7.213225
sample estimates:
mean in group 0 mean in group 1
       15.48868        12.62826
```

Cohens_d	CI	CI_low	CI_high
<dbl>	<dbl>	<dbl>	<dbl>
0.1926675	0.95	-0.09990935	0.4849261

1 row

```
    Wilcoxon rank sum test with continuity correction

data:  Benzo_1000_Prop by coisplit
W = 7371, p-value = 0.3754
alternative hypothesis: true location shift is not equal to 0


    Kendall's rank correlation tau

data:  varicare$Benzo_1000_Prop and varicare$coi
z = -0.4246, p-value = 0.6711
alternative hypothesis: true tau is not equal to 0
sample estimates:
        tau
-0.01816155
```

5.3 Perception of Low-Value Prescriptions

5.3.1 Antibiotics

Hide

Analyses For the Manuscript: Association between Risk Literacy and Va...

```
describeBy(varicare$Antibio_1000_Prop, varicare$AntibioH_bin, mat = T)
leveneTest(varicare$Antibio_1000_Prop, varicare$AntibioH_bin)
t.test(Antibio_1000_Prop ~ AntibioH_bin, data = varicare, var.equal = T)
effectsize::cohens_d(Antibio_1000_Prop ~ AntibioH_bin, data = varicare)

wilcox.test(Antibio_1000_Prop ~ AntibioH_bin, data = varicare)
```

	ite...	group1	vars	n	mean	sd	median	trimmed	mad
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
X11	1	0	1	241	42.80099	35.08450	33.38385	36.57610	14.60967
X12	2	1	1	63	47.36517	38.82718	35.61664	39.64022	17.82828

2 rows | 1-10 of 16 columns

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	1.202168	0.2737622
	302	NA	NA

2 rows

```
    Two Sample t-test

data:  Antibio_1000_Prop by AntibioH_bin
t = -0.89887, df = 302, p-value = 0.3694
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 -14.556343   5.427986
sample estimates:
mean in group 0 mean in group 1
       42.80099        47.36517
```

Cohens_d	CI	CI_low	CI_high
<dbl>	<dbl>	<dbl>	<dbl>
-0.12719	0.95	-0.404606	0.1504362

1 row

Wegwarth O, *et al. BMJ Qual Saf* 2024;0:1–8. doi: 10.1136/bmjqs-2023-016979

```
    Wilcoxon rank sum test with continuity correction

data:  Antibio_1000_Prop by AntibioH_bin
W = 7224.5, p-value = 0.5552
alternative hypothesis: true location shift is not equal to 0
```

5.3.1.1 Control Analysis with STAR-PU adjusted Antibiotics prescription

Hide

```
describeBy(varicare$starab, varicare$AntibioH_bin, mat = T)
leveneTest(varicare$starab, varicare$AntibioH_bin)

t.test(starab ~ AntibioH_bin, data = varicare, var.equal = T)
effectsize::cohens_d(starab ~ AntibioH_bin, data = varicare)

wilcox.test(starab ~ AntibioH_bin, data = varicare)
```

	ite...	group1	vars	n	mean	sd	median	trimmed	mad
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
X11	1	0	1	241	76.71311	65.33706	59.73868	64.52609	27.48446
X12	2	1	1	63	82.67230	69.51046	65.71441	68.94030	30.34782

2 rows | 1-10 of 16 columns

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	0.5948272	0.4411615
	302	NA	NA

2 rows

```
    Two Sample t-test

data:  starab by AntibioH_bin
t = -0.63602, df = 302, p-value = 0.5252
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 -24.39697  12.47857
sample estimates:
mean in group 0 mean in group 1
       76.71311        82.67230
```

Analyses For the Manuscript: Association between Risk Literacy and Va...

Cohens_d <dbl>	CI <dbl>	CI_low <dbl>	CI_high <dbl>
-0.08999731	0.95	-0.3673516	0.1875058

1 row

```
    Wilcoxon rank sum test with continuity correction

data:  starab by AntibioH_bin
W = 7272.5, p-value = 0.6082
alternative hypothesis: true location shift is not equal to 0
```

5.3.2 Opioids

Hide

```
describeBy(varicare$Opioids_1000_Prop, varicare$OpioidH_bin, mat = T)
leveneTest(varicare$Opioids_1000_Prop, varicare$OpioidH_bin)
t.test(Opioids_1000_Prop ~ OpioidH_bin, data = varicare, var.equal = T)
effectsize::cohens_d(Opioids_1000_Prop ~ OpioidH_bin, data = varicare)

wilcox.test(Opioids_1000_Prop ~ OpioidH_bin, data = varicare)
```

	ite... <chr>	group1 <chr>	vars <dbl>	n <dbl>	mean <dbl>	sd <dbl>	median <dbl>	trimmed <dbl>	mad <dbl>
X11	1	0	1	113	47.84464	38.20707	37.49816	41.37694	21.79194
X12	2	1	1	191	51.68701	62.84121	32.95122	38.93114	21.93540

2 rows | 1-10 of 16 columns

	Df <int>	F value <dbl>	Pr(>F) <dbl>
group	1	1.764737	0.1850377
	302	NA	NA

2 rows

```
    Two Sample t-test

data:  Opioids_1000_Prop by OpioidH_bin
t = -0.58856, df = 302, p-value = 0.5566
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 -16.68923   9.00450
sample estimates:
mean in group 0 mean in group 1
       47.84464        51.68701
```

Cohens_d	CI	CI_low	CI_high
<dbl>	<dbl>	<dbl>	<dbl>
-0.06985126	0.95	-0.3024704	0.1628835

1 row

```
    Wilcoxon rank sum test with continuity correction

data:  Opioids_1000_Prop by OpioidH_bin
W = 11676, p-value = 0.2324
alternative hypothesis: true location shift is not equal to 0
```

5.3.3 Benzodiazepines

Hide

```
describeBy(varicare$Benzo_1000_Prop, varicare$BenzoH_bin, mat = T)
leveneTest(varicare$Benzo_1000_Prop, varicare$BenzoH_bin)
t.test(Benzo_1000_Prop ~ BenzoH_bin, data = varicare, var.equal = T)
effectsize::cohens_d(Benzo_1000_Prop ~ BenzoH_bin, data = varicare)

wilcox.test(Benzo_1000_Prop ~ BenzoH_bin, data = varicare)
```

	ite...	group1	vars	n	mean	sd	median	trimmed	mad
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
X11	1	0	1	87	15.74330	15.11249	12.49944	13.05162	8.557225
X12	2	1	1	217	14.66161	14.78554	10.99444	12.00801	7.646772

2 rows | 1-10 of 16 columns

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>

Analyses For the Manuscript: Association between Risk Literacy and Va...

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	0.08787223	0.7671036
	302	NA	NA

2 rows

```
    Two Sample t-test

data:  Benzo_1000_Prop by BenzoH_bin
t = 0.57289, df = 302, p-value = 0.5671
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 -2.633861  4.797254
sample estimates:
mean in group 0 mean in group 1
       15.74330        14.66161
```

Cohens_d	CI	CI_low	CI_high
<dbl>	<dbl>	<dbl>	<dbl>
0.07269773	0.95	-0.1761411	0.3214164

1 row

```
    Wilcoxon rank sum test with continuity correction

data:  Benzo_1000_Prop by BenzoH_bin
W = 9995, p-value = 0.423
alternative hypothesis: true location shift is not equal to 0
```

5.4 Figure

5.4.1 Risk literacy

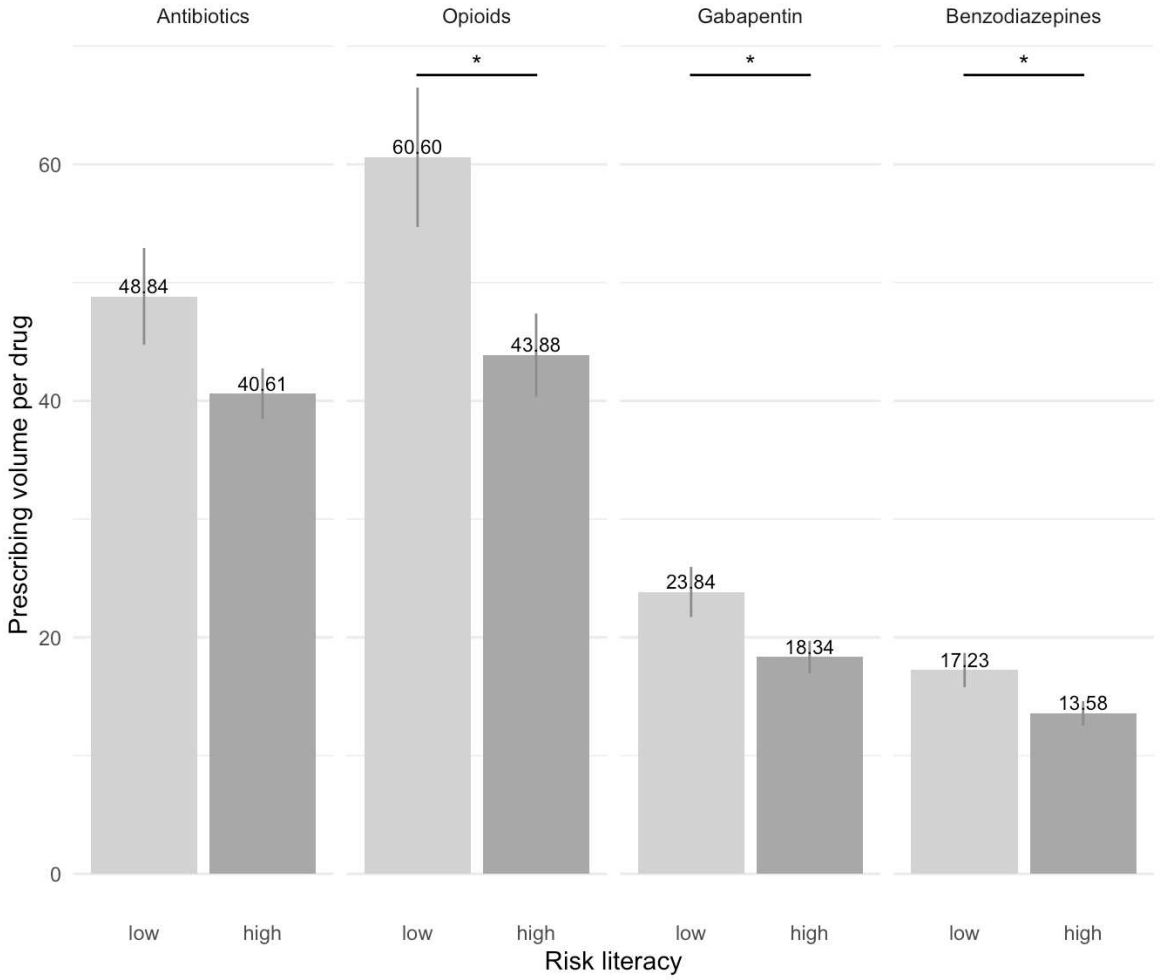
Hide

Analyses For the Manuscript: Association between Risk Literacy and Va...

```
graph.data <- rbind(varicare, varicare, varicare, varicare)

graph.data$Rsplit <- as.factor(graph.data$Rsplit)

graph.data$prescriptions <- NA
graph.data$drug <- rep(1:4, each = 304)
graph.data$prescription[graph.data$drug == 1] <- graph.data$Antibio_1000_Prop[gr
        aph.data$drug ==
    1]
graph.data$prescription[graph.data$drug == 2] <- graph.data$Opioids_1000_Prop[gr
        aph.data$drug ==
    2]
graph.data$prescription[graph.data$drug == 3] <- graph.data$Gaba_1000_Prop[grap
        h.data$drug ==
    3]
graph.data$prescription[graph.data$drug == 4] <- graph.data$Benzo_1000_Prop[grap
        h.data$drug ==
    4]

graph.data$drug <- as.factor(graph.data$drug)
levels(graph.data$drug) <- c("Antibiotics", "Opioids", "Gabapentin", "Benzodiaze
        pines")
levels(graph.data$Rsplit) <- c("low", "high")

# drop ns as lines
sigFunc = function(x) {
    if (x < 0.001) {
        "***"
    } else if (x < 0.01) {
        "**"
    } else if (x < 0.05) {
        "*"
    } else {
        NA
    }
}

F1plot <- ggplot(graph.data, aes(y = prescription, x = Rsplit, fill = Rsplit)) +
    geom_bar(position = "dodge", stat = "summary") + stat_summary(fun.data = "me
        an_se",
    geom = "linerange", color = "grey55", ) + facet_grid(. ~ drug) + stat_summar
        y(aes(label = sprintf("%.2f",
    round(after_stat(y), 2))), fun = mean, geom = "text", size = 3, vjust = -0.2
        5) +
    scale_fill_manual(values = c("lightgrey", "darkgrey")) + labs(x = "Risk lite
        racy",
    y = "Prescribing volume per drug") + theme_minimal() + theme(legend.position
        = "none",
    panel.grid.major.x = element_blank()) + geom_signif(comparisons = list(c("lo
        w",
    "high")), map_signif_level = sigFunc, y_position = 60, tip_length = 0, test
        = "t.test",
    margin_top = 0.017, vjust = 0.4)
```

Analyses For the Manuscript: Association between Risk Literacy and Va...

```
F1plot
```

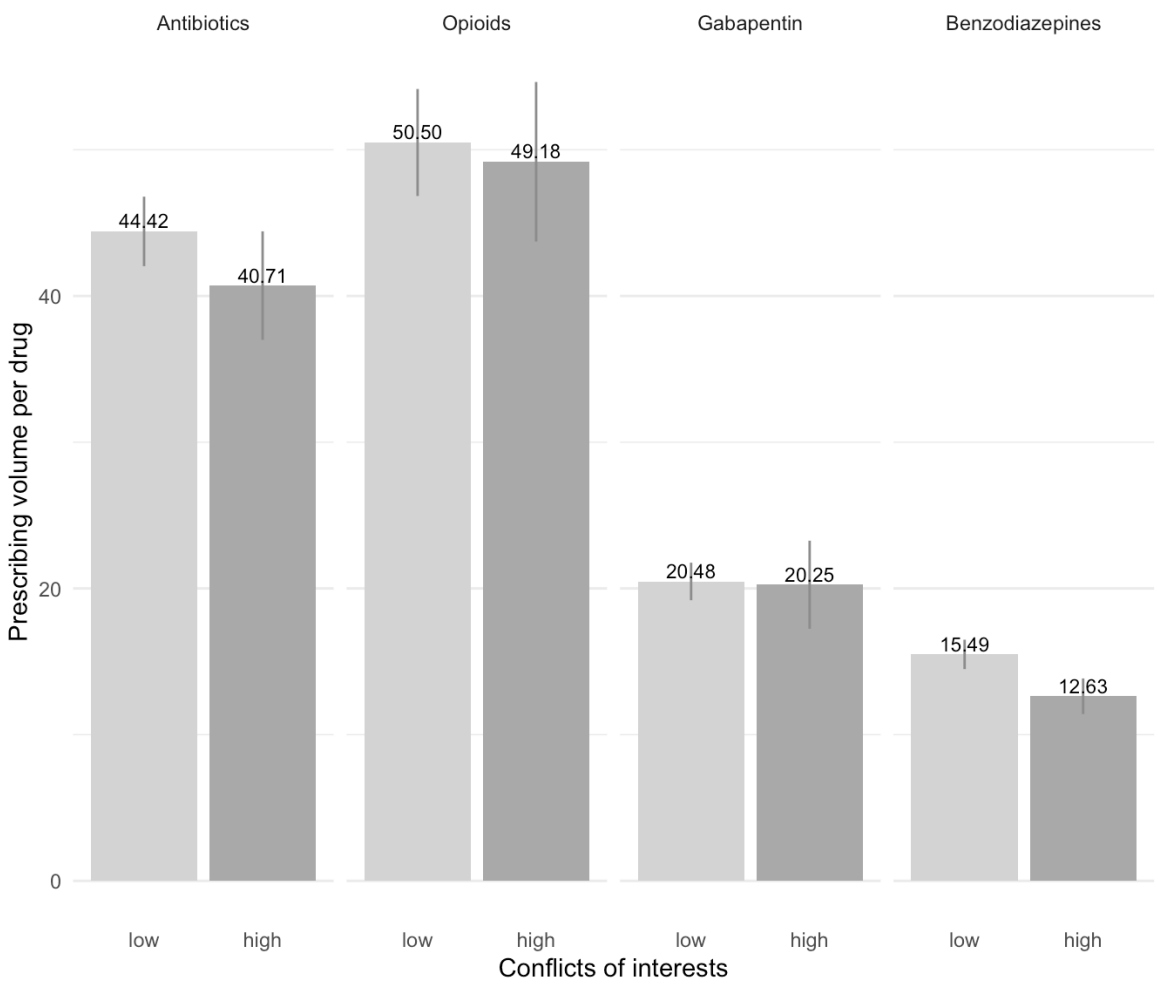


5.4.2 Conflict of Interests

Hide

Analyses For the Manuscript: Association between Risk Literacy and Va...

```
graph.data$coisplit <- as.factor(graph.data$coisplit)
levels(graph.data$coisplit) <- c("low", "high")
F2plot <- ggplot(graph.data, aes(y = prescription, x = coisplit, fill = coispli
        t)) +
    geom_bar(position = "dodge", stat = "summary") + stat_summary(fun.data = "me
        an_se",
    geom = "linerange", color = "grey55", ) + facet_grid(. ~ drug) + stat_summar
        y(aes(label = sprintf("%.2f",
    round(after_stat(y), 2))), fun = mean, geom = "text", size = 3, vjust = -0.2
        5) +
    scale_fill_manual(values = c("lightgrey", "darkgrey")) + labs(x = "Conflicts
        of interests",
    y = "Prescribing volume per drug") + theme_minimal() + theme(legend.position
        = "none",
    panel.grid.major.x = element_blank())



F2plot
```

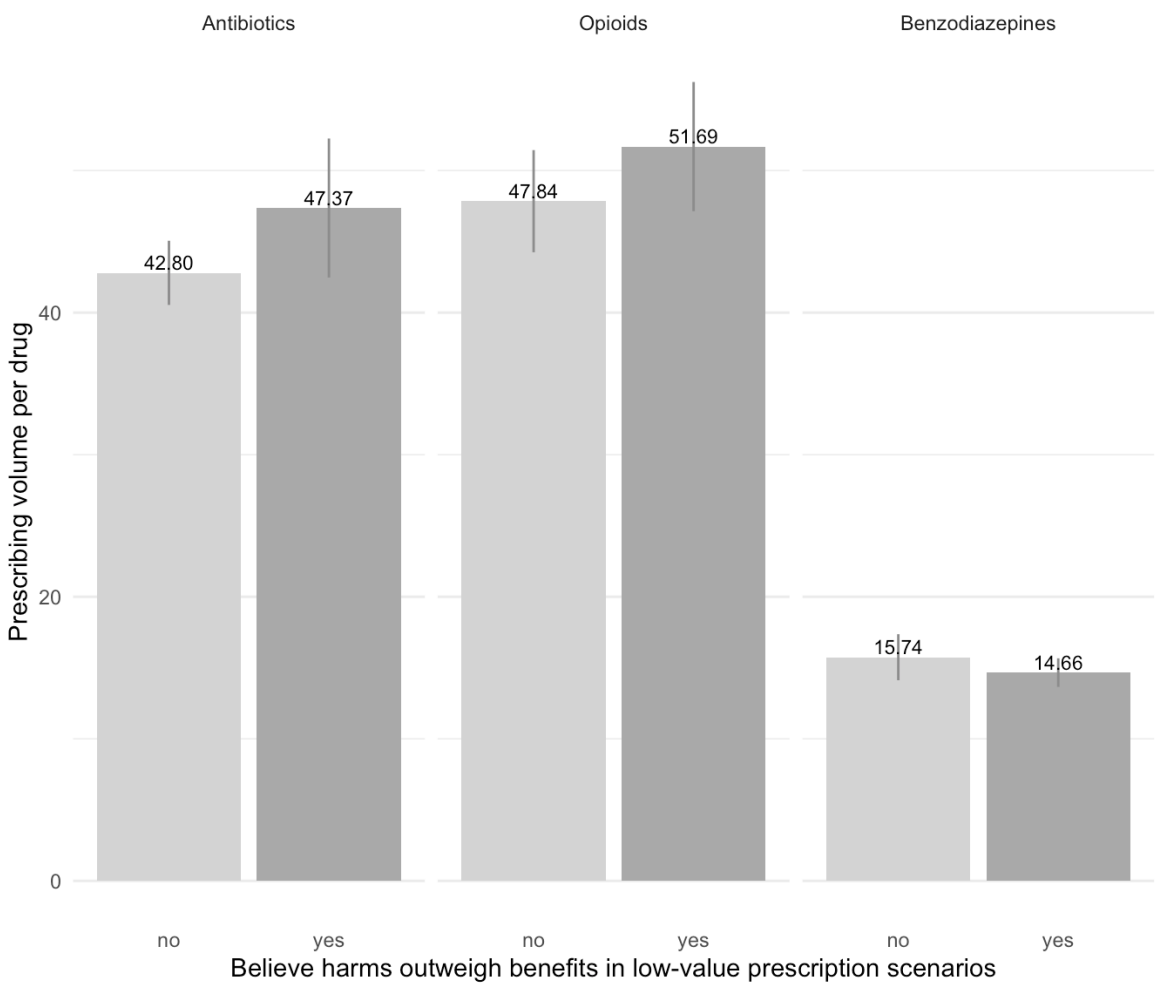


5.4.3 Perception of Low-value Prescriptions

Hide

```
graph.data$bhspec <- NA
graph.data$bhspec[graph.data$drug == "Antibiotics"] <- graph.data$AntibioH_bin[g
        raph.data$drug ==
    "Antibiotics"]
graph.data$bhspec[graph.data$drug == "Opioids"] <- graph.data$OpioidH_bin[graph.
        data$drug ==
    "Opioids"]
graph.data$bhspec[graph.data$drug == "Benzodiazepines"] <- graph.data$BenzoH_bin
        [graph.data$drug ==
    "Benzodiazepines"]

graph.data$bhspec <- as.factor(graph.data$bhspec)
levels(graph.data$bhspec) <- c("no", "yes")

graph.data.cl <- graph.data[is.na(graph.data$bhspec) == F, ]

F3plot <- ggplot(graph.data.cl, aes(y = prescription, x = bhspec, fill = bhspe
        c)) +
    geom_bar(position = "dodge", stat = "summary") + stat_summary(fun.data = "me
        an_se",
    geom = "linerange", color = "grey55", ) + facet_grid(. ~ drug) + stat_summar
        y(aes(label = sprintf("%.2f",
    round(after_stat(y), 2))), fun = mean, geom = "text", size = 3, vjust = -0.2
        5) +
    scale_fill_manual(values = c("lightgrey", "darkgrey")) + labs(x = "Believe h
        arms outweigh benefits in low-value prescription scenarios",
    y = "Prescribing volume per drug") + theme_minimal() + theme(legend.position
        = "none",
    panel.grid.major.x = element_blank())

F3plot
```

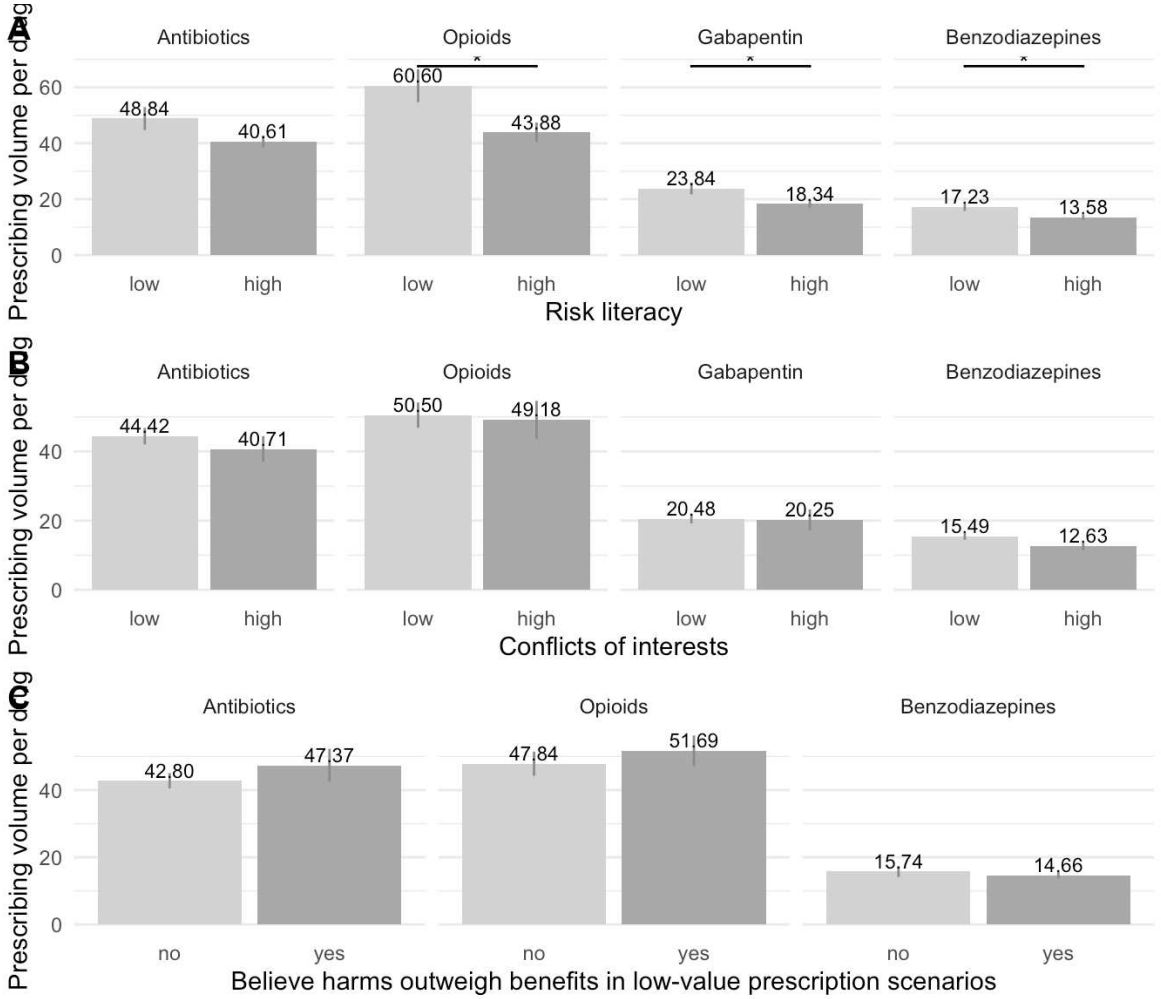
Analyses For the Manuscript: Association between Risk Literacy and Va...



5.4.4 Final Combination

Hide

```
figurealt <- ggarrange(F1plot, F2plot, F3plot, labels = c("A", "B", "C"), ncol =
        1,
    nrow = 3)
# ggarrange(p1, p2, widths = c(1.5,2))

figurealt
```



6 Other Associations

6.1 Risk Literacy

6.1.1 Demography

Hide

Analyses For the Manuscript: Association between Risk Literacy and Va...

```
y.r <- xtabs(~Years_Profession + Rsplit, data = varicare)
use_labels(varicare, table(Years_Profession, Rsplit))
DescTools::MultinomCI(y.r[, 1])
DescTools::MultinomCI(y.r[, 2])
summary(y.r)
CramerV(y.r)
wilcox.test(Years_Profession ~ Rsplit, data = varicare)

size.r <- xtabs(~s5_Range_number_physician_practice + Rsplit, data = varicare)
use_labels(varicare, table(s5_Range_number_physician_practice, Rsplit))
DescTools::MultinomCI(size.r[, 1])
DescTools::MultinomCI(size.r[, 2])
summary(size.r)
CramerV(size.r)
wilcox.test(s5_Range_number_physician_practice ~ Rsplit, data = varicare)


describeBy(varicare$Patient_lsize, varicare$Rsplit, mat = T)
leveneTest(varicare$Patient_lsize, varicare$Rsplit)
t.test(Patient_lsize ~ Rsplit, data = varicare, var.equal = T)

cor.test(varicare$Patient_lsize, varicare$R, method = "kendall")
```

Analyses For the Manuscript: Association between Risk Literacy and Va...

```
                Rsplit
Years_Profession  0  1
   <10 years     23 40
   10 -19 years  42 74
   20 - 29 years 26 49
   30 - 39 years 19 21
   ≥40 years      6  4
                     est     lwr.ci    upr.ci
<10 years     0.19827586 0.11206897 0.2980193
10 -19 years  0.36206897 0.27586207 0.4618124
20 - 29 years 0.22413793 0.13793103 0.3238813
30 - 39 years 0.16379310 0.07758621 0.2635365
≥40 years     0.05172414 0.00000000 0.1514675
                    est     lwr.ci     upr.ci
<10 years     0.2127660 0.13829787 0.28739181
10 -19 years  0.3936170 0.31914894 0.46824288
20 - 29 years 0.2606383 0.18617021 0.33526415
30 - 39 years 0.1117021 0.03723404 0.18632798
≥40 years     0.0212766 0.00000000 0.09590245
Call: xtabs(formula = ~Years_Profession + Rsplit, data = varicare)
Number of cases in table: 304
Number of factors: 2
Test for independence of all factors:
    Chisq = 4.148, df = 4, p-value = 0.3863
    Chi-squared approximation may be incorrect
[1] 0.1168147

    Wilcoxon rank sum test with continuity correction

data:  Years_Profession by Rsplit
W = 11708, p-value = 0.2603
alternative hypothesis: true location shift is not equal to 0

                                  Rsplit
s5_Range_number_physician_practice  0  1
                                1     2  1
                                2     7 10
                                4-5  21 59
                                6-10 53 66
                                ≥10  33 52
            est     lwr.ci    upr.ci
1    0.01724138 0.00000000 0.1188287
2    0.06034483 0.00000000 0.1619322
4-5  0.18103448 0.09482759 0.2826218
6-10 0.45689655 0.37068966 0.5584839
≥10  0.28448276 0.19827586 0.3860701
             est    lwr.ci     upr.ci
1    0.005319149 0.0000000 0.08414756
2    0.053191489 0.0000000 0.13201990
4-5  0.313829787 0.2393617 0.39265820
6-10 0.351063830 0.2765957 0.42989224
```


Wegwarth O, *et al. BMJ Qual Saf* 2024;0:1–8. doi: 10.1136/bmjqs-2023-016979

```
≥10  0.276595745 0.2021277 0.35542416
Call: xtabs(formula = ~s5_Range_number_physician_practice + Rsplit,
    data = varicare)
Number of cases in table: 304
Number of factors: 2
Test for independence of all factors:
    Chisq = 7.975, df = 4, p-value = 0.09251
    Chi-squared approximation may be incorrect
[1] 0.1619644

    Wilcoxon rank sum test with continuity correction

data:  s5_Range_number_physician_practice by Rsplit
W = 11698, p-value = 0.2609
alternative hypothesis: true location shift is not equal to 0
```

	it...	group1	vars	n	mean	sd	median	trimmed	mad
	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
X11	1	0	1	116	12490.75	8827.301	10708.42	11204.13	5837.985
X12	2	1	1	188	13662.80	10614.945	10866.75	11638.89	6434.360

2 rows | 1-10 of 16 columns

	Df	F value	Pr(>F)
	<int>	<dbl>	<dbl>
group	1	0.7848525	0.3763661
	302	NA	NA

2 rows

```
    Two Sample t-test

data:  Patient_lsize by Rsplit
t = -0.99548, df = 302, p-value = 0.3203
alternative hypothesis: true difference in means between group 0 and group 1 is
not equal to 0
95 percent confidence interval:
 -3488.947  1144.843
sample estimates:
mean in group 0 mean in group 1
       12490.75        13662.80


    Kendall's rank correlation tau

data:  varicare$Patient_lsize and varicare$R
z = 0.69441, p-value = 0.4874
alternative hypothesis: true tau is not equal to 0
sample estimates:
       tau
0.02872432
```

6.1.2 COI

Hide

```
coi.r <- xtabs(~coisplit + Rsplit, data = varicare)
coi.r
DescTools::MultinomCI(coi.r[, 1])
DescTools::MultinomCI(coi.r[, 2])
summary(coi.r)
Phi(coi.r)
cor.test(varicare$coi, varicare$R, method = "kendall")
```

```
        Rsplit
coisplit   0   1
       0  88 161
       1  28  27
        est    lwr.ci    upr.ci
0 0.7586207 0.6896552 0.8405474
1 0.2413793 0.1724138 0.3233060
       est    lwr.ci    upr.ci
0 0.856383 0.8138298 0.9084998
1 0.143617 0.1010638 0.1957338
Call: xtabs(formula = ~coisplit + Rsplit, data = varicare)
Number of cases in table: 304
Number of factors: 2
Test for independence of all factors:
    Chisq = 4.627, df = 1, p-value = 0.03148
[1] 0.1233668

    Kendall's rank correlation tau

data:  varicare$coi and varicare$R
z = -2.4978, p-value = 0.0125
alternative hypothesis: true tau is not equal to 0
sample estimates:
       tau
-0.1149081
```

6.1.3 Perception of Low-value Prescriptions

Hide

```
BHR.r <- xtabs(~BHRsplit + Rsplit, data = varicare)
BHR.r
DescTools::MultinomCI(BHR.r[, 1])
DescTools::MultinomCI(BHR.r[, 2])
summary(BHR.r)
Phi(BHR.r)
cor.test(varicare$BHR, varicare$R, method = "kendall")
```

```
        Rsplit
BHRsplit   0   1
       0  59  66
       1  57 122
        est    lwr.ci    upr.ci
0 0.5086207 0.4224138 0.6066564
1 0.4913793 0.4051724 0.5894150
        est    lwr.ci    upr.ci
0 0.3510638 0.2872340 0.4245826
1 0.6489362 0.5851064 0.7224549
Call: xtabs(formula = ~BHRsplit + Rsplit, data = varicare)
Number of cases in table: 304
Number of factors: 2
Test for independence of all factors:
    Chisq = 7.355, df = 1, p-value = 0.006686
[1] 0.1555477

    Kendall's rank correlation tau

data:  varicare$BHR and varicare$R
z = 3.5562, p-value = 0.0003763
alternative hypothesis: true tau is not equal to 0
sample estimates:
      tau
0.1658972
```

6.2 Conflict of Interests

6.2.1 Demography

Hide

Analyses For the Manuscript: Association between Risk Literacy and Va...

```
y.coi <- xtabs(~Years_Profession + coisplit, data = varicare)
y.coi
summary(y.coi)
CramerV(y.coi)
wilcox.test(Years_Profession ~ coisplit, data = varicare)

# split to simplify complex relationship
varicare$Years_Professionsh <- NA
varicare$Years_Professionsh[varicare$Years_Profession < 3] <- 0
varicare$Years_Professionsh[varicare$Years_Profession > 2] <- 1

ys.coi <- xtabs(~Years_Professionsh + coisplit, data = varicare)
ys.coi
summary(ys.coi)
Phi(ys.coi)

size.coi <- xtabs(~s5_Range_number_physician_practice + coisplit, data = varicar
        e)
size.coi
summary(size.coi)
CramerV(size.coi)
wilcox.test(s5_Range_number_physician_practice ~ coisplit, data = varicare)
```


Wegwarth O, *et al. BMJ Qual Saf* 2024;0:1–8. doi: 10.1136/bmjqs-2023-016979

Analyses For the Manuscript: Association between Risk Literacy and Va...

```
                coisplit
Years_Profession   0   1
   <10 years      54   9
   10 -19 years  101  15
   20 - 29 years  52  23
   30 - 39 years  37   3
   ≥40 years       5   5
Call: xtabs(formula = ~Years_Profession + coisplit, data = varicare)
Number of cases in table: 304
Number of factors: 2
Test for independence of all factors:
    Chisq = 20.602, df = 4, p-value = 0.0003796
    Chi-squared approximation may be incorrect
[1] 0.2603289

    Wilcoxon rank sum test with continuity correction

data:  Years_Profession by coisplit
W = 5812.5, p-value = 0.06727
alternative hypothesis: true location shift is not equal to 0

                  coisplit
Years_Professionsh   0   1
                 0 155  24
                 1  94  31
Call: xtabs(formula = ~Years_Professionsh + coisplit, data = varicare)
Number of cases in table: 304
Number of factors: 2
Test for independence of all factors:
    Chisq = 6.446, df = 1, p-value = 0.01112
[1] 0.1456154
                                  coisplit
s5_Range_number_physician_practice  0  1
                              1     3  0
                              2    13  4
                              4-5  72  8
                              6-10 91 28
                              ≥10  70 15
Call: xtabs(formula = ~s5_Range_number_physician_practice + coisplit,
    data = varicare)
Number of cases in table: 304
Number of factors: 2
Test for independence of all factors:
    Chisq = 6.922, df = 4, p-value = 0.14
    Chi-squared approximation may be incorrect
[1] 0.1509002

    Wilcoxon rank sum test with continuity correction

data:  s5_Range_number_physician_practice by coisplit
W = 6293, p-value = 0.3222
```

```
alternative hypothesis: true location shift is not equal to 0
```

6.2.2 Perception of Low-value Prescriptions

Hide

```
BHR.coi <- xtabs(~BHRsplit + coisplit, data = varicare)
BHR.coi
summary(BHR.coi)
Phi(BHR.coi)
cor.test(varicare$BHR, varicare$coi, method = "kendall")
```

```
        coisplit
BHRsplit   0   1
       0  95  30
       1 154  25
Call: xtabs(formula = ~BHRsplit + coisplit, data = varicare)
Number of cases in table: 304
Number of factors: 2
Test for independence of all factors:
    Chisq = 5, df = 1, p-value = 0.02535
[1] 0.1282489

    Kendall's rank correlation tau

data:  varicare$BHR and varicare$coi
z = -2.9022, p-value = 0.003706
alternative hypothesis: true tau is not equal to 0
sample estimates:
       tau
-0.1400363
```

6.3 Perception of Low-value Prescriptions

6.3.1 Demographics

Hide

Analyses For the Manuscript: Association between Risk Literacy and Va...

```
y.BHR <- xtabs(~Years_Profession + BHRsplit, data = varicare)
y.BHR
summary(y.BHR)
CramerV(y.BHR)
wilcox.test(Years_Profession ~ BHRsplit, data = varicare)


size.BHR <- xtabs(~s5_Range_number_physician_practice + BHRsplit, data = varicar
        e)
size.BHR
summary(size.BHR)
CramerV(size.BHR)
wilcox.test(s5_Range_number_physician_practice ~ BHRsplit, data = varicare)
```


Wegwarth O, *et al. BMJ Qual Saf* 2024;0:1–8. doi: 10.1136/bmjqs-2023-016979

```
                BHRsplit
Years_Profession  0  1
   <10 years     29 34
   10 -19 years  40 76
   20 - 29 years 31 44
   30 - 39 years 21 19
   ≥40 years      4  6
Call: xtabs(formula = ~Years_Profession + BHRsplit, data = varicare)
Number of cases in table: 304
Number of factors: 2
Test for independence of all factors:
    Chisq = 4.885, df = 4, p-value = 0.2993
    Chi-squared approximation may be incorrect
[1] 0.1267586

    Wilcoxon rank sum test with continuity correction

data:  Years_Profession by BHRsplit
W = 11602, p-value = 0.5662
alternative hypothesis: true location shift is not equal to 0

                                  BHRsplit
s5_Range_number_physician_practice  0  1
                              1     2  1
                              2     9  8
                              4-5  33 47
                              6-10 45 74
                              ≥10  36 49
Call: xtabs(formula = ~s5_Range_number_physician_practice + BHRsplit,
    data = varicare)
Number of cases in table: 304
Number of factors: 2
Test for independence of all factors:
    Chisq = 2.3806, df = 4, p-value = 0.6661
    Chi-squared approximation may be incorrect
[1] 0.08849304

    Wilcoxon rank sum test with continuity correction

data:  s5_Range_number_physician_practice by BHRsplit
W = 10866, p-value = 0.6531
alternative hypothesis: true location shift is not equal to 0
```

7 Version Information

Last update on 2023-11-13 at 2023-11-13 18:11:56 with R version 4.2.2.