

Urine\_Dep

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Enter author note here.1

The authors made the following contributions. HaoChen: Conceptualization, Writing - Original Draft Preparation, Writing - Review & Editing; Ernst-August Doelle: Writing - Review & Editing, Supervision.

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## Abstract

One or two sentences providing a **basic introduction** to the field, comprehensible to a scientist in any discipline. Two to three sentences of **more detailed background**, comprehensible to scientists in related disciplines. One sentence clearly stating the **general problem** being addressed by this particular study. One sentence summarizing the main result (with the words “**here we show**” or their equivalent). Two or three sentences explaining what the **main result** reveals in direct comparison to what was thought to be the case previously, or how the main result adds to previous knowledge. One or two sentences to put the results into a more **general context**. Two or three sentences to provide a **broader perspective**, readily comprehensible to a scientist in any discipline.

*Keywords:* keywords

Word count: X

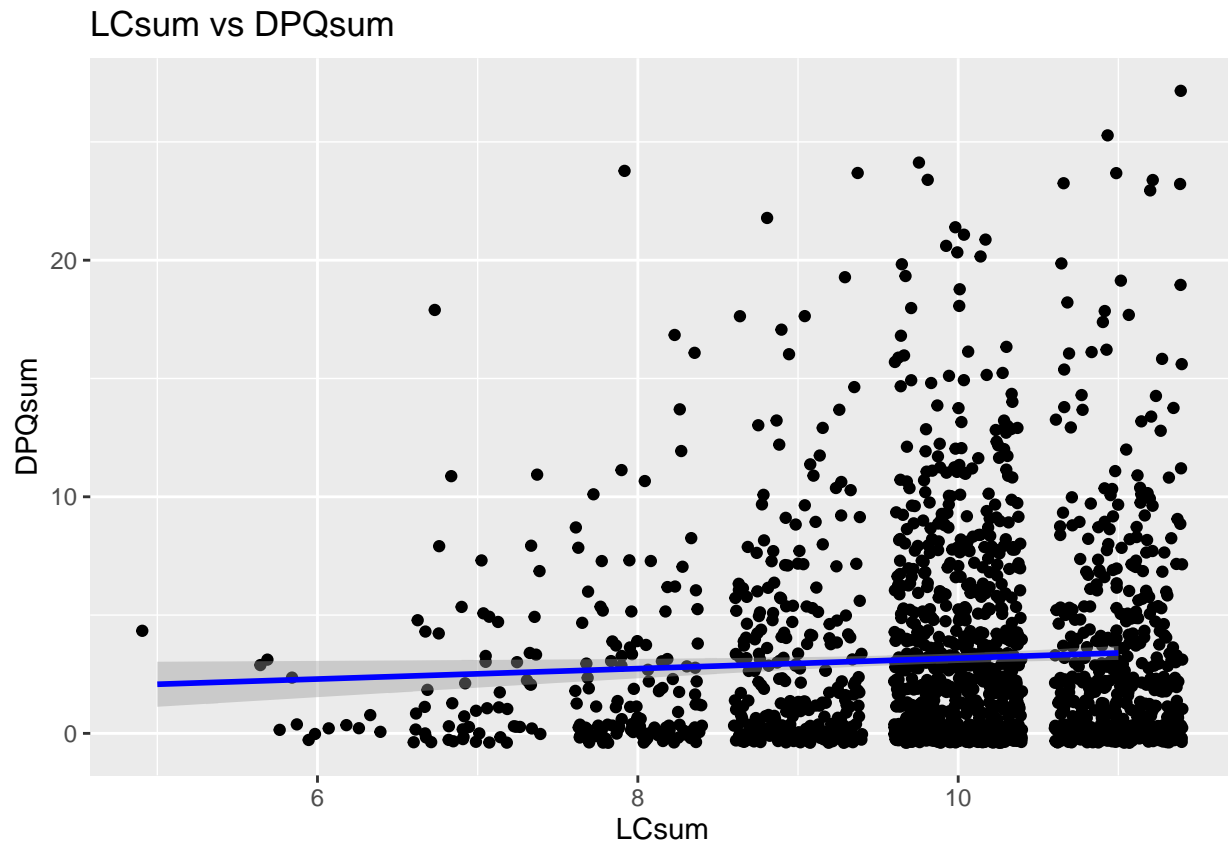
## Urine\_Dep

```
## # A tibble: 6 x 11
```

```
##   DPQ010 DPQ020 DPQ030 DPQ040 DPQ050 DPQ060 DPQ070 DPQ080 DPQ090 DPQ100 SEQN
##   <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl> <dbl>
## 1      0      0      0      0      0      0      0      0      0      0    NA 93708
## 2      1      0      1      0      0      0      0      0      0      0      0 93711
## 3      0      0      1      0      0      0      0      0      0      0      0 93712
## 4      1      0      0      1      0      0      0      0      0      0      0 93714
## 5     NA     NA     NA     NA     NA     NA     NA     NA     NA     NA     NA 93718
## 6      0      0      1      0      0      0      0      0      0      0      0 93722
```

Here to reference my depression measure gender difference  
 plot.Figure\(**ref?**\)(fig:DPQgenderdiff-plot)

Here to reference my LCsum and DPQ sum linear regression plot.  
 Figure\(**ref?**\)(fig:LCDPQ-plot)



Here to reference my racial demographic table ([ref?](#))(racial\_demographics)

```
## \begin{table}
## \centering
## \caption{(\#tab:racial_demographics)Racial Demographics in NHANES Data}
## \centering
## \begin{tabular}[t]{>{}c||c}
## \hline
## \textbf{Race} & \textbf{Count}\\
## \hline
## \textbf{\cellcolor{gray!10}{Mexican American}} & \cellcolor{gray!10}{263}\\
## \hline
## \textbf{Non-Hispanic Asian} & 262\\
```

```
## \hline
## \textbf{\cellcolor{gray!10}{Non-Hispanic Black}} & \cellcolor{gray!10}{430}\\
## \hline
## \textbf{Non-Hispanic White} & 636\\
## \hline
## \textbf{\cellcolor{gray!10}{Other}} & \cellcolor{gray!10}{104}\\
## \hline
## \textbf{Other Hispanic} & 164\\
## \hline
## \end{tabular}
## \end{table}
```

## Methods

### Participants

### Material

### Procedure

### Data analysis

We used R (Version 4.3.2; R Core Team, 2023) and the R-packages *dplyr* (Version 1.1.4; Wickham, François, Henry, Müller, & Vaughan, 2023), *forcats* (Version 1.0.0; Wickham, 2023a), *ggplot2* (Version 3.4.4; Wickham, 2016), *kableExtra* (Version 1.4.0; Zhu, 2024), *knitr* (Version 1.45; Xie, 2015), *lubridate* (Version 1.9.3; Grolemund & Wickham, 2011), *papaja* (Version 0.1.2; Aust & Barth, 2023), *purrr* (Version 1.0.2; Wickham & Henry, 2023), *readr* (Version 2.1.4; Wickham, Hester, & Bryan, 2023), *stringr* (Version 1.5.1; Wickham, 2023b), *tibble* (Version 3.2.1; Müller & Wickham, 2023), *tidyr* (Version

1.3.0; Wickham, Vaughan, & Girlich, 2023), *tidyverse* (Version 2.0.0; Wickham et al., 2019), and *tinylabels* (Version 0.2.4; Barth, 2023) for all our analyses.

```
## Warning in cor.test.default(fix_nhanes_data$LCsum, fix_nhanes_data$DPQsum, :  
## Cannot compute exact p-value with ties  
  
##  
## Spearman's rank correlation rho  
##  
## data: fix_nhanes_data$LCsum and fix_nhanes_data$DPQsum  
## S = 1038255815, p-value = 0.191  
## alternative hypothesis: true rho is not equal to 0  
## sample estimates:  
## rho  
## 0.03034425  
  
## Warning in cor.test.default(fix_nhanes_data[[var]], fix_nhanes_data$DPQsum, :  
## Cannot compute exact p-value with ties  
  
## Warning in cor.test.default(fix_nhanes_data[[var]], fix_nhanes_data$DPQsum, :  
## Cannot compute exact p-value with ties  
  
## Warning in cor.test.default(fix_nhanes_data[[var]], fix_nhanes_data$DPQsum, :  
## Cannot compute exact p-value with ties  
  
## Warning in cor.test.default(fix_nhanes_data[[var]], fix_nhanes_data$DPQsum, :  
## Cannot compute exact p-value with ties
```

```
## Warning in cor.test.default(fix_nhanes_data[[var]], fix_nhanes_data$DPQsum, :
## Cannot compute exact p-value with ties
```

```
## Warning in cor.test.default(fix_nhanes_data[[var]], fix_nhanes_data$DPQsum, :
## Cannot compute exact p-value with ties
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## Warning in cor.test.default(fix_nhanes_data[[var]], fix_nhanes_data$DPQsum, :
## Cannot compute exact p-value with ties
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## Cannot compute exact p-value with ties
```

```
## Warning in cor.test.default(fix_nhanes_data[[var]], fix_nhanes_data$DPQsum, :
## Cannot compute exact p-value with ties
```

##	Variable	R_Score	P_Value
## rho	URXUBA	-0.0004281156	0.98549843
## rho1	URXUCD	0.0503757996	0.03234614
## rho2	URXUC0	0.0361856511	0.12434322
## rho3	URXUCS	0.0023723363	0.91977296
## rho4	URXUM0	0.0041575011	0.85989247
## rho5	URXUMN	-0.0272955238	0.24642729

```
## rho6    URXUPB -0.0428280493 0.06889063
## rho7    URXUSB  0.0404663801 0.08566191
## rho8    URXUSN  0.0566022171 0.01617140
## rho9    URXUTL  0.0013211775 0.95526871
## rho10   URXUTU  0.0554684370 0.01843443
```

## Results

## Discussion



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