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Supplemental Material

Association of Tailpipe-Related and Nontailpipe–Related Air Pollution Exposure with Cognitive Decline in the Chicago Health and Aging Project

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Supplement – Quantitative bias analysis simulation

R Code

The following code replicates the simulation study results provided in the main text. It is heavily based on code published to accompany Mayeda et al. (2018), which can be found at *https://github.com/ermayeda/education_cognitive_decline_simulation*.

Generating intercepts

First, we present a function that estimates the intercept for the logistic regression used to generate predicted probabilities of death. We assumed that the probability of death was given by the following equation in agreement with Figure S1:

$$\Pr(S_i = 0) = \frac{\exp\{\gamma_{0,c} + \gamma_1 I(Q_i = 2) + \gamma_2 I(Q_i = 3) + \gamma_3 U_i + \gamma_4 I(Q_i = 2)U_i + \gamma_5 I(Q_i = 3)U_i\}}{1 + \exp\{\gamma_{0,c} + \gamma_1 I(Q_i = 2) + \gamma_2 I(Q_i = 3) + \gamma_3 U_i + \gamma_4 I(Q_i = 2)U_i + \gamma_5 I(Q_i = 3)U_i\}}$$

where I is an indicator function and Q_i denotes the pseudo-individual's TRAP exposure, with 1 corresponding to the first/lowest tertile of exposure (i.e.,"low"), 2 corresponding to the second tertile of exposure (i.e., "medium"), and 3 corresponding to the third/highest tertile of exposure (i.e., "high"). The values of $\gamma_1, \ldots \gamma_5$ are chosen as part of the simulation, and a root finding procedure is applied to estimate the $\gamma_{0,c}$ that gives approximately the correct marginal probability of death, as given by life tables in Arias (2015) National Vital Statistics Reports, Vol. 64, No. 11. The parameter matrices produced by this code are used in the next code chunk.

```
#Hard code the non-intercept parameters
g_2nd <- log(c(1.05,
               1.25,
               1.25,
               1.50,
               1.50,
               1.25,
               1.25,
               1.50,
               1.50))

g_3rd <- log(c(1.25,
               1.75,
               1.75,
               2.25,
               2.25,
               1.75,
               1.75,
               2.25,
               2.25))
```

```r
g_u <- log(c(0.9, rep(c(0.7, 0.8), 4)))

g_int_2nd <- log(c(1,
                   1,
                   1,
                   1,
                   1,
                   0.9,
                   0.9,
                   0.8,
                   0.8))

g_int_3rd <- log(c(1,
                   1,
                   1,
                   1,
                   1,
                   0.7,
                   0.7,
                   0.5,
                   0.5))

sim_params <- data.frame(g_2nd, g_3rd, g_u, g_int_2nd, g_int_3rd)

#These come from survival probabilities in Arias (2015) for Black men,
#Black women, White men, and White women

p_surv_bm60 <- 36790/1e5
p_surv_bw60 <- 38761/1e5
p_surv_wm60 <- 61933/1e5
p_surv_ww60 <- 68462/1e5

p_surv_bm65 <- 29314/1e5
p_surv_bw65 <- 30852/1e5
p_surv_wm65 <- 52964/1e5
p_surv_ww65 <- 60499/1e5

p_surv_bm75 <- 18854/1e5
p_surv_bw75 <- 17216/1e5
p_surv_wm75 <- 29205/1e5
p_surv_ww75 <- 32777/1e5

p_surv_bm85 <- 1747/1e5
p_surv_bw85 <- 3029/1e5
p_surv_wm85 <- 5145/1e5
p_surv_ww85 <- 7152/1e5
```

```
####

#Obtain intercepts

get_g0 <- function(x, pdie, mean_2, mean_3){
  pdie - exp(x + g_2nd*mean_2 + g_3rd*mean_3 + g_u*mean_u + g_int_2nd*mean_2*
mean_u + g_int_3rd*mean_3*mean_u)/(1 + exp(x + g_2nd*mean_2 + g_3rd*mean_3 +
g_u*mean_u + g_int_2nd*mean_2*mean_u + g_int_3rd*mean_3*mean_u))
}


mean_u = 0

g0_bm60 <- rep(0, nrow(sim_params))
g0_bw60 <- rep(0, nrow(sim_params))
g0_wm60 <- rep(0, nrow(sim_params))
g0_ww60 <- rep(0, nrow(sim_params))

g0_bm65 <- rep(0, nrow(sim_params))
g0_bw65 <- rep(0, nrow(sim_params))
g0_wm65 <- rep(0, nrow(sim_params))
g0_ww65 <- rep(0, nrow(sim_params))

g0_bm75 <- rep(0, nrow(sim_params))
g0_bw75 <- rep(0, nrow(sim_params))
g0_wm75 <- rep(0, nrow(sim_params))
g0_ww75 <- rep(0, nrow(sim_params))

g0_bm85 <- rep(0, nrow(sim_params))
g0_bw85 <- rep(0, nrow(sim_params))
g0_wm85 <- rep(0, nrow(sim_params))
g0_ww85 <- rep(0, nrow(sim_params))

for(i in 1:nrow(sim_params)){
  g_2nd <- sim_params[i,"g_2nd"]
  g_3rd <- sim_params[i, "g_3rd"]
  g_u <- sim_params[i, "g_u"]
  g_int_2nd <- sim_params[i, "g_int_2nd"]
  g_int_3rd <- sim_params[i, "g_int_3rd"]

  #root finding for intercepts for race by sex/gender, for age 65 and 75
  g0_bm65[i] <- uniroot(get_g0, interval=c(-5,5), pdie=1-p_surv_bm65, mean_2
= 0.322, mean_3 = 0.576)$root
  g0_bw65[i] <- uniroot(get_g0, interval=c(-5,5), pdie=1-p_surv_bw65, mean_2
= 0.322, mean_3 = 0.576)$root
  g0_wm65[i] <- uniroot(get_g0, interval=c(-5,5), pdie=1-p_surv_wm65, mean_2
= 0.358, mean_3 = 0.085)$root
  g0_ww65[i] <- uniroot(get_g0, interval=c(-5,5), pdie=1-p_surv_ww65, mean_2
= 0.358, mean_3 = 0.085)$root
```

```
  g0_bm75[i] <- uniroot(get_g0, interval=c(-5,5), pdie=1-p_surv_bm75, mean_2
= 0.322, mean_3 = 0.576)$root
  g0_bw75[i] <- uniroot(get_g0, interval=c(-5,5), pdie=1-p_surv_bw75, mean_2
= 0.322, mean_3 = 0.576)$root
  g0_wm75[i] <- uniroot(get_g0, interval=c(-5,5), pdie=1-p_surv_wm75, mean_2
= 0.358, mean_3 = 0.085)$root
  g0_ww75[i] <- uniroot(get_g0, interval=c(-5,5), pdie=1-p_surv_ww75, mean_2
= 0.358, mean_3 = 0.085)$root



}


g0_65_matrix <- cbind(sim_params,
                      g0_bm65,
                      g0_bw65,
                      g0_wm65,
                      g0_ww65)

g0_75_matrix <- cbind(sim_params,
                      g0_bm75,
                      g0_bw75,
                      g0_wm75,
                      g0_ww75)
```

Carrying out the simulation study

The next code chunk does the simulation study. Whereas Mayeda et al. (2018) present their simulation code as a set of nested functions, we present our code as a single chunk for simplicity. Below is the code for $B = 2000$ iterations of the age 65 study. This code iterates over a set over parameter values encoded in the parameter matrix, which is created in the prior code chunk above. It assumes that this matrix is in the user's environment, and that the *tidyverse*, *lme4*, and *MASS* libraries have been loaded.

The TRAP exposures for Black and White pseudo-participants are based on observed nitrogen dioxide distributions seen in the Chicago Health and Aging Project. We assumed that the true difference in the mean rate of cognitive change was $\beta = -0.003$.

This code includes some time metric reporting to assess how long the simulations run. If desired, this can be removed without affecting the simulation.

```
Age = 65
Bsim = 2000


t.beta = -0.003 #total causal effect of air pollution on annual rate of cogni
tive decline
N = 1e5 #total number of possible CHAP participants
```

```r
sampSize = 1e4 #target number of selected CHAP participants
t.int = 3 #time between cognitive assessment intervals
n.obs = 6 #total number of cognitive assessments

s2z0 = 0.2   # variance of random cognitive intercept
s2z1 = 0.005 # variance of random cognitive slope
sz01 = 0.01  #  covariance of random intercept and random slope
s2e = 0.70   # variance of unexplained variation in Cij
rho = 0      # correlation between noise terms for Cij
s2d = 0      # variance of measurement error of Cij
b00 = 0      # cognitive intercept for those with average air pollution expos
ure (A=0)
b01 = 0   # effect of a 1 ppm in air pollution on cognitive intercept
b02 = 0      # effect of U=1 on cognitive intercept
b10 = -0.006 # effect of time itself on cognitive slope
b11 =  -0.003 #effect of air pollution on cognitive slope
b12 = 0.3

no2_black_mean <- 19.88
no2_white_mean <- 17.02

no2_black_sd <- 2.07
no2_white_sd <- 1.80


b.err = c(s2z0,sz01,sz01,s2z1)


w.err = sqrt(0.7)
#These are hold overs from Mayeda et al. (2018) for cases where measurement
#error and other biases are of interest. Here, they are set to 0.
a.err = 0
m.err = 0

#In CHAP:

#10.3% of Black participants <= 33rd percentile of exposure
#55.7% of White participants <= 33rd percentile of exposure

#32.2% of Black participants > 33rd but <= 67th percentile of exposure
#35.8% of White participants > 33rd but <= 67th percentile of exposure

#57.6% of Black participants > 67th percentile of exposure
#8.5% of White participants > 67th percentile of exposure

data_gen <- function(){

  ## Create data frame of population
  df = data.frame(id = 1:N)
```

```
  # Assign the participants a race and sex/gender. For simplicity, equal %s

  df$race <- rep(c("White", "Black"), times=N/2)
  df$sex <- c(rep("Male", times=N/4), rep("Female", times=N/4), rep("Male", t
imes=N/4), rep("Female", times=N/4))

  df <- arrange(df, race)

  # Step 1: Generate air pollution exposure variable
  df$exposure = rnorm(N, mean = 18.8, sd=2.4)

  no2_black <- rnorm(N/2, mean=no2_black_mean, sd=no2_black_sd)
  no2_white <- rnorm(N/2, mean=no2_white_mean, sd=no2_white_sd)
  exposure <- c(no2_black, no2_white)

  df$exposure <- exposure


  df$p_tertile2 <- ifelse(df$race == "Black", 0.322, 0.358)
  df$p_tertile3 <- ifelse(df$race == "Black", 0.576, 0.085)
  df$tertile2 <- rbinom(N, 1, prob=df$p_tertile2)
  df$tertile3 <- rbinom(N, 1, prob=df$p_tertile3)

  # Step 2: Generate U
  #df$U = rbinom(N, size=1, prob=p_u)
  df$U = rnorm(N, mean=0, sd=1)

  # Step 3: Generate selection variable

  bm_subset <- filter(df, sex=="Male" & race=="Black")
  bw_subset <- filter(df, sex=="Female" & race=="Black")
  wm_subset <- filter(df, sex=="Male" & race=="White")
  ww_subset <- filter(df, sex=="Female" & race=="White")


  lin.pred_bm = with(bm_subset, exp(g0_bm65 + g_2nd*tertile2 + g_3rd*tertile3
+ g_u*U + g_int_2nd*tertile2*U + g_int_3rd*tertile3*U))
  bm_subset$p_survived = with(bm_subset, lin.pred_bm/(1+lin.pred_bm))
  bm_subset$survived = unlist(lapply(1:nrow(bm_subset),function(i){ifelse(run
if(1)<bm_subset$p_survived[i],0,1)}))

  lin.pred_bw = with(bw_subset, exp(g0_bw65 + g_2nd*tertile2 + g_3rd*tertile3
+ g_u*U + g_int_2nd*tertile2*U + g_int_3rd*tertile3*U))
  bw_subset$p_survived = with(bw_subset, lin.pred_bw/(1+lin.pred_bw))
  bw_subset$survived = unlist(lapply(1:nrow(bw_subset),function(i){ifelse(run
if(1)<bw_subset$p_survived[i],0,1)}))

  lin.pred_wm = with(wm_subset, exp(g0_wm65 + g_2nd*tertile2 + g_3rd*tertile3
+ g_u*U + g_int_2nd*tertile2*U + g_int_3rd*tertile3*U))
  wm_subset$p_survived = with(wm_subset, lin.pred_wm/(1+lin.pred_wm))
```

```r
  wm_subset$survived = unlist(lapply(1:nrow(wm_subset),function(i){ifelse(run
if(1)<wm_subset$p_survived[i],0,1)}))

  lin.pred_ww = with(ww_subset, exp(g0_ww65 + g_2nd*tertile2 + g_3rd*tertile3
+ g_u*U + g_int_2nd*tertile2*U + g_int_3rd*tertile3*U))
  ww_subset$p_survived = with(ww_subset, lin.pred_ww/(1+lin.pred_ww))
  ww_subset$survived = unlist(lapply(1:nrow(ww_subset),function(i){ifelse(run
if(1)<ww_subset$p_survived[i],0,1)}))

  df <- bind_rows(bm_subset, bw_subset, wm_subset, ww_subset)


  # Step 4: Generate cognitive function values at each cognitive assessment.
The study will include 6 cognitive assessment waves 3 years apart*/

  # Generate random terms for cognitive slope and intercept, zeta_0i (z0i) an
d zeta_1i (z1i),where zeta_0i and zeta_1i covary
  Sig = matrix(unlist(b.err),nrow=2,ncol=2)
  df = data.frame(df,b = mvrnorm(N,mu = c(0,0),Sigma = Sig))

  # Generate visit times
  time = seq(0,t.int*(n.obs-1),t.int)
  df.long = df[rep(seq_len(nrow(df)), each=n.obs),]
  df.long$time = rep(time,N)

  # Generate autoregressive noise term (unexplained variance in Cij) for each
visit
  df$alpha_ij = sqrt((1-a.err*a.err)*w.err)

  epsilon0 = rnorm(N,0,sqrt(w.err))
  autoerr = matrix(0,N*n.obs)
  df.long$autoerr = for(i in 1:N){
    autoerr[n.obs*(i-1)+1] = epsilon0[i]
    for(j in 2:(n.obs)){
      autoerr[n.obs*(i-1)+j] = a.err*autoerr[n.obs*(i-1)+j-1]+rnorm(1,0,sqrt(
(1-a.err*a.err)*w.err))
    }
  }

  df.long$true_cogfxn  = with(df.long, b00 + b01*exposure + b02*U +(b10 + b11
*exposure + b12*U)*time + b.1 + b.2*time + autoerr)

  df.long$delta = rnorm(N*n.obs, 0,  sqrt(m.err))
  df.long$measured_cogfxn = with(df.long,true_cogfxn+delta)

  #Return Final Data
  r.list = list(df.long = df.long,
                #g0 = g0,
                tB = t.beta,
                sampSize = sampSize)
```

```
  return(r.list)
}


simResults = function(B, trueB){
  start_time <- Sys.time()
  est_b_vec <- rep(0, times=B)
  emp_coverage_vec <- rep(0, times=B)

  for (i in 1:B){
    dG = data_gen()
    size = dG$sampSize
    df.long = dG$df.long
    df = df.long[!duplicated(df.long$id),]
    dGS = subset(df,survived==1)
    sampSize_black_male = sample(dGS[which(dGS$race=="Black" & dGS$sex=="Male
"),"id"], size=0.24*size)
    sampSize_black_female = sample(dGS[which(dGS$race=="Black" & dGS$sex=="Fe
male"),"id"], size=0.41*size)
    sampSize_white_male = sample(dGS[which(dGS$race=="White" & dGS$sex=="Male
"), "id"], size=0.13*size)
    sampSize_white_female = sample(dGS[which(dGS$race=="White" & dGS$sex=="Fe
male"), "id"], size=0.22*size)
    sampSize = c(sampSize_black_male, sampSize_black_female, sampSize_white_m
ale, sampSize_white_female)
    dfSamp.long = subset(df.long,id%in%sampSize)
    dfSamp = dfSamp.long[!duplicated(dfSamp.long$id),]


    ## run mixed effects model
    f1 = lmer(measured_cogfxn~exposure + time + exposure:time +(time|id),
              data = dfSamp.long)

    est_b <- fixef(f1)[['exposure:time']]
    est_b_sd <- t(diag(vcov(f1))^0.5)[[4]]

    U_CI <- est_b + qnorm(0.975)*est_b_sd
    L_CI <- est_b - qnorm(0.975)*est_b_sd

    emp_coverage = ifelse(trueB >= L_CI & trueB <= U_CI, 1, 0)

    est_b_vec[i] <- est_b
    emp_coverage_vec[i] <- emp_coverage

  }
  #print(est_b)
  mean_beta <- mean(est_b_vec)
  bias_perc <- (mean(est_b_vec)-trueB)/trueB*100
  mean_coverage <- mean(emp_coverage_vec)
```

```
  results_list <- list("g_2nd" = g_2nd,
                       "g_3rd" = g_3rd,
                       "g_U" = g_u,
                       "g_int_2nd" = g_int_2nd,
                       "g_int_3rd" = g_int_3rd,
                       "est_b"=est_b_vec,
                       "mean_b" = mean_beta,
                       "bias" = bias_perc,
                       "coverage" = mean_coverage)

  saveRDS(results_list,file = 'INSERT FILE PATH HERE')


  cat(paste0("Mean Empirical Cognitive Decline: ", mean_beta, "\n"))
  cat(paste0("Bias percentage: ", bias_perc, "\n"))
  cat(paste0("Percent CI coverage: ", mean_coverage, "\n"))

  end_time <- Sys.time()
  print(end_time - start_time)
  cat(paste0("\n"))
  cat(paste0("\n"))
}


######

set.seed(247)


for(i in 1:nrow(g0_65_matrix)){

  g_2nd <- g0_65_matrix[i, "g_2nd"]
  g_3rd <- g0_65_matrix[i, "g_3rd"]
  g_u <- g0_65_matrix[i, "g_u"]
  g_int_2nd <- g0_65_matrix[i, "g_int_2nd"]
  g_int_3rd <- g0_65_matrix[i, "g_int_3rd"]

  g0_bm65 <- g0_65_matrix[i, "g0_bm65"]
  g0_bw65 <- g0_65_matrix[i, "g0_bw65"]
  g0_wm65 <- g0_65_matrix[i, "g0_wm65"]
  g0_ww65 <- g0_65_matrix[i, "g0_ww65"]

  iter <- i
  simResults(B=Bsim, trueB= b11)

}
```

Generating results

In the code above, results were assembled into a list that includes the simulation parameters used, the estimated cognitive decline coefficients, the mean of these coefficients, the percentage bias, and the 95% CI coverage. This list is saved based on a file path and name provided by the user. Here, we show code that displays the results for the fourth row in Table 2, which uses the parameters in the fourth row of `g0_65_matrix`. The percentage bias can be accessed via `my_data[[3]]` where `my_data.RDA` is the file that was saved as part of the fourth simulation study.

```
my_result[["bias"]]

## [1] -94.43659
```

The overall results of our simulations are given in Table 3 in the main text.

Supplement – Assigning 3-year exposure windows

This section provides further details of how we assigned 3-year exposure windows to each participant in our analytic sample.

Figure S1: Timeline of CHAP (1993-2012) indicating (i) windows during which participants were recruited/enrolled into CHAP, (ii) the window in which we have NO_X and NO_2 predicted concentrations, and (iii) the temporal ordering of TRAP exposure windows and the period in which participants were followed for cognitive decline.

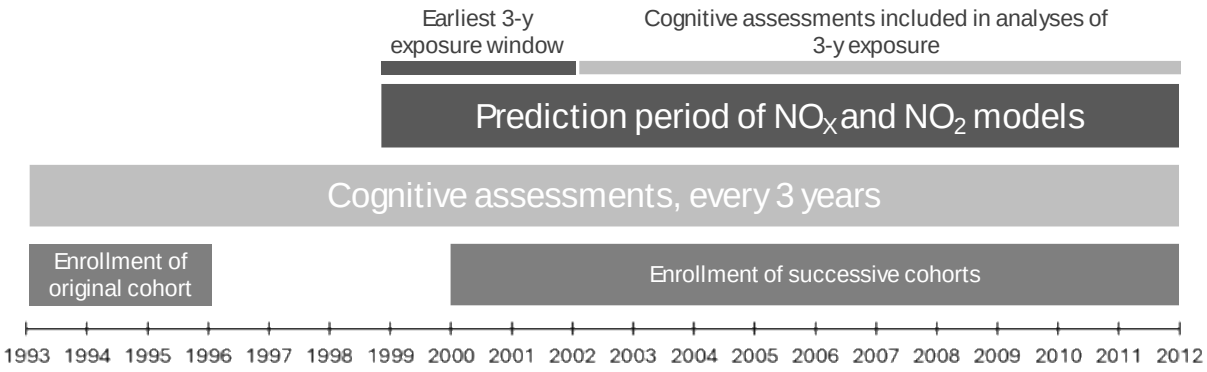
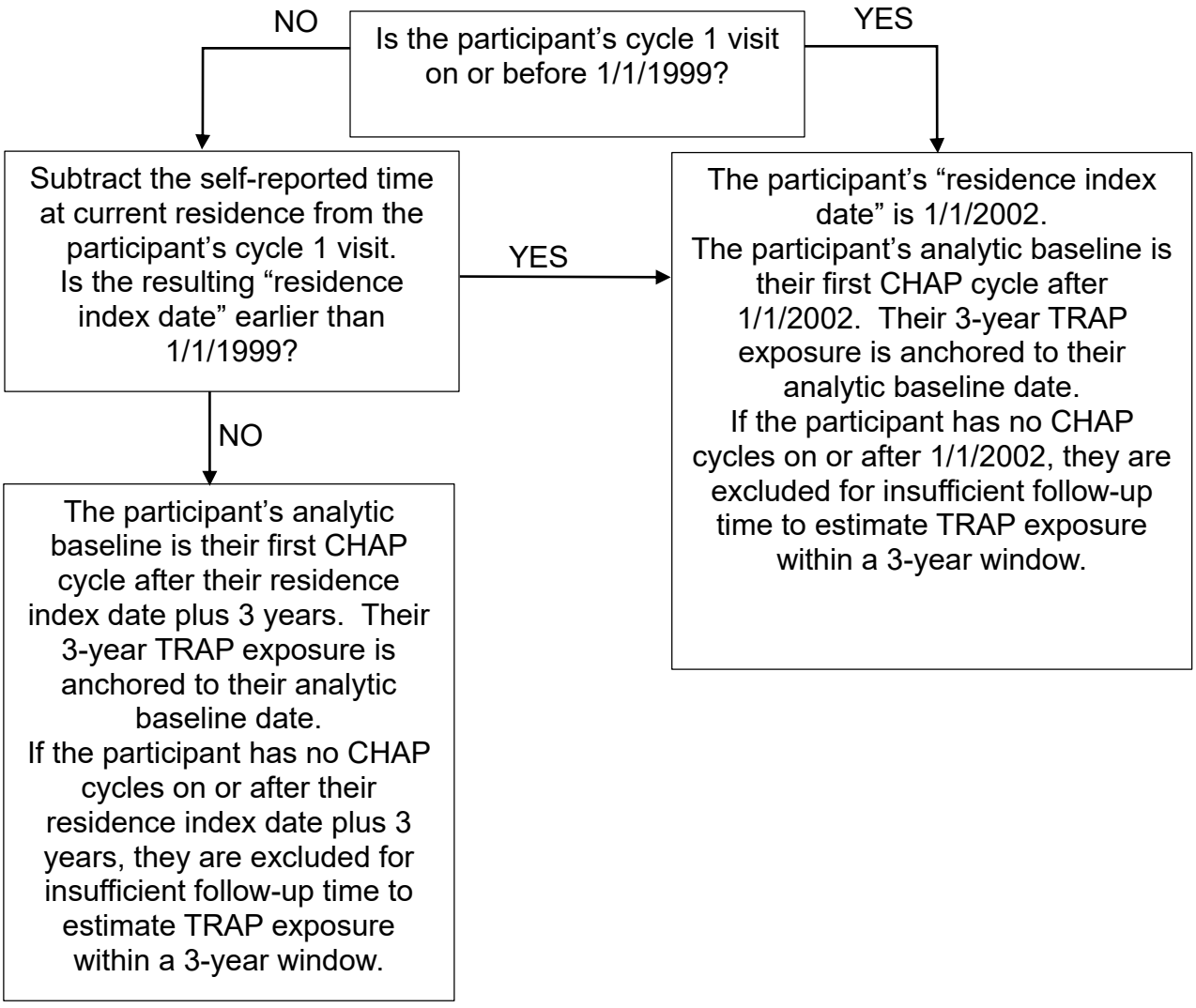


Figure S2: Algorithm by which we assigned participants in our analyses a 3-year exposure window, which in term determined their analytic baseline.



Toy examples

Using the toy dataset below in Table S4, we illustrate how the algorithm in Figure S2 can be used to assign participants an analytic baseline visit (which is the end of their 3-year TRAP exposure window).

Table S1. Dataset containing 5 hypothetical participants in our study who entered CHAP at different times.

ID	Time at current residence	Cycle 1	Cycle 2	Cycle 3	Cycle 4	Cycle 5	Cycle 6
1111	n/a	8/1/1993	10/13/1997	2/4/2001	5/30/2004	4/10/2008	3/18/2012
1112	n/a	10/10/1993	7/2/1996	9/10/1999			
1113	n/a	7/12/1994	11/11/1997	2/1/2001	12/12/2003		
1114	21.5 years	5/5/2005	9/14/2008	3/22/2011			
1115	2.9 years	2/16/2005	4/28/2008	1/12/2011			

Example: Participant 1111

This participant entered CHAP on 8/1/1993, which is before 1/1/1999. Following the algorithm flowchart, we assign a residence index date of 1/1/2002. The first CHAP cycle after this residence index date is 5/30/2004, which becomes the participant's analytic baseline. Finally, we define their 3-year TRAP exposure window to be 5/30/2001 to 5/30/2004 (note that the end date is anchored to the analytic baseline). If this participant were in our analytic dataset, they would contribute 3 waves of data to our primary analyses (5/30/2004, 4/10/2008, and 3/18/2012).

Example: Participant 1112

This participant entered CHAP on 10/10/1993, which is before 1/1/1999. Therefore, we assign them a residence index date of 1/1/2002. However, this participant did not complete any CHAP visits on or after this index date (their last cycle date was 9/10/1999). We exclude this participant from our analyses due to insufficient follow-up time to estimate a 3-year TRAP exposure.

Example: Participant 1113

This participant entered CHAP on 7/12/1994, which is before 1/1/1999. We therefore assign a residence index date of 1/1/2002. They completed a CHAP cycle on 12/12/2003, which becomes their analytic baseline. We define their 3-year TRAP exposure window to be 12/12/2000 to 12/12/2003, and this hypothetical participant would contribute 1 wave of data to our primary analyses (12/12/2003).

Note that this participant would not be included in a sensitivity analysis based on 5-year TRAP exposure. To see this, replace every mention of “3 years” in the algorithm above with “5 years.” By following this modified algorithm, you will eventually assign this participant a residence index date of 1/1/2004 (5 years after 1/1/1999). However, this participant has no CHAP cycles after 12/12/2003, so they would be excluded for insufficient follow-up time to estimate a 5-year TRAP exposure, even though they were included in our 3-year (primary) analyses.

Example: Participant 1114

This participant entered CHAP after 1/1/1999 on 5/5/2005. We therefore need to assign a residence index date based on their entry date and their self-reported time at their current residence. Subtracting 21.5 years from 5/5/2005 clearly results in a date before 1/1/1999; therefore, this participant’s residential index date is 1/1/2002 per our algorithm. The CHAP visit following this index date is 5/5/2005 – in this case, the participant’s analytic baseline equals their true baseline. We define their 3-year TRAP exposure window to be 5/5/2002 to 5/5/2005, and they contribute 3 waves of data to our analyses.

Example: Participant 1115

This participant entered on 2/16/2005, which is after 1/1/1999. Therefore, we assign a residence index date based on their entry date and their self-reported time at their current residence. Subtracting 2.9 years from 2/16/2005 results in a date of 3/25/2002, assuming 2.9 years is equal to 365.25 days/year * 2.9 years = 1059 days after rounding. This date is after 1/1/2002, so we assign this participant a residence index date of 3/25/2002 according to our algorithm. The participant’s analytic baseline is the CHAP visit following this index date, which is 4/28/2008. Their 3-year exposure window is defined to be 4/28/2005 to 4/28/2008, and they contribute 2 waves of data to our primary analyses (4/28/2008 and 1/12/2011).

Supplement – Inverse probability weight model fit

In the main text, we report sensitivity analyses involving inverse probability of continuation weights (IPCW). These weights are defined as the product of an IPCW due to not dying and an IPCW due to not dropping out.

In Table S5, we report the c-statistics from each pooled logistic regression model used to construct these weights. Due to concerns about the lower c-statistics for the IPCW model(s) for not dropping out, we conducted additional IPCW sensitivity analyses using only the IPCW due to not dying (estimated from models with acceptable discriminatory ability based on the c-statistic).

In Tables S6-S9, we report the estimated coefficients from each pooled logistic regression model used to construct IPCWs. Overall, we see that while many of the associations between covariates and the probability of dying are in the expected direction (e.g., those with poor self-rated health have much higher odds of dying compared to those with excellent self-rated health), the associations between covariates and the probability of not dropping out are often counter-to-expectations. Although the purpose of these models is to predict mortality or dropout rather than estimate effects of any given factor on the risk of these outcomes, these preliminary results helped our decision to focus on unweighted results for our primary analyses and explore weighted results through sensitivity analyses.

Table S2: C-statistics from models predicting either continuation due to not dropping out or continuation due to not dying among participants in our analytic sample (N=6,061)

TRAP species	C-statistic, model predicting continuation due to not dropping out*	C-statistic, model predicting continuation due to not dying*
NO_X	0.612	0.764
NO_2	0.611	0.765
$PM_{2.5\text{-}10,Cu}$	0.611	0.764
$PM_{2.5\text{-}10,Zn}$	0.614	0.764

*Our predictive models included the following covariates: sex, race, age, years of educational attainment, smoking status, alcohol consumption within the previous two weeks, Nagi disability score, self-rated health, self-reported diabetes mellitus status at the analytic baseline visit, social network score, and global cognition score at the prior visit. Each model additionally adjusted for the TRAP species of interest, which resulted in 4 separate models predicting continuation due to not dropping out and 4 separate models predicting continuation due to not dying.

Table S3: Results from pooled logistic regression models for dropout or death in our analytic sample (N=6,061), adjusting for NO_X and other relevant covariates.

Covariate*	**OR for dropout**	**OR for death**
Age	0.96	1.06
Male sex (reference: Female sex)	0.91	1.71
Black (reference: non-Black)	1.47	0.60
Smoking status		
Never	1.00 (ref)	1.00 (ref)
Former	0.99	1.32
Current	0.88	2.41
Alcohol consumption		
0 drinks/day	1.00 (ref)	1.00 (ref)
Up to 1 drink/day	0.87	0.89
2 or more drinks/day	0.98	1.20
Educational attainment		
Less than 9 years	1.00 (ref)	1.00 (ref)
9-12 years	1.14	1.14
13-16 years	1.05	1.06
17 or more years	0.94	0.88
Baseline diabetes	0.78	1.70
Self-rated health		
Excellent	1.00 (ref)	1.00 (ref)
Good	1.01	1.25
Fair	0.92	1.74
Poor	0.94	2.45
Social network score	1.00	0.99
Nagi disability score	1.04	0.92
Global cognitive score	0.82	0.56
3-year NO_X exposure	0.96	1.01

OR = odds ratio

*Odds ratios are given for a 1 unit increase in covariate values unless otherwise specified.

Table S4: Results from pooled logistic regression models for dropout or death in our analytic sample (N=6,061), adjusting for NO_2 and other relevant covariates.

Covariate*	**OR for dropout**	**OR for death**
Age	0.96	1.07
Male sex (reference: Female sex)	0.91	1.84
Black (reference: non-Black)	1.32	0.63
Smoking status		
Never	1.00 (ref)	1.00 (ref)
Former	0.99	1.33
Current	0.87	2.22
Alcohol consumption		
0 drinks/day	1.00 (ref)	1.00 (ref)
Up to 1 drink/day	0.87	0.85
2 or more drinks/day	0.97	0.85
Educational attainment		
Less than 9 years	1.00 (ref)	1.00 (ref)
9-12 years	1.16	1.13
13-16 years	1.06	1.08
17 or more years	0.96	0.94
Baseline diabetes	0.79	1.62
Self-rated health		
Excellent	1.00 (ref)	1.00 (ref)
Good	1.01	1.29
Fair	0.92	1.98
Poor	0.95	2.67
Social network score	1.00	0.99
Nagi disability score	1.04	0.91
Global cognitive score	0.82	0.55
3-year NO_2 exposure	0.93	1.04

OR = odds ratio

*Odds ratios are given for a 1 unit increase in covariate values unless otherwise specified.

Table S5: Results from pooled logistic regression models for dropout or death in our analytic sample (N=6,061), adjusting for $PM_{2.5\text{-}10,Cu}$ and other relevant covariates.

Covariate*	**OR for dropout**	**OR for death**
Age	0.96	1.07
Male sex (reference: Female sex)	0.91	1.84
Black (reference: non-Black)	1.34	0.68
Smoking status		
Never	1.00 (ref)	1.00 (ref)
Former	0.99	1.33
Current	0.87	2.23
Alcohol consumption		
0 drinks/day	1.00 (ref)	1.00 (ref)
Up to 1 drink/day	0.88	0.85
2 or more drinks/day	0.99	0.84
Educational attainment		
Less than 9 years	1.00 (ref)	1.00 (ref)
9-12 years	1.16	1.11
13-16 years	1.09	1.07
17 or more years	1.02	0.92
Baseline diabetes	0.80	1.61
Self-rated health		
Excellent	1.00 (ref)	1.00 (ref)
Good	1.01	1.30
Fair	0.92	1.98
Poor	0.94	2.67
Social network score	1.00	1.00
Nagi disability score	1.04	0.91
Global cognitive score	0.82	0.55
3-year $PM_{2.5\text{-}10,Cu}$ exposure	0.93	1.00

OR = odds ratio

**Odds ratios are given for a 1 unit increase in covariate values unless otherwise specified.

Table S6: Results from pooled logistic regression models for dropout or death in our analytic sample (N=6,061), adjusting for $PM_{2.5–10,Zn}$ and other relevant covariates.

Covariate*	**OR for dropout**	**OR for death**
Age	0.96	1.07
Male sex (reference: Female sex)	0.91	1.84
Black (reference: non-Black)	1.07	0.69
Smoking status		
Never	1.00 (ref)	1.00 (ref)
Former	0.99	1.33
Current	0.87	2.23
Alcohol consumption		
0 drinks/day	1.00 (ref)	1.00 (ref)
Up to 1 drink/day	0.88	0.85
2 or more drinks/day	0.99	0.84
Educational attainment		
Less than 9 years	1.00 (ref)	1.00 (ref)
9-12 years	1.17	1.12
13-16 years	1.09	1.07
17 or more years	1.01	0.92
Baseline diabetes	0.80	1.61
Self-rated health		
Excellent	1.00 (ref)	1.00 (ref)
Good	1.01	1.30
Fair	0.91	1.98
Poor	0.94	2.67
Social network score	1.00	0.99
Nagi disability score	1.04	0.91
Global cognitive score	0.82	0.55
3-year $PM_{2.5-10,Zn}$ exposure	0.98	1.00

OR = odds ratio

*Odds ratios are given for a 1 unit increase in covariate values unless otherwise specified.

Supplement – Spearman correlations for TRAP concentrations

Assessing spatial stability over time

In the main text, we assume that TRAP concentrations remain spatially stable over time. To test this assumption, we estimated 1-year average concentrations for NO_X and NO_2 over the entire range of predictions that we have, from 1999 until 2012, and then we estimated Spearman rank correlations between these concentrations over time. We observe that these correlations are quite high, even for 1-year averages that are separated by several years. This suggests that, at least in terms of rank order, TRAP concentrations within the catchment area of the Chicago Health and Aging Project were relatively stable over time, and our assumption of stability for the other TRAP species ($PM_{2.5\text{-}10,Cu}$ and $PM_{2.5\text{-}10,Zn}$) and other time frames (i.e., pre-1999) is justifiable.

Table S7: Spearman rank correlations of predicted annual average NOx concentrations, from 1999 through 2012, at all CHAP locations (N=8,473 unique locations).*

	1999 (47.9)	2000 (43.7)	2001 (43.0)	2002 (39.9)	2003 (42.1)	2004 (38.5)	2005 (36.4)	2006 (32.9)	2007 (31.3)	2008 (28.1)	2009 (26.7)	2010 (23.8)	2011 (20.7)	2012 (27.4)
1999	1.0000	0.9997	0.9978	0.9933	0.9894	0.9260	0.9567	0.9905	0.9900	0.9852	0.9671	0.8222	0.8124	0.7691
2000	0.9997	1.0000	0.9989	0.9953	0.9879	0.9217	0.9538	0.9904	0.9900	0.9852	0.9659	0.8169	0.8073	0.7625
2001	0.9978	0.9989	1.0000	0.9987	0.9800	0.9040	0.9399	0.9840	0.9836	0.9777	0.9545	0.7919	0.7819	0.7344
2002	0.9933	0.9953	0.9987	1.0000	0.9698	0.8840	0.9238	0.9758	0.9755	0.9686	0.9415	0.7652	0.7549	0.7043
2003	0.9894	0.9879	0.9800	0.9698	1.0000	0.9692	0.9882	0.9985	0.9982	0.9978	0.9928	0.8924	0.8846	0.8485
2004	0.9260	0.9217	0.9040	0.8840	0.9692	1.0000	0.9951	0.9609	0.9608	0.9672	0.9861	0.9735	0.9689	0.9491
2005	0.9567	0.9538	0.9399	0.9238	0.9882	0.9951	1.0000	0.9830	0.9830	0.9870	0.9970	0.9489	0.9432	0.9161
2006	0.9905	0.9904	0.9840	0.9758	0.9985	0.9609	0.9830	1.0000	0.9999	0.9993	0.9915	0.8812	0.8738	0.8345
2007	0.9900	0.9900	0.9836	0.9755	0.9982	0.9608	0.9830	0.9999	1.0000	0.9994	0.9917	0.8817	0.8744	0.8350
2008	0.9852	0.9852	0.9777	0.9686	0.9978	0.9672	0.9870	0.9993	0.9994	1.0000	0.9951	0.8940	0.8873	0.8490
2009	0.9671	0.9659	0.9545	0.9415	0.9928	0.9861	0.9970	0.9915	0.9917	0.9951	1.0000	0.9319	0.9264	0.8938
2010	0.8222	0.8169	0.7919	0.7652	0.8924	0.9735	0.9489	0.8812	0.8817	0.8940	0.9319	1.0000	0.9997	0.9949
2011	0.8124	0.8073	0.7819	0.7549	0.8846	0.9689	0.9432	0.8738	0.8744	0.8873	0.9264	0.9997	1.0000	0.9958
2012	0.7691	0.7625	0.7344	0.7043	0.8485	0.9491	0.9161	0.8345	0.8350	0.8490	0.8938	0.9949	0.9958	1.0000

*Below each year in the first row is the predicted mean concentration of NO_X for that year (in ppb), across all CHAP locations.

Table S8: Spearman rank correlations of predicted annual average NO_2 concentrations, from 1999 through 2012, at all CHAP locations (N=8,473 unique locations).*

	1999 (19.2)	2000 (18.8)	2001 (19.2)	2002 (18.2)	2003 (19.7)	2004 (17.8)	2005 (18.1)	2006 (16.7)	2007 (16.2)	2008 (15.7)	2009 (14.5)	2010 (14.2)	2011 (13.6)	2012 (13.3)
1999	1.0000	0.9998	1.0000	0.9993	0.9993	0.9965	0.9979	0.9960	0.9956	0.9940	0.9803	0.9775	0.9622	0.9728
2000	0.9998	1.0000	0.9999	0.9997	0.9989	0.9971	0.9985	0.9970	0.9968	0.9954	0.9823	0.9796	0.9648	0.9754
2001	1.0000	0.9999	1.0000	0.9994	0.9993	0.9969	0.9983	0.9965	0.9961	0.9945	0.9814	0.9786	0.9637	0.9741
2002	0.9993	0.9997	0.9994	1.0000	0.9980	0.9973	0.9986	0.9978	0.9978	0.9967	0.9841	0.9817	0.9671	0.9778
2003	0.9993	0.9989	0.9993	0.9980	1.0000	0.9974	0.9983	0.9958	0.9948	0.9932	0.9821	0.9795	0.9657	0.9745
2004	0.9965	0.9971	0.9969	0.9973	0.9974	1.0000	0.9997	0.9992	0.9984	0.9979	0.9926	0.9909	0.9806	0.9874
2005	0.9979	0.9985	0.9983	0.9986	0.9983	0.9997	1.0000	0.9993	0.9987	0.9980	0.9904	0.9884	0.9768	0.9848
2006	0.9960	0.9970	0.9965	0.9978	0.9958	0.9992	0.9993	1.0000	0.9997	0.9994	0.9930	0.9914	0.9806	0.9887
2007	0.9956	0.9968	0.9961	0.9978	0.9948	0.9984	0.9987	0.9997	1.0000	0.9997	0.9925	0.9908	0.9795	0.9884
2008	0.9940	0.9954	0.9945	0.9967	0.9932	0.9979	0.9980	0.9994	0.9997	1.0000	0.9940	0.9925	0.9820	0.9905
2009	0.9803	0.9823	0.9814	0.9841	0.9821	0.9926	0.9904	0.9930	0.9925	0.9940	1.0000	0.9997	0.9964	0.9990
2010	0.9775	0.9796	0.9786	0.9817	0.9795	0.9909	0.9884	0.9914	0.9908	0.9925	0.9997	1.0000	0.9975	0.9995
2011	0.9622	0.9648	0.9637	0.9671	0.9657	0.9806	0.9768	0.9806	0.9795	0.9820	0.9964	0.9975	1.0000	0.9980
2012	0.9728	0.9754	0.9741	0.9778	0.9745	0.9874	0.9848	0.9887	0.9884	0.9905	0.9990	0.9995	0.9980	1.0000

*Below each year in the first row is the predicted mean concentration of NO_2 for that year (in ppb), across all CHAP locations.

Assessing correlation between TRAP and community noise

In Table 2 of the main text, we presented estimated Spearman rank correlations between estimated TRAP concentrations, averaged over 3 years prior to analytic baseline. Below, we expand this table to include community noise levels, which we included in our outcome models for cognitive decline.

Table S9: Spearman rank correlations between estimated TRAP concentrations, averaged over 3 years prior to analytic baseline, and community noise levels (N=6,601).

	NO_X	NO_2	$PM_{2.5-10,Cu}$	$PM_{2.5-10,Zn}$	Community noise
NO_X	1.00				
NO_2	0.91	1.00			
$PM_{10-2.5,Cu}$	0.63	0.71	1.00		
$PM_{10-2.5,Zn}$	-0.10	-0.13	-0.18	1.00	
Community noise	0.02	0.02	0.12	0.07	1.00