Supplementary Digital Content for "Measurement error correction for predicted spatiotemporal air pollution exposures."
eTable 1. Parameter estimates for spatiotemporal model of ambient $\mathrm{PM}_{2.5}$.

|  | Estimate | Standard Error |
| :--- | :---: | :---: |
| Spatiotemporal Covariates |  |  |
| Temperature $\left(10^{\circ} \mathrm{C}\right)$ | 0.037 | 0.037 |
| Wind Speed (10 m/s) | -0.249 | 0.060 |
| Relative Humidity (10\%) | -0.015 | 0.010 |
| Long-term Mean |  |  |
| Intercept | 1.744 | 1.117 |
| Percent Forest Cover (\%) | -0.003 | 0.001 |
| Distance to Emissions Point Source (10 km) | -0.059 | 0.025 |
| Log of Range Parameter (km) | 4.179 | 0.506 |
| Log of Sill Parameter | -4.507 | 0.314 |
| Time Trend Coefficients | 0.073 |  |
| Intercept | 0.013 | 0.044 |
| Elevation (100m) | 0.001 | $<0.006$ |
| Percent Forest Cover (\%) | -0.030 | 0.015 |
| Local Road Length (10 km) | -0.056 | 0.026 |
| Highway Length (10 km) | 5.253 | 0.635 |
| Log of Range Parameter (km) | -5.371 | 0.534 |
| Log of Sill Parameter |  |  |
| Spatiotemporal Residual | -3.130 | 0.09 |
| Log of Range Parameter (km) | -4.782 | 0.030 |
| Log of Sill Parameter |  |  |
| Log of Nugget Parameter |  | 0.075 |


eFigure 1. $\mathrm{PM}_{2.5}$ time trend estimated from monitoring data. Trend is shown on the standardized scale.

eFigure 2. Observations and cross-validated predictions of two-week average $\mathrm{PM}_{2.5}$ concentrations $\left(\mu \mathrm{g} / \mathrm{m}^{3}\right)$ from 2002 through 2006. The 1-1 line is drawn for reference.
eTable 2. Estimated difference in birth weight (in grams) associated with $1 \mu \mathrm{~g} / \mathrm{m}^{3}$ higher ambient average $\mathrm{PM}_{2.5}$ during the specified trimester, among births to mothers in all counties. Bootstrap corrections are based upon 1,000 bootstrap samples.

| Cohort | Correction | Trimester | Estimate | Std. Err |
| :--- | :--- | :---: | :---: | :---: |
| Statewide | Non- | 1 | 0.43 | 0.55 |
|  | Parametric | 2 | -0.65 | 0.56 |
|  |  | 3 | -0.51 | 0.58 |
|  |  |  |  |  |
|  | Parameter | 1 | 0.28 | 0.68 |
|  |  | 2 | -0.63 | 0.67 |
|  |  | 3 | -0.65 | 0.61 |

eTable 3. Estimated difference in birth weight (in grams) associated with $1 \mu \mathrm{~g} / \mathrm{m}^{3}$ higher ambient average $\mathrm{PM}_{2.5}$ during the third trimester in the restricted cohort. The degrees of freedom (df) per year in the health model reflects different amount of temporal smoothing.

| df per year | Estimate | Std. Err | 95\% CI |
| :---: | :---: | :---: | :---: |
| 1 | -0.70 | 0.39 | $(-1.46,0.05)$ |
| 2 | -0.75 | 0.69 | $(-2.10,0.59)$ |
| 3 | -1.98 | 0.77 | $(-3.50,-0.46)$ |
| 4 | -2.36 | 0.78 | $(-3.89,-0.83)$ |
| 5 | -2.31 | 0.79 | $(-3.85,-0.77)$ |
| 6 | -2.44 | 0.80 | $(-4.00,-0.88)$ |
| 7 | -2.38 | 0.80 | $(-3.95,-0.80)$ |
| 8 | -2.33 | 0.80 | $(-3.90,-0.75)$ |

```
# Example code for running the non-parametric bootstrap and the
# parameter bootstrap.
# First are three auxiliary functions,
# followed by a description of the R
# objects in the accompanying data file,
# followed then by code for running the
# bootstrap procedures.
# For each bootstrap (non-parametric and
# parameter), the code is in two parts.
# The first part deals with the exposure
# data, the second part with the health
# analysis.
```

```
#############################
```

\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#

# create_timemx()

# create_timemx()

# 

# 

# Function for creating a list of time-space linkages

# Function for creating a list of time-space linkages

# 

# 

# INPUT:

# INPUT:

# gridIDs -- vector of grid IDs

# gridIDs -- vector of grid IDs

# dates -- optional data frame for supplying the conception, trimester,

# dates -- optional data frame for supplying the conception, trimester,

# and birth dates

# and birth dates

# obsdates -- dates for which exposures are available. gestational

# obsdates -- dates for which exposures are available. gestational

# dates will be matched to the closest date in this vector

# dates will be matched to the closest date in this vector

# concep.date -- conception dates

# concep.date -- conception dates

# T2 -- dates of start of second trimester

# T2 -- dates of start of second trimester

# T3 -- dates of start of third trimester

# T3 -- dates of start of third trimester

# dob -- dates of birth

# dob -- dates of birth

# 

# 

# OUTPUT: A list of length equal to the number of

# OUTPUT: A list of length equal to the number of

# unique grid IDs. Each element in the list is

# unique grid IDs. Each element in the list is

# a set of three sparse matrices (one for each

# a set of three sparse matrices (one for each

# trimester).The number of rows is equal to

# trimester).The number of rows is equal to

# the number of obsdates. The number of columns

# the number of obsdates. The number of columns

# depends upon how many births occurred in that

# depends upon how many births occurred in that

# grid cell. Columns of the matrix sum to 1,

# grid cell. Columns of the matrix sum to 1,

# with non-zero entries corresponding to the

# with non-zero entries corresponding to the

# interval of the corresponding trimester.

# interval of the corresponding trimester.

# This is designed to allow for easily computing

# This is designed to allow for easily computing

# averages in the bootstrap procedure by simple

# averages in the bootstrap procedure by simple

# matrix multiplication.

# matrix multiplication.

# 

# 

create_timemx <- functionCgridIDs, dates=NULL, obsdates,
create_timemx <- functionCgridIDs, dates=NULL, obsdates,
concep.date=dates$concep.date, T2=dates$T2, T3=dates$T3, dob=dates$dob){

```
concep.date=dates$concep.date, T2=dates$T2, T3=dates$T3, dob=dates$dob){
```

```
T1.int <- findInterval(concep.date, obsdates)
T2.int <- findInterval(T2, obsdates)
T3.int <- findInterval(T3, obsdates)
dob.int <- findInterval(dob, obsdates)
newdates <- data.frame(T1.int=T1.int, T2.int=T2.int, T3.int=T3.int,
dob.int=dob.int)
ndates <- length(obsdates)
grid.list = sort(unique(gridIDs))
time.mx <- vector("list", length=length(grid.list))
names(time.mx) <- grid.list
for (i in 1:length(grid.list)) {
        grid.i = grid.list[i]
## Extract birth records in grid cell i
use = which(gridIDs == grid.i)
dat.i <- newdates[use,]
## Calculate exposure indicators
time.mx[[i]]$T1 <- Matrix(mapply(createExpInd,a = dat.i$T1.int, b =
dat.i$T2.int, n= ndates), sparse=TRUE, dimnames=list(NULL, rownames(dat.i)))
time.mx[[i]]$T2 <- Matrix(mapply (createExpInd,a = dat.i$T2.int, b =
dat.i$T3.int, n= ndates), sparse=TRUE, dimnames=list(NULL, rownames(dat.i)))
time.mx[[i]]$T3 <- Matrix(mapply (createExpInd,a = dat.i$T3.int, b =
dat.i$dob.int, n= ndates), sparse=TRUE, dimnames=list(NULL, rownames(dat.i)))
}
return(time.mx)
}
# Helper function for getting the indices
# corresponding to exposure. Creates
# an n-vector, with zeros everywhere
# except from indices a to b, in which
# there are equal values that sum to 1.
# This makes exposure assignment easily
# done through matrix multiplication.
createExpInd <- function(a, b, n) {
x <- numeric(n)
x[a:b] <- 1/(b-a + 1)
return(x)
}
```

```
# make_exposure_assignment()
#
# Function for making exposure assignment
#
# INPUT:
# obs -- matrix of exposure observations
# time.list -- list output from create_timemx()
#
# OUTPUT:
# expos -- matrix of average exposures
# for each subject (row) and trimester (column)
#
make_exposure_assignment <- function(obs, time.list){
# Get location name list
locnamelist <- sapply(time.list, function(w) colnames(w$T1))
# Vector of location names, for assigning to rows of output matrix
locnames <- unlist(locnamelist, use.names=FALSE)
# Vector of location counts per grid, to allow for
# efficient index creation, all to avoid (slow!) name
# matching within the loop
indvec <- cumsum(c(1, sapply(locnamelist, length)))
expos <- matrix(data=0, nrow=length(locnames), ncol=3)
rownames(expos) <- locnames
colnames(expos) <- c("T1", "T2", "T3")
for (i in 1:length(time.list) ){
    grid.i = names(time.list)[i]
    ## Extract 2-week time-series for grid cell i
    exp.i = obs[, colnames(obs) == grid.i]
    # ## Fill in exposure estimates
    T1 <- as.vector(exp.i %*% time.list[[i]]$T1)
    T2 <- as.vector(exp.i %*% time.list[[i]]$T2)
    T3 <- as.vector(exp.i %*% time.list[[i]]$T3)
    inds <- indvec[i]:(indvec[i+1]-1)
    expos[inds, ] <- cbind(T1, T2, T3)
}
return(expos)
}
```

```
library(SpatioTemporal)
library(MASS)
#####################
# Load the Data #
#####################
load("GA_PM25_Birthweight.RData")
# Objects included:
# pm.stmodel -- the STmodel object containing the monitoring data
# and model specifications
# pm.stdata -- the STdata object containing the monitoring data
# grid.stdata -- an STdata object containing covariate information
# at grid locations. Used for making predictions.
# est.pm.stmodel -- an estimateSTmodel object containing parameter
# estimates for the exposure prediction model
# pm.aqsgrid.stmodel -- an STmodel object for simulating data
# at AQS and grid locations simultaneously.
# bwdata -- Synthetic birth weight data. These were generated using
# random dates, random locations, and random birth weights
# and thus differ from the observed data used in the
# manuscript analysis.
# Note: See the SpatioTemporal package help files for more
# information about structure of the STmodel and STdata objects.
```

```
#########################
```

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# Fit original models

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```
```

fitT1 = lm (bwt~T1.exp, data = bwdata)

```
fitT1 = lm (bwt~T1.exp, data = bwdata)
lmT1coef <- coef(fitT1)
lmT1coef <- coef(fitT1)
lmT1sigma <- summary(fitT1)$sigma
lmT1sigma <- summary(fitT1)$sigma
fitT2 = lm (bwt~T2.exp, data = bwdata)
fitT2 = lm (bwt~T2.exp, data = bwdata)
lmT2coef <- coef(fitT2)
lmT2coef <- coef(fitT2)
lmT2sigma <- summary(fitT2)$sigma
lmT2sigma <- summary(fitT2)$sigma
fitT3 = lm (bwt~T3.exp, data = bwdata)
fitT3 = lm (bwt~T3.exp, data = bwdata)
lmT3coef <- coef(fitT3)
lmT3coef <- coef(fitT3)
lmT3sigma <- summary(fitT3)$sigma
```

lmT3sigma <- summary(fitT3)\$sigma

```
```

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# 

# Non-Parametric Bootstrap

# 

\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#

# Extract spatial covariates

mon.covars <- pm.stdata\$covars

# Spatiotemporal covariates

mon.st.covars <- pm.stdata\$SpatioTemporal

# Monitor observations matrix

mon.obs <- createDataMatrix(pm.stdata)

# Monitor IDs

mon.list <- colnames(mon.obs)
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# NP Bootstrap, Part 1

# Monitor Sampling

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# Code shown here as a loop over B=2 iterations.

# These can also be run in parallel.

B <-2
for (i in 1:B){
seed <- i
set.seed(seed)
mons.i <- sample(mon.list, replace=T)
mon.obs.i <- mon.obs[, mons.i]
colnames(mon.obs.i) <- 1:ncol(mon.obs.i) \# Give arbitrary monitor IDs
mon.covars.i <- mon.covars[match(mons.i, mon.covars\$ID), ]
mon.covars.i $x[duplicated(mons.i)] <-
jitter(mon.covars.i$x[duplicated(mons.i)], amount=0.3) \# Jitter by 300m in
each direction
mon.covars.i \$y[duplicated(mons.i)] <- jitter(mon.covars.i
\$y[duplicated(mons.i)], amount=0.3)
mon.covars.i $ID <- 1:length(mons.i) # Give arbitrary monitor IDs
mon.st.covars.i <- mon.st.covars[, mons.i, ]
dimnames(mon.st.covars.i)[[2]] <- 1:length(mons.i) # Give arbitrary IDs
pm.stdata.i <- createSTdata(obs= mon.obs.i, covars= mon.covars.i,
SpatioTemporal = mon.st.covars.i)
pm.stdata.i$trend <- pm.stmodel$trend # Add the original trend
pm.stdata.i$trend.fnc <- pm.stmodel\$trend.fnc \# Add the original trend

# Model Setup

LUR <- list (~ forest_2001 + dist_emiss_2002, ~elevation+forest_2001 +

```
```

local_length + highway_length)
cov.beta <- list(covf = "exp", nugget = F)
cov.nu <- list (covf = "exp", nugget = T)
locations <- list (coords =c("x", "y"), long.lat = c("long", "lat"))
pm.stmodel.i <-createSTmodel(pm.stdata.i, LUR=LUR, ST=c("tmp", "wspd", "rh"),
cov.beta=cov.beta, cov.nu=cov.nu, locations=locations)

# Estimate model parameters

## This may take a long time!

x.init<-cbind (c(3, -4, 3, -5, 3, -3, -5), rep (0, 7))
est.pm.stmodel.i <- estimate (pm.stmodel.i, x.init, type="p")

# Make predictions

## This may take a long time!

grid.pred.temp.i <- predict(object= pm.stmodel.i , x= est.pm.stmodel.i,
STdata= grid.stdata, pred.var=FALSE, Nmax=2000)
EX.i <- grid.pred.temp.i\$EX

# Save the results, if desired

stdatafilename <- paste0("nonparametric_bootstrap_stdata_seed", seed,
".RData")
save(mons.i, EX.i, est.pm.stmodel.i, file=stdatafilename)
}
\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#

# NP Bootstrap, Part 2

# Health Analysis

\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#\#
obsdates <- seq(as.Date('2001/1/1'), as.Date('2006/12/11'), by="14 days")

# Create list of time-space linkage information, to facilitate

# simpler computation of trimester exposures

tm <- create_timemx(gridIDs= bwdata\$grid, dates= bwdata, obsdates= obsdates)

# Matrix for estimates

coefMX <- matrix(NA, nrow=3, ncol=B, dimnames=list(c("T1", "T2", "T3"), 1:B))

# Loop over simulated exposures

for (i in 1:B){

# Load the ST data for this bootstrap run

stdata.boot.filename <- paste0("nonparametric_bootstrap_stdata_seed", i,
".RData")
load(stdata.boot.filename, verbose=TRUE)
obsPred.i <- exp(EX.i)
expPred <- make_exposure_assignment(obs= obsPred.i, time.list=tm)
bwdata.i <- bwdata

```
```

bwdata.i$T1.exp <- expPred[match(rownames(bwdata), rownames(expPred)), "T1"]
bwdata.i$T2.exp <- expPred[match(rownames(bwdata), rownames(expPred)), "T2"]
bwdata.i\$T3.exp <- expPred[match(rownames(bwdata), rownames(expPred)), "T3"]
subj.i <- sample(nrow(bwdata.i), replace=TRUE)
bwdata.i <- bwdata.i[subj.i, ]

```
```


# Fit Models

```
# Fit Models
fitT1.i = lm ( bwt~T1.exp, data = bwdata.i )
fitT1.i = lm ( bwt~T1.exp, data = bwdata.i )
coefs <- c(coef(fitT1.i)[2])
coefs <- c(coef(fitT1.i)[2])
fitT2.i = lm ( bwt~T2.exp, data = bwdata.i )
fitT2.i = lm ( bwt~T2.exp, data = bwdata.i )
coefs <- c(coefs, coef(fitT2.i)[2])
coefs <- c(coefs, coef(fitT2.i)[2])
fitT3.i = lm ( bwt~T3.exp, data = bwdata.i )
fitT3.i = lm ( bwt~T3.exp, data = bwdata.i )
coefs <- c(coefs, coef(fitT3.i)[2])
coefs <- c(coefs, coef(fitT3.i)[2])
coefMX[, i] <- coefs
coefMX[, i] <- coefs
}
}
# Bootstrap corrected estimate for Trimester 1 is:
# Bootstrap corrected estimate for Trimester 1 is:
2* lmT1coef["T1.exp"] - mean(coefMX["T1",])
2* lmT1coef["T1.exp"] - mean(coefMX["T1",])
###############################
# #
# Parameter Bootstrap #
# #
###############################
############################
# Parameter Boot., Part 1 #
# Exposure Simulation #
############################
# Code shown here as a loop over B=2 iterations.
# These can also be run in parallel.
B <-2
for (i in 1:B){
seed <- i
set.seed(seed)
# Simulate the data
pm.sim <- simulate(pm.aqsgrid.stmodel, nsim=1, x=coef(est.pm.stmodel)$par,
nugget.unobs=exp(coef(est.pm.stmodel)$par[length(coef(est.pm.stmodel)$par)]))
# Put into space-time matrix form
obs <- exp(createDataMatrix(obs=pm.sim$obs[[1]]$obs,
date=pm.sim$obs[[1]]$date, ID=pm.sim$obs[[1]]$ID))
```

```
# Create new STmodel object, with new 'monitor' data
new.pm.stmodel <- pm.stmodel
new.pm.stmodel$obs <- pm.sim$obs[[1]][pm.sim$obs[[1]]$ID %in%
pm.stmodel$locations$ID,]
# Sample new exposure parameters
#
Sigma <- solve(-est.pm.stmodel$res.best$hessian.all)
parest <- mvrnorm(n=1, mu=est.pm.stmodel$res.best$par.all$par, Sigma=Sigma)
# Make predictions
# Note this may take a long time!
grid.pred.temp <- predict(object= new.pm.stmodel , x= parest, STdata=
grid.stdata, pred.var=FALSE, Nmax=2000)
EX <- grid.pred.temp$EX
rm(grid.pred.temp)
# Save the results, if desired
stdatafilename <- paste0("parameter_bootstrap_stdata_seed", seed, ".RData")
save(obs, EX, parest, file=stdatafilename)
}
############################
# Parameter Boot., Part 2 #
# Health Analysis #
############################
# Create list of time-space linkage information, to facilitate
# simpler computation of trimester exposures
obsdates <- seq(as.Date('2001/1/1'), as.Date('2006/12/11'), by="14 days")
tm <- create_timemx(gridIDs= bwdata$grid, dates= bwdata, obsdates= obsdates)
# Matrix for estimates
coefMX <- matrix(NA, nrow=3, ncol=B, dimnames=list(c("T1", "T2", "T3"), 1:B))
# Loop over simulated exposures
for (i in 1:B){
set.seed(1e5 + i)
# Load the simulated exposure observations and predictions
stfilename <- paste0("parameter_bootstrap_stdata_seed", i, ".RData")
load(stfilename, verbose=TRUE)
###########################################
# Simulate new Health Data, using bootstrapped
# exposure data at subject locations
# Make Exposure Assignments
```

```
exp <- make_exposure_assignment(obs=obs, time.list=tm)
lmMMT1.i <- cbind(1, T1.exp=exp[match(rownames(bwdata),rownames(exp)), "T1"])
lmMMT2.i <- cbind(1, T2.exp=exp[match(rownames(bwdata),rownames(exp)), "T2"])
lmMMT3.i <- cbind(1, T3.exp=exp[match(rownames(bwdata),rownames(exp)), "T3"])
# Simulate the health data
T1bwt_mean <- lmMMT1.i %*% lmT1coef
T2bwt_mean <- lmMMT2.i %*% lmT2coef
T3bwt_mean <- lmMMT3.i %*% lmT3coef
eps <- matrix(rnorm(n=3*nrow(bwdata)), nrow=nrow(bwdata), ncol=3)
T1bwt <- T1bwt_mean + lmT1sigma*eps[, 1]
T2bwt <- T2bwt_mean + lmT2sigma*eps[, 2]
T3bwt <- T3bwt_mean + lmT3sigma*eps[, 3]
###########################################
# Compute predicted exposures, using
# predictions developed from simulated
# monitor data.
# Make Exposure Assignments
obsPred <- exp(EX)
expPred <- make_exposure_assignment(obs=obsPred, time.list=tm)
# Replace model matrices with predictions
lmMMT1.i <- cbind(1, T1.exp= expPred[match(rownames(bwdata),
rownames(expPred)), "T1"])
lmMMT2.i <- cbind(1, T2.exp= expPred[match(rownames(bwdata),
rownames(expPred)), "T2"])
lmMMT3.i <- cbind(1, T3.exp= expPred[match(rownames(bwdata),
rownames(expPred)), "T3"])
fitT1.i <- solve(crossprod(lmMMT1.i), crossprod(lmMMT1.i, T1bwt))
coefs <- c(T1=fitT1.i[2])
rm(fitT1.i, lmMMT1.i); gc()
fitT2.i <- solve(crossprod(lmMMT2.i), crossprod(lmMMT2.i, T2bwt))
coefs <- c(coefs, T2=fitT2.i[2])
rm(fitT2.i, lmMMT2.i); gc()
fitT3.i <- solve(crossprod(lmMMT3.i), crossprod(lmMMT3.i, T3bwt))
coefs <- c(coefs, T3=fitT3.i[2])
rm(fitT3.i, lmMMT3.i); gc()
coefMX[, i] <- coefs
}
# Bootstrap corrected estimate for Trimester 1 is:
2* lmT1coef["T1.exp"] - mean(coefMX["T1",])
```

