```r
# Code for aggregating consumer exposures

# Written by CG at ICF in January 2024

# Last updated 03/04/2024 HAF


#User defined fraction absorbed values by pathway

  fabs_derm = 1 #fabs_dermal already accounted for in CEM results

  fabs_ing = 0.775 #fabs_ing depends on logKow based on Fang and Stapleton (2014)

  fabs_inh = 0.5 #fabs_inh assumed to be 0.5 for all chemicals


# Number of people in simulation

  n_people <- 100000


# Importing libraries needed

library(readxl)

library(base)

library(data.table)


# Set working directory

setwd(dirname(rstudioapi::getSourceEditorContext()$path)) #This should automatically set the working
directory


# Import input file

cpsc_data   <- read_xlsx("10_35656-01-0_Aggregate_Estimate_Inputs _2024-01-20_v2.xlsx")

adjustments <- read_xlsx("Probability_Adjustments_Aggregate_Estimate_Inputs _Tier3_2024-03-
11.xlsx")


# Make copy of data to edit

data1 <- cpsc_data[,c(1,5:13)]

data2 <- copy(adjustments)
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# Variable of unique number of scenarios (18 in current version)
n_cem <- uniqueN(data1$`CPSC Scenario #`)


# Make new column that indexes each scenario and repeats 7 times in same scenario (7 ages)
data1$index <- c(1:nrow(data1))
data_unadj  <- copy(data1)


#Create totals. Broken out to easily alter or add adjustments when needed
data1$Total_Derm <- data1$A_DER1 + data1$A_DER2 * data2$DermalAdj + data1$A_DER3
data1$Total_Ing  <- data1$A_ING1 + data1$A_ING2 * data2$MouthingAdj + data1$A_ING3
data1$Total_Inh  <- data1$A_INH1G + data1$A_INH1P


data_unadj$Total_Derm <- data1$A_DER1 + data1$A_DER2 + data1$A_DER3
data_unadj$Total_Ing  <- data1$A_ING1 + data1$A_ING2  + data1$A_ING3
data_unadj$Total_Inh  <- data1$A_INH1G + data1$A_INH1P


# Random number generator
RNGkind("Mersenne-Twister")


# Set seed and x1 is matrix with unique number of scenarios
set.seed(100)
x1_temp <- matrix(runif(n_people*n_cem), nrow = n_cem, ncol = n_people)
 x1 <- apply(x1_temp, 2, function(x) rep(x, each = 7))


# Probabilities from each scenario
 probs1 <- data2$Probability1
 probs2 <- data2$Probability2
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# x2 is matrix with unique number of scenarios

x2_temp <- matrix(runif(n_people*n_cem), nrow = n_cem, ncol = n_people)

  x2 <- apply(x2_temp, 2, function(x) rep(x, each = 7))


ages <- uniqueN(data2$Receptor)
# Initializing exposure pathway vectors

  total_dermal_unadj <- matrix(0,nrow = ages, ncol = n_people)

  total_ingestion_unadj <- matrix(0,nrow = ages, ncol = n_people)

  total_inhalation_unadj <- matrix(0,nrow = ages, ncol = n_people)


  total_dermal_adj <- matrix(0,nrow = ages, ncol = n_people)

  total_ingestion_adj <- matrix(0,nrow = ages, ncol = n_people)

  total_inhalation_adj <- matrix(0,nrow = ages, ncol = n_people)


  total_dermal_prob <- matrix(0,nrow = ages, ncol = n_people)

  total_ingestion_prob <- matrix(0,nrow = ages, ncol = n_people)

  total_inhalation_prob <- matrix(0,nrow = ages, ncol = n_people)


  total_dermal <- matrix(0,nrow = ages, ncol = n_people)

  total_ingestion <- matrix(0,nrow = ages, ncol = n_people)

  total_inhalation <- matrix(0,nrow = ages, ncol = n_people)


# For loop to go over every person, for total exposure via dermal, ingestion, inhalation
for (i in 1:n_people){


  #Select relevant scenarios based on p1 (p2 below). 0 = not selected , otherwise 1.
  y1 <- as.integer(x1[, i] <= probs1)
  y2 <- as.integer(x2[, i] <= probs2)
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intersect = y1*y2  #All scenarios that are selected from both probabilities


# Total route exposure is sum of the intersection of when total route is less than the prob
  # UnAdj (the original CEM output)
    total_dermal_unadj[, i] <- rowSums(matrix(data_unadj$Total_Derm, nrow = ages))


    total_ingestion_unadj[, i] <- rowSums(matrix(data_unadj$Total_Ing, nrow = ages))


    total_inhalation_unadj[, i] <- rowSums(matrix(data_unadj$Total_Inh, nrow = ages))


  # Adj (CEM output with adjustments)
    total_dermal_adj[, i] <- rowSums(matrix(data1$Total_Derm, nrow = ages))


    total_ingestion_adj[, i] <- rowSums(matrix(data1$Total_Ing, nrow = ages))


    total_inhalation_adj[, i] <- rowSums(matrix(data1$Total_Inh, nrow = ages))


  # Prob (averages across population including non-users, uses adjusted CEM output)
    total_dermal_prob[, i] <- rowSums(matrix(data1$Total_Derm*intersect, nrow = ages))


    total_ingestion_prob[, i] <- rowSums(matrix(data1$Total_Ing*intersect, nrow = ages))


    total_inhalation_prob[, i] <- rowSums(matrix(data1$Total_Inh*intersect, nrow = ages))


  # Fabs (population average of absorbed dose, now with fraction absorbed values)
    total_dermal[, i] <- rowSums(matrix(data1$Total_Derm*intersect, nrow = ages)) * fabs_derm


    total_ingestion[, i] <- rowSums(matrix(data1$Total_Ing*intersect, nrow = ages)) * fabs_ing
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    total_inhalation[, i] <- rowSums(matrix(data1$Total_Inh*intersect, nrow = ages)) * fabs_inh
}


#Output
  #Make tables
    table1 = cbind(rowMeans(total_dermal_unadj),
rowMeans(total_ingestion_unadj),rowMeans(total_inhalation_unadj),

            rowMeans(total_dermal_unadj) + rowMeans(total_ingestion_unadj) +
rowMeans(total_inhalation_unadj))

    rownames(table1) <- unique(data2$Receptor)

    colnames(table1) <- c('DermalUnadj',        'IngestionUnadj',        'InhalationUnadj',
        'TotalUnadj')


    table2= cbind(rowMeans(total_dermal_adj),
rowMeans(total_ingestion_adj),rowMeans(total_inhalation_adj),

            rowMeans(total_dermal_adj) + rowMeans(total_ingestion_adj) +
rowMeans(total_inhalation_adj))

    rownames(table2) <- unique(data2$Receptor)

    colnames(table2) <- c('DermalAdj',    'IngestionAdj',   'InhalationAdj',  'TotalAdj')


    table3= cbind(rowMeans(total_dermal_prob),
rowMeans(total_ingestion_prob),rowMeans(total_inhalation_prob),

            rowMeans(total_dermal_prob) + rowMeans(total_ingestion_prob) +
rowMeans(total_inhalation_prob))

    rownames(table3) <- unique(data2$Receptor)

    colnames(table3) <- c('DermalProbs','IngestionProbs',        'InhalationProbs',        'TotalProbs')


    table4= cbind(rowMeans(total_dermal), rowMeans(total_ingestion),rowMeans(total_inhalation),

            rowMeans(total_dermal) + rowMeans(total_ingestion) + rowMeans(total_inhalation))

    rownames(table4) <- unique(data2$Receptor)

    colnames(table4) <- c('DermalFabs',  'IngestionFabs', 'InhalationFabs',        'TotalFabs')
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#Combine tables
  Table <- cbind(table1,table2,table3,table4)


#Write to csv
  write.csv(Table, "10_35656-01-0_Consumer_Aggregate_Results_2024-01-20_v2_ReverseOrder.csv")


#Reorder Rows and write to csv
  Table2 = Table[c("Infant1", "Infant2", "Child1", "Child2", "Youth1", "Youth2" , "Adult"), ]
  write.csv(Table2, "10_35656-01-0_Consumer_Aggregate_Results_2024-01-20_v2.csv")


#Write to csv the individual scenarios adjusted for mouthing and dermal
  write.csv(data1,"10_35656-01-0_Individual_Scenarios_Adjusted_2024-01-20_v2.csv")
```