# Inequality in Environmental Exposure Across Population Groups

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## Contents

# 1 Location, Population, and Pollution

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## 1.1 Simulate Population Distribution over Location and Demographics

Use the binomial distribution to generate heterogenous demographic break-down by location. There are N demographic cells, and the binomial distribution provides the probability mass in each of the N cell. Different bernoulli "win" chance for each location. There is also probability distribution over population in each location.

First, construct empty population share dataframe:

```r
# 7 different age groups and 12 different locationso
it_N_pop_groups <- 7
it_M_location <- 12
# Matrix of demographics by location
mt_pop_data_frac <- matrix(data=NA, nrow=it_M_location, ncol=it_N_pop_groups)
colnames(mt_pop_data_frac) <- paste0('popgrp', seq(1,it_N_pop_groups))
rownames(mt_pop_data_frac) <- paste0('location', seq(1,it_M_location))
# Display
mt_pop_data_frac %>% kable() %>% kable_styling_fc()
```

Second, generate conditional population distribution for each location, and then multiply by the share of population in each locality:

```r
# Share of population per location
set.seed(123)
ar_p_loc <- dbinom(0:(3*it_M_location-1), 3*it_M_location-1, 0.5)
it_start <- length(ar_p_loc)/2-it_M_location/2
ar_p_loc <- ar_p_loc[it_start:(it_start+it_M_location+1)]
ar_p_loc <- ar_p_loc/sum(ar_p_loc)
```

|  | popgrp1 | popgrp2 | popgrp3 | popgrp4 | popgrp5 | popgrp6 | popgrp7 |
|---|---|---|---|---|---|---|---|
| location1 | NA | NA | NA | NA | NA | NA | NA |
| location2 | NA | NA | NA | NA | NA | NA | NA |
| location3 | NA | NA | NA | NA | NA | NA | NA |
| location4 | NA | NA | NA | NA | NA | NA | NA |
| location5 | NA | NA | NA | NA | NA | NA | NA |
| location6 | NA | NA | NA | NA | NA | NA | NA |
| location7 | NA | NA | NA | NA | NA | NA | NA |
| location8 | NA | NA | NA | NA | NA | NA | NA |
| location9 | NA | NA | NA | NA | NA | NA | NA |
| location10 | NA | NA | NA | NA | NA | NA | NA |
| location11 | NA | NA | NA | NA | NA | NA | NA |
| location12 | NA | NA | NA | NA | NA | NA | NA |

```r
# Different bernoulli "win" probability for each location
set.seed(234)
# ar_fl_unif_prob <- sort(runif(it_M_location)*(0.25)+0.4)
ar_fl_unif_prob <- sort(runif(it_M_location))

# Generate population proportion by locality
for (it_loc in 1:it_M_location ) {
  ar_p_pop_condi_loc <- dbinom(0:(it_N_pop_groups-1), it_N_pop_groups-1, ar_fl_unif_prob[it_loc])
  mt_pop_data_frac[it_loc,] <- ar_p_pop_condi_loc*ar_p_loc[it_loc]
}

# Sum of cells, should equal to 1
print(paste0('pop frac sum = ', sum(mt_pop_data_frac)))
```

```
## [1] "pop frac sum = 0.962953679726938"
```

```r
# Display
round(mt_pop_data_frac*100, 2) %>%
  kable(caption='Share of population in each location and demographic cell') %>%
  kable_styling_fc()
```

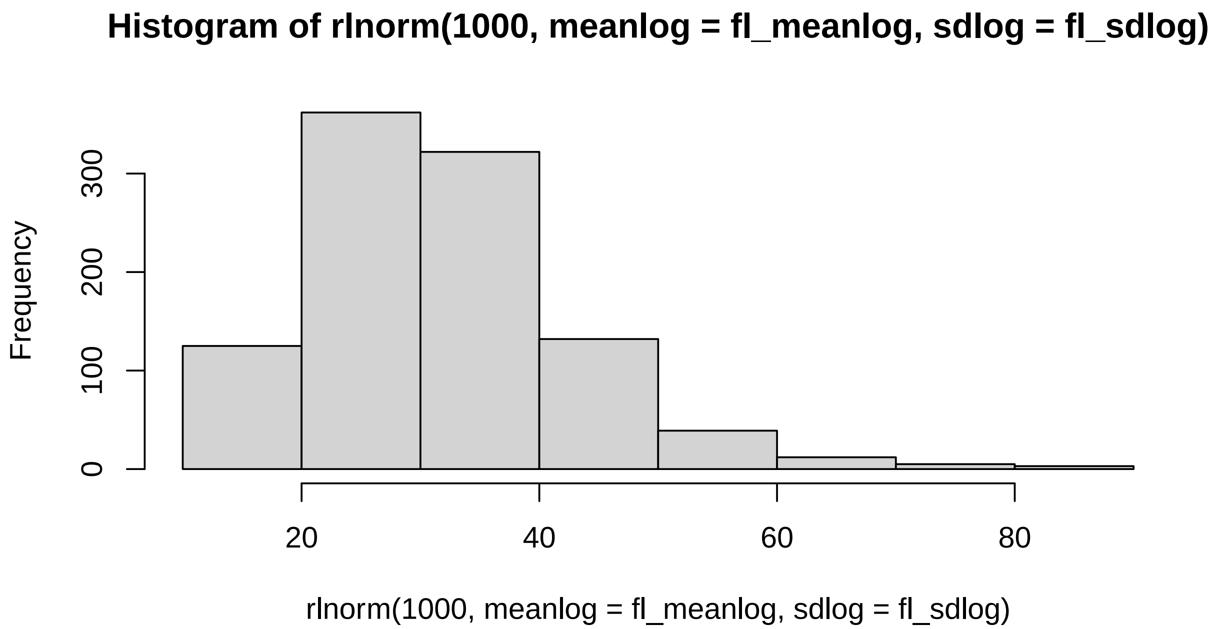
Share of population in each location and demographic cell

|  | popgrp1 | popgrp2 | popgrp3 | popgrp4 | popgrp5 | popgrp6 | popgrp7 |
|---|---|---|---|---|---|---|---|
| location1 | 1.09 | 0.13 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 |
| location2 | 1.63 | 0.70 | 0.13 | 0.01 | 0.00 | 0.00 | 0.00 |
| location3 | 0.59 | 1.40 | 1.39 | 0.74 | 0.22 | 0.03 | 0.00 |
| location4 | 0.06 | 0.43 | 1.29 | 2.09 | 1.90 | 0.92 | 0.19 |
| location5 | 0.07 | 0.55 | 1.73 | 2.89 | 2.71 | 1.36 | 0.28 |
| location6 | 0.02 | 0.26 | 1.19 | 2.89 | 3.93 | 2.85 | 0.86 |
| location7 | 0.01 | 0.10 | 0.66 | 2.23 | 4.26 | 4.33 | 1.83 |
| location8 | 0.00 | 0.06 | 0.47 | 1.83 | 4.03 | 4.72 | 2.31 |
| location9 | 0.00 | 0.03 | 0.27 | 1.26 | 3.28 | 4.55 | 2.63 |
| location10 | 0.00 | 0.02 | 0.20 | 0.96 | 2.57 | 3.68 | 2.19 |
| location11 | 0.00 | 0.00 | 0.00 | 0.04 | 0.40 | 2.05 | 4.38 |
| location12 | 0.00 | 0.00 | 0.00 | 0.02 | 0.24 | 1.28 | 2.82 |

## 1.2 Simulate Enviromental Exposure

Use log-normal distribution to describe average daily PM10 exposures distribution by locality:

```
fl_meanlog <- 3.4
fl_sdlog <- 0.35
hist(rlnorm(1000, meanlog = fl_meanlog, sdlog = fl_sdlog))
```



First, draw pollution measure for each locality:

```
# draw
set.seed(123)
ar_pollution_loc <- rlnorm(it_M_location, meanlog = fl_meanlog, sdlog = fl_sdlog)
# pollution dataframe
# 5 by 3 matrix

# Column Names
ar_st_varnames <- c('location','avgdailypm10')

# Combine to tibble, add name col1, col2, etc.
tb_loc_pollution <- as_tibble(ar_pollution_loc) %>%
  rowid_to_column(var = "id") %>%
  rename_all(~c(ar_st_varnames)) %>%
  mutate(location = paste0('location', location))

# Display
kable(tb_loc_pollution) %>% kable_styling_fc()
```

Second, reshape population data:

```
# Reshape population data, so each observation is location/demo
df_pop_data_frac_long <- as_tibble(mt_pop_data_frac, rownames='location') %>%
```

| location | avgdailypm10 |
|---|---:|
| location1 | 24.62676 |
| location2 | 27.64481 |
| location3 | 51.70466 |
| location4 | 30.71275 |
| location5 | 31.35114 |
| location6 | 54.61304 |
| location7 | 35.20967 |
| location8 | 19.24456 |
| location9 | 23.56121 |
| location10 | 25.63653 |
| location11 | 45.99021 |
| location12 | 33.98553 |

```
  pivot_longer(cols = starts_with('popgrp'),
               names_to = c('popgrp'),
               names_pattern = paste0("popgrp(.*)"),
               values_to = "pop_frac")
```

Third, join with pollution data:

```
# Reshape population data, so each observation is location/demo
df_pop_pollution_long <- df_pop_data_frac_long %>%
  left_join(tb_loc_pollution, by='location')

# display
df_pop_pollution_long[1:round(it_N_pop_groups*2.5),] %>% kable() %>% kable_styling_fc()
```

| location | popgrp | pop_frac | avgdailypm10 |
|---|---|---:|---:|
| location1 | 1 | 0.0109366 | 24.62676 |
| location1 | 2 | 0.0013417 | 24.62676 |
| location1 | 3 | 0.0000686 | 24.62676 |
| location1 | 4 | 0.0000019 | 24.62676 |
| location1 | 5 | 0.0000000 | 24.62676 |
| location1 | 6 | 0.0000000 | 24.62676 |
| location1 | 7 | 0.0000000 | 24.62676 |
| location2 | 1 | 0.0163003 | 27.64481 |
| location2 | 2 | 0.0070132 | 27.64481 |
| location2 | 3 | 0.0012573 | 27.64481 |
| location2 | 4 | 0.0001202 | 27.64481 |
| location2 | 5 | 0.0000065 | 27.64481 |
| location2 | 6 | 0.0000002 | 27.64481 |
| location2 | 7 | 0.0000000 | 27.64481 |
| location3 | 1 | 0.0058760 | 51.70466 |
| location3 | 2 | 0.0140000 | 51.70466 |
| location3 | 3 | 0.0138984 | 51.70466 |
| location3 | 4 | 0.0073587 | 51.70466 |

## 1.3 Compute Demographic Group Specific Exposure Distributions

What is the p10, median, p90 and mean pollution exposure for each demographic group?

1. group by population group

2. sort by pollution exposure within group
3. generate population group specific conditional population weights
4. generate population CDF for each population group (sorted by pollution)

```
# Follow four steps above
df_pop_pollution_by_popgrp_cdf <- df_pop_pollution_long %>%
  arrange(popgrp, avgdailypm10) %>%
  group_by(popgrp) %>%
  mutate(cdf_pop_condi_popgrp_sortpm10 = cumsum(pop_frac/sum(pop_frac)),
         pmf_pop_condi_popgrp_sortpm10 = (pop_frac/sum(pop_frac)))
# display
df_pop_pollution_by_popgrp_cdf[1:round(it_N_pop_groups*5.5),] %>%
  kable() %>% kable_styling_fc_wide()
```

| location | popgrp | pop_frac | avgdailypm10 | cdf_pop_condi_popgrp_sortpm10 | pmf_pop_condi_popgrp_sortpm10 |
|---|---|---|---:|---:|---:|
| location8 | 1 | 0.0000364 | 19.24456 | 0.0010453 | 0.0010453 |
| location9 | 1 | 0.0000151 | 23.56121 | 0.0014804 | 0.0004351 |
| location1 | 1 | 0.0109366 | 24.62676 | 0.3156484 | 0.3141680 |
| location10 | 1 | 0.0000104 | 25.63653 | 0.3159471 | 0.0002988 |
| location2 | 1 | 0.0163003 | 27.64481 | 0.7841942 | 0.4682471 |
| location4 | 1 | 0.0005879 | 30.71275 | 0.8010816 | 0.0168874 |
| location5 | 1 | 0.0007392 | 31.35114 | 0.8223166 | 0.0212350 |
| location12 | 1 | 0.0000000 | 33.98553 | 0.8223168 | 0.0000002 |
| location7 | 1 | 0.0000681 | 35.20967 | 0.8242718 | 0.0019550 |
| location11 | 1 | 0.0000000 | 45.99021 | 0.8242721 | 0.0000003 |
| location3 | 1 | 0.0058760 | 51.70466 | 0.9930669 | 0.1687948 |
| location6 | 1 | 0.0002413 | 54.61304 | 1.0000000 | 0.0069331 |
| location8 | 2 | 0.0006400 | 19.24456 | 0.0172871 | 0.0172871 |
| location9 | 2 | 0.0003150 | 23.56121 | 0.0257947 | 0.0085076 |
| location1 | 2 | 0.0013417 | 24.62676 | 0.0620374 | 0.0362427 |
| location10 | 2 | 0.0002235 | 25.63653 | 0.0680736 | 0.0060362 |
| location2 | 2 | 0.0070132 | 27.64481 | 0.2575157 | 0.1894421 |
| location4 | 2 | 0.0042712 | 30.71275 | 0.3728918 | 0.1153760 |
| location5 | 2 | 0.0055479 | 31.35114 | 0.5227547 | 0.1498629 |
| location12 | 2 | 0.0000004 | 33.98553 | 0.5227662 | 0.0000116 |
| location7 | 2 | 0.0010378 | 35.20967 | 0.5508009 | 0.0280347 |
| location11 | 2 | 0.0000008 | 45.99021 | 0.5508213 | 0.0000203 |
| location3 | 2 | 0.0140000 | 51.70466 | 0.9289930 | 0.3781718 |
| location6 | 2 | 0.0026287 | 54.61304 | 1.0000000 | 0.0710070 |
| location8 | 3 | 0.0046896 | 19.24456 | 0.0638166 | 0.0638166 |
| location9 | 3 | 0.0027290 | 23.56121 | 0.1009539 | 0.0371373 |
| location1 | 3 | 0.0000686 | 24.62676 | 0.1018872 | 0.0009333 |
| location10 | 3 | 0.0020006 | 25.63653 | 0.1291118 | 0.0272246 |
| location2 | 3 | 0.0012573 | 27.64481 | 0.1462207 | 0.0171089 |
| location4 | 3 | 0.0129304 | 30.71275 | 0.3221799 | 0.1759592 |
| location5 | 3 | 0.0173492 | 31.35114 | 0.5582709 | 0.2360910 |
| location12 | 3 | 0.0000141 | 33.98553 | 0.5584625 | 0.0001916 |
| location7 | 3 | 0.0065945 | 35.20967 | 0.6482016 | 0.0897391 |
| location11 | 3 | 0.0000242 | 45.99021 | 0.6485305 | 0.0003290 |
| location3 | 3 | 0.0138984 | 51.70466 | 0.8376617 | 0.1891312 |
| location6 | 3 | 0.0119295 | 54.61304 | 1.0000000 | 0.1623383 |
| location8 | 4 | 0.0183277 | 19.24456 | 0.1224562 | 0.1224562 |
| location9 | 4 | 0.0126118 | 23.56121 | 0.2067219 | 0.0842656 |

## 1.4 Compute the Gini Index by Population Subgroup

The Gini index from fs_gini_disc.

```
ffi_dist_gini_random_var_pos_test <- function(ar_x_sorted, ar_prob_of_x) {
  fl_mean <- sum(ar_x_sorted*ar_prob_of_x);
  ar_mean_cumsum <- cumsum(ar_x_sorted*ar_prob_of_x);
  ar_height <- ar_mean_cumsum/fl_mean;
  fl_area_drm <- sum(ar_prob_of_x*ar_height);
  fl_area_below45 <- sum(ar_prob_of_x*(cumsum(ar_prob_of_x)/sum(ar_prob_of_x)))
  fl_gini_index <- (fl_area_below45-fl_area_drm)/fl_area_below45
  return(fl_gini_index)
}
```

Compute Gini index for sub-group:

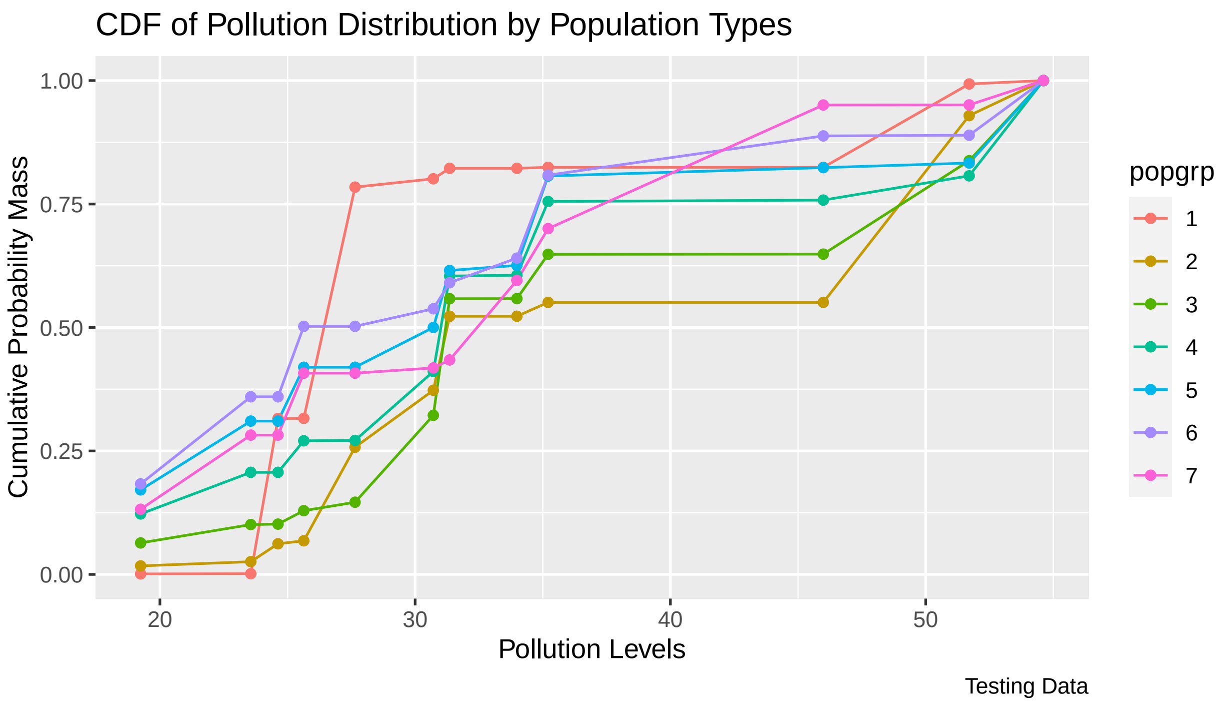
```
# Compute GINI by group
df_pop_pollu_gini <- df_pop_pollution_by_popgrp_cdf %>%
  group_by(popgrp) %>%
  do(popgrp_gini = ffi_dist_gini_random_var_pos_test(
    .$avgdailypm10, .$pmf_pop_condi_popgrp_sortpm10)) %>%
  unnest(c(popgrp_gini)) %>%
  left_join(df_pop_pollution_by_popgrp_cdf %>%
              group_by(popgrp) %>% slice(1L) %>%
              select(popgrp)
              , by="popgrp")
# Display
df_pop_pollu_gini %>% kable() %>% kable_styling_fc()
```

| popgrp | popgrp_gini |
|---|---|
| 1 | 0.1206861 |
| 2 | 0.1075096 |
| 3 | 0.1380319 |
| 4 | 0.1543002 |
| 5 | 0.1680265 |
| 6 | 0.1754309 |
| 7 | 0.1453136 |

## 1.5 Visualize the Distributions

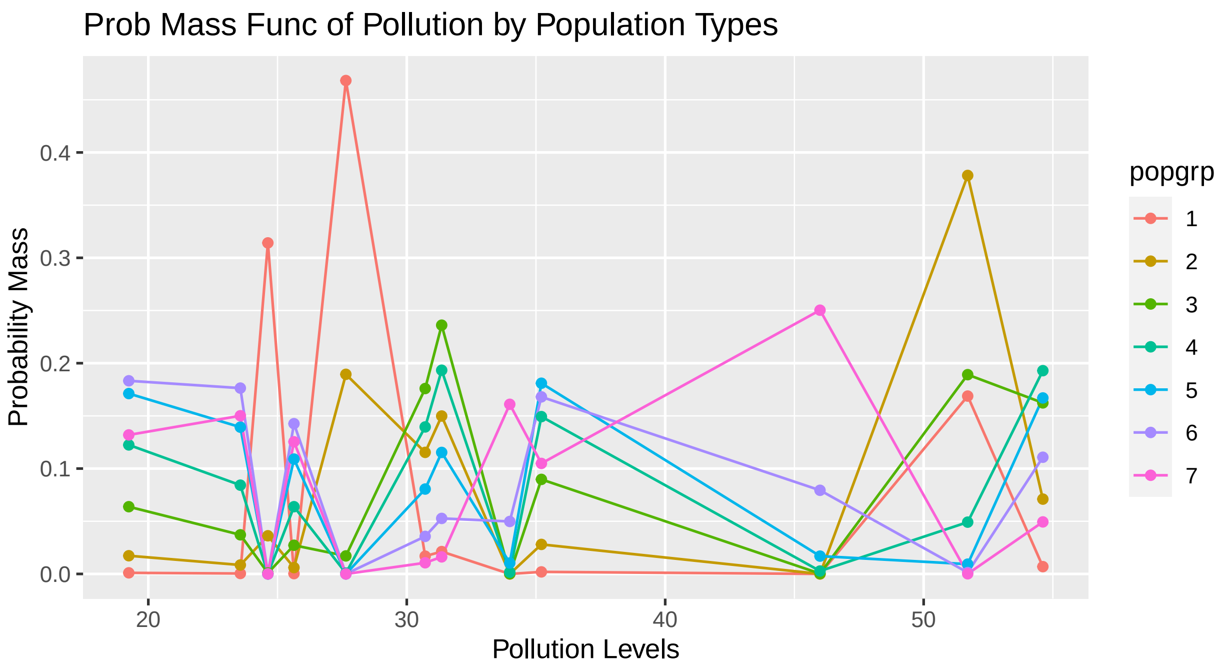
Visualizing distributions. Visualize the CDF:

```
# Visaulize Distributions, CDF for different population groups
lineplot <- df_pop_pollution_by_popgrp_cdf %>%
    select(popgrp, avgdailypm10, cdf_pop_condi_popgrp_sortpm10 ) %>%
    ggplot(aes(x=avgdailypm10, y=cdf_pop_condi_popgrp_sortpm10,
               colour=popgrp)) +
        geom_line() +
        geom_point() +
        labs(title = 'CDF of Pollution Distribution by Population Types',
             x = 'Pollution Levels',
             y = 'Cumulative Probability Mass',
             caption = 'Testing Data')
print(lineplot)
```



Visualize the Probability Mass (real data should look much less chaotic than this):

```
# Visaulize Distributions, CDF for different population groups
lineplot_pmf <- df_pop_pollution_by_popgrp_cdf %>%
    select(popgrp, avgdailypm10, pmf_pop_condi_popgrp_sortpm10 ) %>%
    ggplot(aes(x=avgdailypm10, y=pmf_pop_condi_popgrp_sortpm10,
               colour=popgrp)) +
        geom_line() +
        geom_point() +
        labs(title = 'Prob Mass Func of Pollution by Population Types',
             x = 'Pollution Levels',
             y = 'Probability Mass',
             caption = 'Testing Data')
print(lineplot_pmf)
```



Testing Data

## 1.6 Various Quantiles

Measure quantiles of pollution exposures for different population groups:

1. Consider CDF larger than current quantile of interest.
2. Slice group-specific CDF that is higher and closest to quantile of interest.
3. Merge results for different quantiles together.

```
# Generate pollution quantiles by population groups
df_pop_pollution_distribution <- df_pop_pollution_by_popgrp_cdf %>%
  group_by(popgrp) %>%
  mutate(pm10_mean = weighted.mean(avgdailypm10, pop_frac)) %>%
  mutate(pm10_sd_gap = pop_frac*(avgdailypm10 - pm10_mean)^2,
         pm10_sd = sqrt(weighted.mean(pm10_sd_gap, pop_frac))) %>%
  select(-pm10_sd_gap) %>%
  filter(cdf_pop_condi_popgrp_sortpm10 >= 0.10) %>%
  slice(1) %>%
  mutate(pm10_p10 = avgdailypm10) %>%
  select(popgrp, pm10_mean, pm10_sd, pm10_p10) %>%
  left_join(df_pop_pollu_gini, by='popgrp') %>%
  left_join(df_pop_pollution_by_popgrp_cdf %>%
              filter(cdf_pop_condi_popgrp_sortpm10 >= 0.20) %>%
              slice(1) %>%
              mutate(pm10_p20 = avgdailypm10) %>%
              select(popgrp, pm10_p20),
            by='popgrp') %>%
  left_join(df_pop_pollution_by_popgrp_cdf %>%
              filter(cdf_pop_condi_popgrp_sortpm10 >= 0.50) %>%
              slice(1) %>%
              mutate(pm10_p50 = avgdailypm10) %>%
              select(popgrp, pm10_p50),
            by='popgrp') %>%
  left_join(df_pop_pollution_by_popgrp_cdf %>%
              filter(cdf_pop_condi_popgrp_sortpm10 >= 0.80) %>%
              slice(1) %>%
              mutate(pm10_p80 = avgdailypm10) %>%
              select(popgrp, pm10_p80),
            by='popgrp') %>%
  left_join(df_pop_pollution_by_popgrp_cdf %>%
              filter(cdf_pop_condi_popgrp_sortpm10 >= 0.90) %>%
              slice(1) %>%
              mutate(pm10_p90 = avgdailypm10) %>%
              select(popgrp, pm10_p90),
            by='popgrp') %>%
  select(popgrp, pm10_mean, pm10_sd, popgrp_gini, everything())
# display
df_pop_pollution_distribution %>%
  kable(caption = 'PM10 Exposure Distribution by Population Groups') %>%
  kable_styling_fc()
```

PM10 Exposure Distribution by Population Groups

| popgrp | pm10_mean | pm10_sd | popgrp_gini | pm10_p10 | pm10_p20 | pm10_p50 | pm10_p80 | pm10_p90 |
|---|---:|---:|---:|---:|---:|---:|---:|---:|
| 1 | 31.07894 | 0.8098981 | 0.1206861 | 24.62676 | 24.62676 | 27.64481 | 30.71275 | 51.70466 |
| 2 | 39.47897 | 1.0628619 | 0.1075096 | 27.64481 | 27.64481 | 31.35114 | 51.70466 | 51.70466 |
| 3 | 37.92901 | 1.2140423 | 0.1380319 | 23.56121 | 30.71275 | 31.35114 | 51.70466 | 54.61304 |
| 4 | 34.86470 | 1.7692120 | 0.1543002 | 19.24456 | 23.56121 | 31.35114 | 51.70466 | 54.61304 |
| 5 | 32.56731 | 2.2367922 | 0.1680265 | 19.24456 | 23.56121 | 30.71275 | 35.20967 | 54.61304 |
| 6 | 31.46626 | 2.0286573 | 0.1754309 | 19.24456 | 23.56121 | 25.63653 | 35.20967 | 54.61304 |
| 7 | 33.50541 | 1.7562952 | 0.1453136 | 19.24456 | 23.56121 | 33.98553 | 45.99021 | 45.99021 |