

# VISUALIZING CUMULATIVE CANCER RISK FROM AIR TOXINS

Using R and Leaflet to create an interactive map to explore cancer risk from air toxins in Oregon

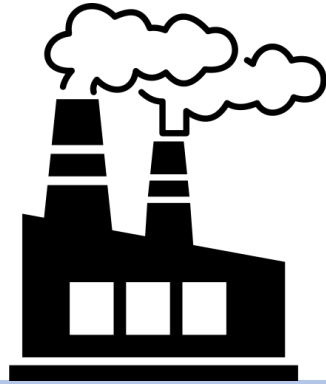
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Presentation to NACAA Air Toxics Committee 5<sup>th</sup> Aug 2021



# BACKGROUND

WHAT IS THE NEED FOR THE VISUALIZATION?



## Division 245 Cleaner Air Oregon Program

Regulates industrial sources of toxic air contaminants



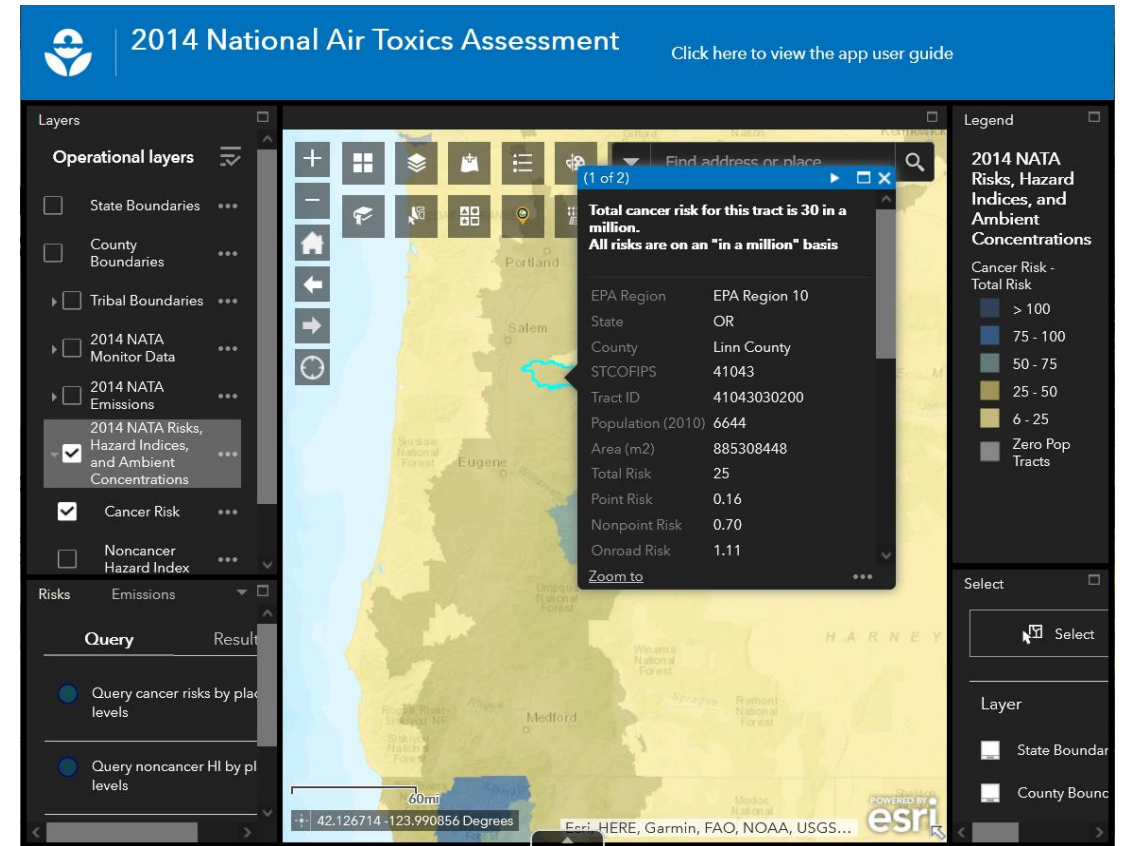
## Division 246 Oregon State Air Toxics Program

Assesses impact of toxic air contaminants from all sources

# CHALLENGE

MAKING NATA 2014 DATA ACCESSIBLE

- Data/analysis challenges
  - OR-specific risk (ambient concentrations, OR TRVs)
- Communication challenges
  - Accessible
  - Local/relevant
  - Interesting

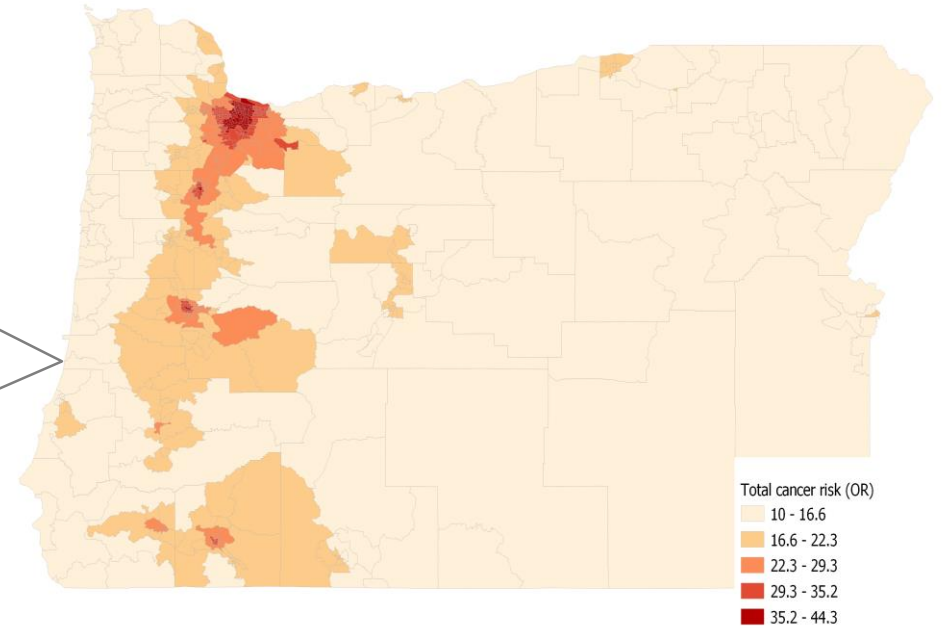


# DATA CHALLENGE

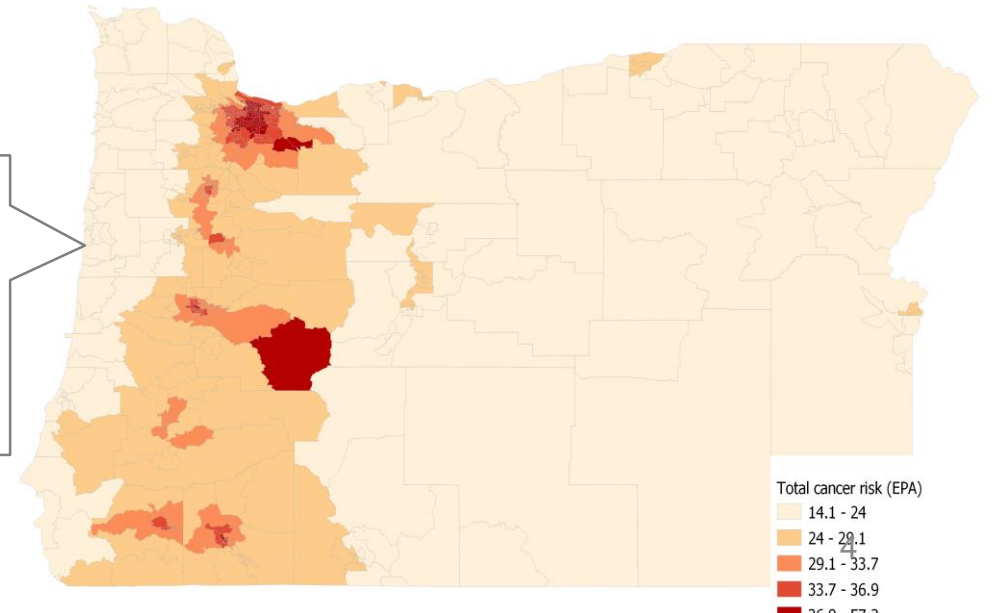
## CALCULATING OR-SPECIFIC RISK

- ❑ Ambient concentrations vs. exposure concentrations
- ❑ OR specific standards
  
- ❑ Fairly straightforward in R:
  - ❑ iterate through list of air toxins
  - ❑ divide the ambient concentration by reference values (TRV) for that air toxin
- ❑ Bind the rows together (for R code, see slide at end of deck)

Cancer risk based on ambient conc. & OR TRVs



Cancer risk based on exp. Conc. & EPA reference values



# COMMUNICATION CHALLENGE

IDENTIFYING RELEVANT DATA & MAKING IT ACCESSIBLE

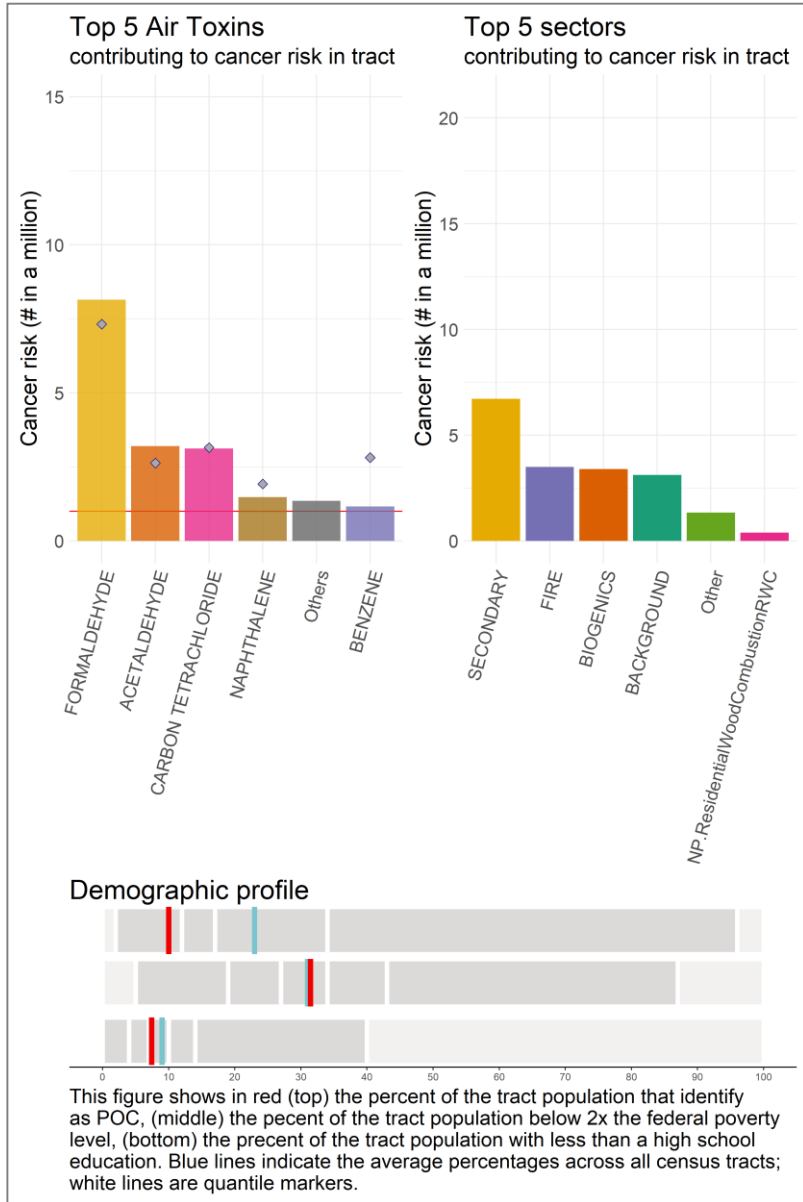
## Making information accessible

- ❑ focus on top five air toxins
- ❑ focus on top five sectors

## Making information local & relevant

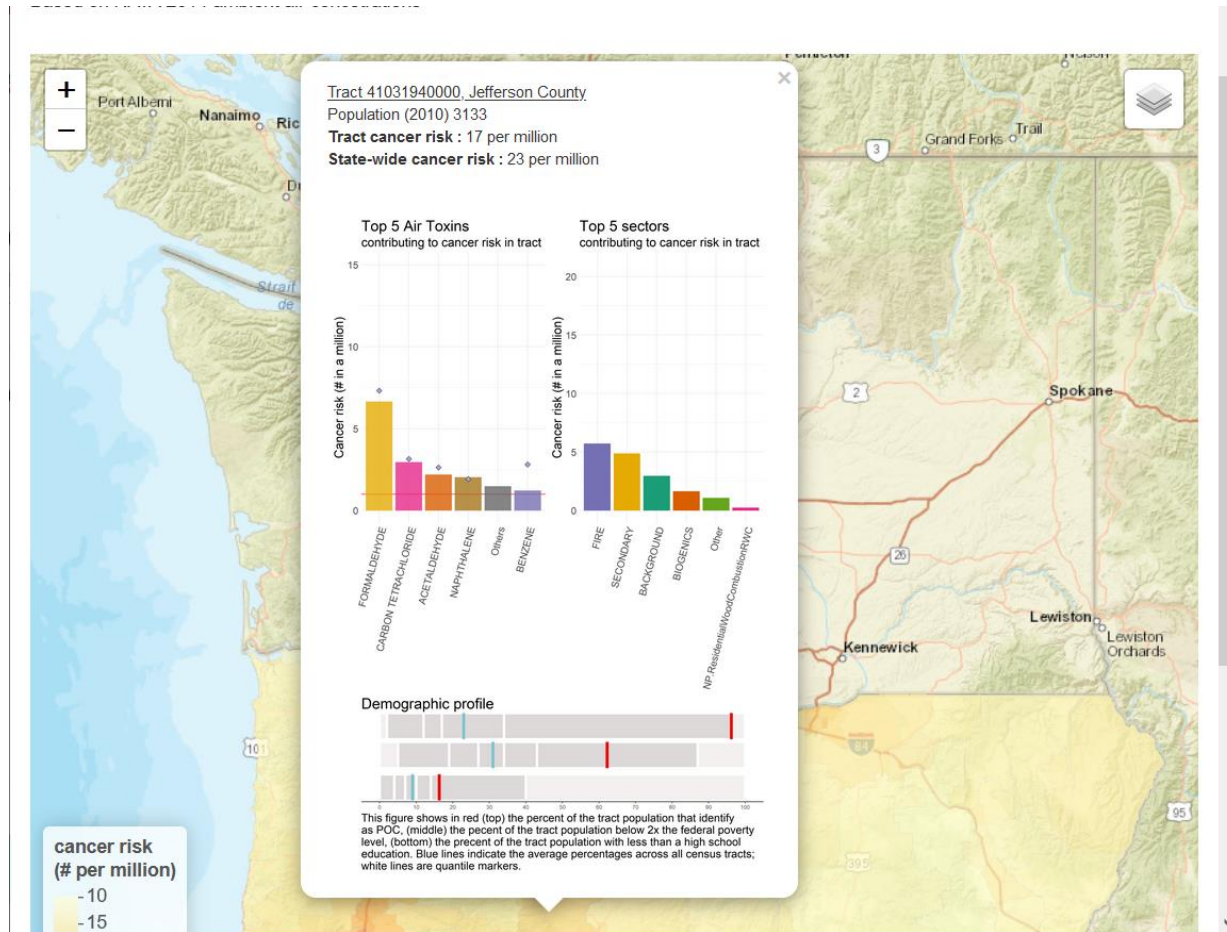
- ❑ create census tract specific information
- ❑ add socio-demographic variables
- ❑ add comparison to state-wide averages

For R code to extract the top 5 air toxins contributing to cancer risk in the tract, see slide at end of deck



# PUTTING IT ALL TOGETHER

## INTERACTIVE MAP WITH TRACT-SPECIFIC DATA VISUALIZATION



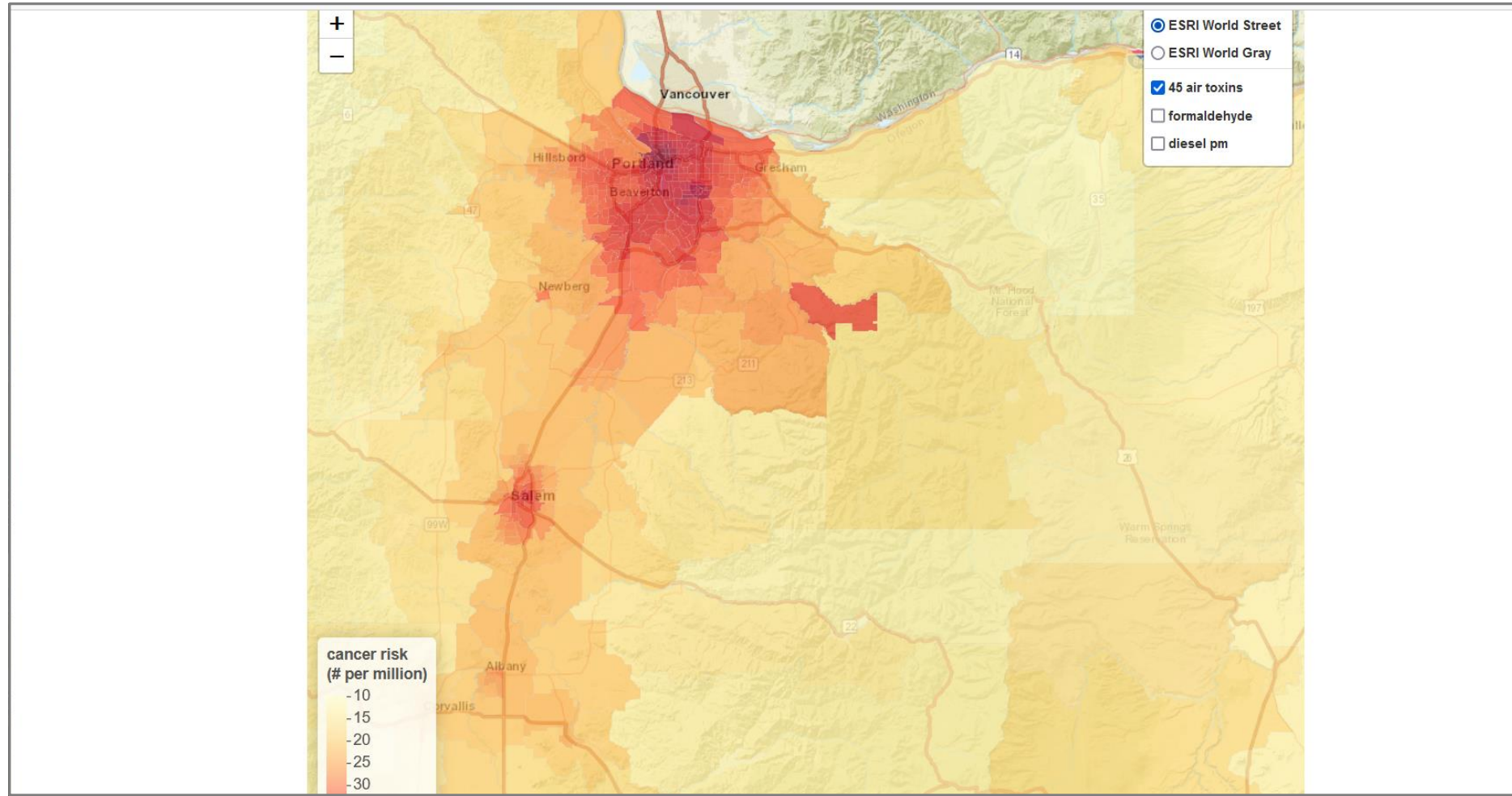
R packages used:

- rgdal
- leaflet
- leafpop
- tidycensus
- patchwork

Map created using RMarkdown, and “published” to DEQ’s Connect Server



# DEMO OF INTERACTIVE MAP

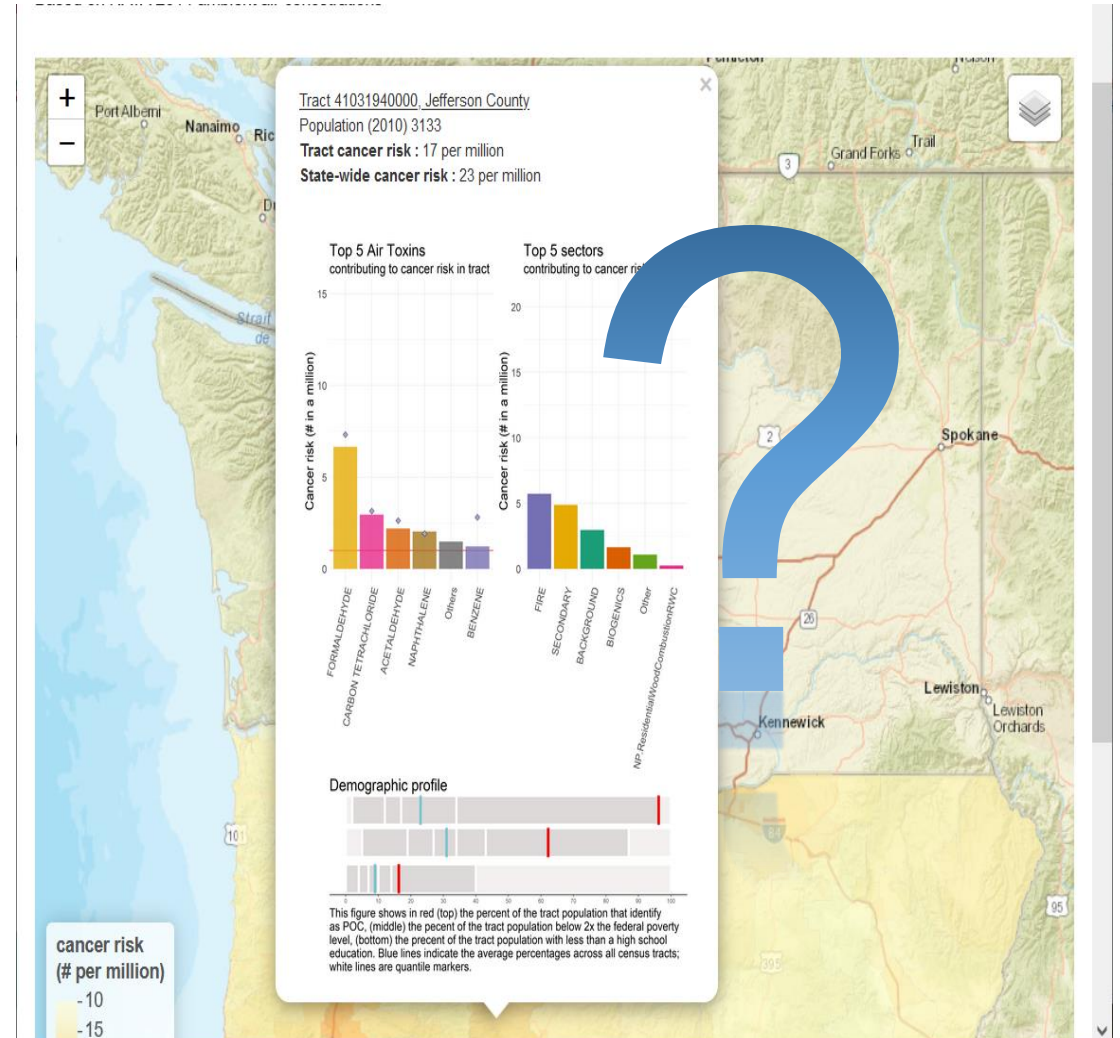


# NEXT STEPS

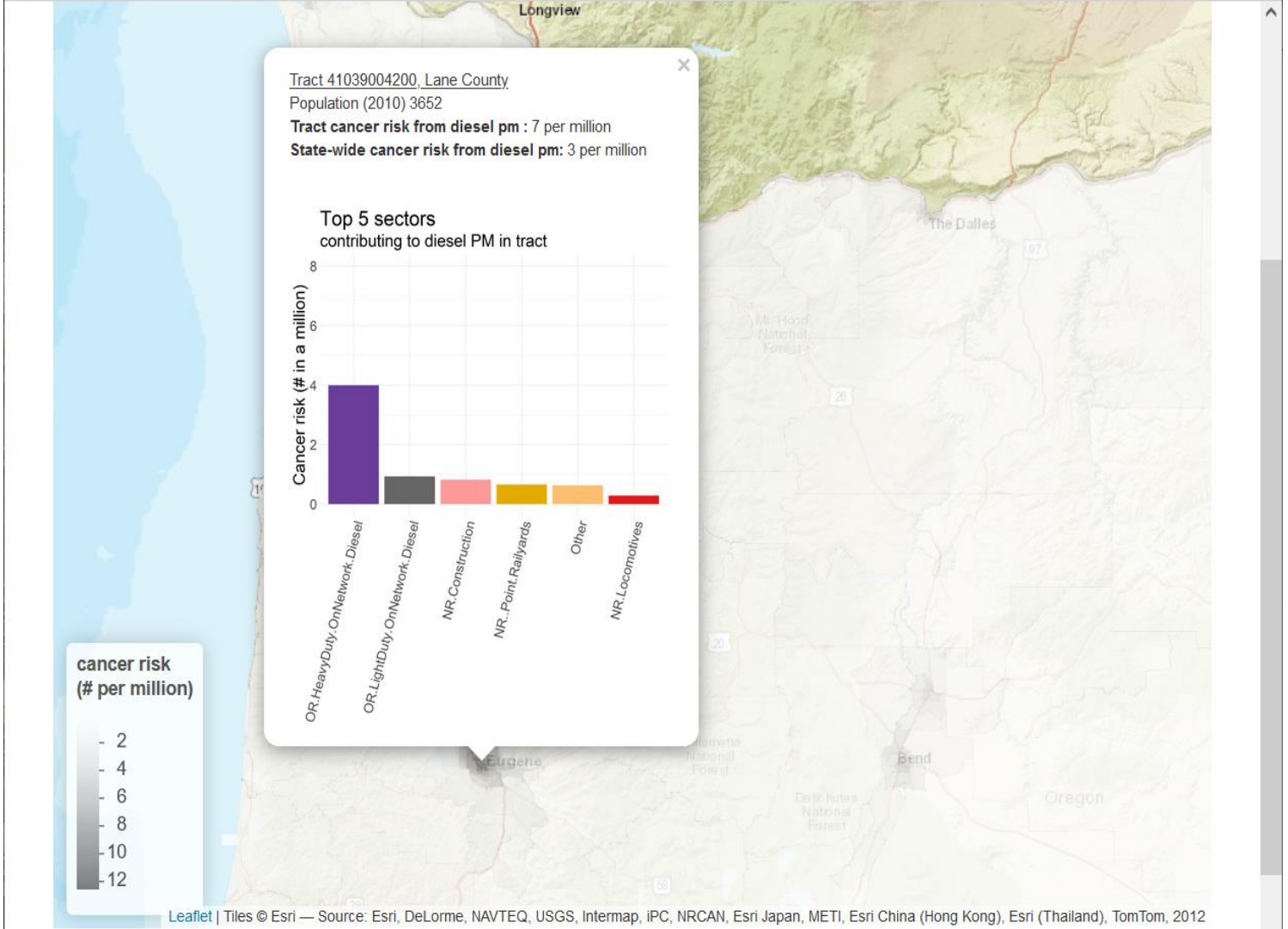
BUT...IS THIS WHAT USERS WANT?

Feedback from community members & advocacy groups

- accessible?
- relevant?
- interesting?
- useful background for providing input on upcoming rule updates?







[https://rstudioconnect.deq.state.or.us/content/bc5c5ebd-002e-47b5-aaa0-9984e66948ae/at\\_risk\\_map.html#close](https://rstudioconnect.deq.state.or.us/content/bc5c5ebd-002e-47b5-aaa0-9984e66948ae/at_risk_map.html#close)

# DISCUSSION

QUESTIONS...

FEEDBACK...

SUGGESTIONS...

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# DATA CHALLENGE

## CALCULATING OR-SPECIFIC RISK

### A “mere” matter of R programming!

```
# calculate cancer risk based on Oregon TRV cancer risk
len <- length(ure_trv$nata.name)                ## ure_trv holds OR TRVs
or_ris <- ris[FALSE, 1:46]                      ## create an empty dataframe with same columns as NATA risk
for ( i in 1:len) {
  if (!is.na(ure_trv$trv_can1_ugm.3[i])) {
    at_exp <- exp %>% filter(Pollutant.Name == ure_trv$nata.name[i]) %>%
      filter(FIPS*10^6 != Tract)                ## filter out state and county summary rows from ambient conc dataframe
    at_ris <- ris[, 1:46] %>% filter(Pollutant.Name == ure_trv$nata.name[i]) %>%
      filter(FIPS*10^6 != Tract)                ## filter out state and county summary rows from risk dataframe
    at_ris[, 8:46] <- 0 ## set risk from sectors to 0 – ready to be filled in by OR-specific values
    at_ris[, 8:46] <- at_exp[, 8:46]/ure_trv$trv_can1_ugm.3[i] ## calculate the risk
    or_ris <- rbind(or_ris, at_ris)              ## bind rows for each air toxin to the or_ris dataframe
    print(paste(as.character(i), ure_trv$nata.name[i])) ## print air toxin just completed
  }
}
## add 'pahpom' to the or_ris table (special case)
pah_ris <- ris[, 1:46] %>% filter(Pollutant.Name == "PAHPOM") %>%
  filter(FIPS*10^6 != Tract)
or_ris <- rbind(or_ris, pah_ris)
```

# ACCESSIBILITY

## IDENTIFYING TOP FIVE TOXINS

```
# extract top five air toxins contributing to cancer risk for each census tract
yat <- at_all %>% group_by(Tract) %>%
  arrange(desc(Total.Cancer.Risk..per.million.)) %>%
  slice(1:5) %>%
  select("Tract", "County", "Population", "Pollutant.Name", "Total.Cancer.Risk..per.million.")
colnames(yat) <- c("Tract", "County", "Population", "Air.Toxin", "Cancer.Risk")

# for each tract, create a "Others" category, summing up cancer risk from remaining air toxins
yato <- at_all %>% group_by(Tract) %>%
  arrange(desc(Total.Cancer.Risk..per.million.)) %>%
  slice(6:n()) %>%
  summarize(County = first(County),
            Population = first(Population),
            Air.Toxin = "Others",
            Cancer.Risk = sum(Total.Cancer.Risk..per.million., na.rm = TRUE))

# combine the two data frames
yat <- bind_rows(yat, yato)
yat <- merge(yat, st_avg, by.x = "Air.Toxin", by.y = "Pollutant.Name", all.x = TRUE)
```