

# Supplementary Figures: Mapping Male Lung Cancer Risk in Washington State

Walker Azam  
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## IID Estimates:

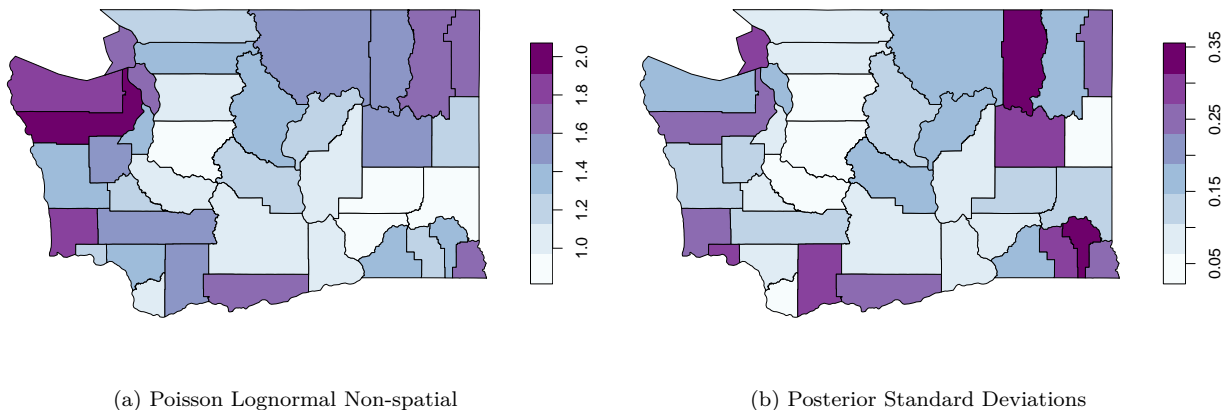


Figure 1: Poisson Lognormal Non-Spatial Mapping

## Supplementary Code Appendix

```
library(knitr)
# Setting up RMarkdown
opts_chunk$set(collapse = TRUE, tidy = TRUE, fig.align = "center", tidy.opts = list(blank = TRUE,
strip.white = TRUE), warning = FALSE, message = FALSE, cache = FALSE, echo = FALSE)
# Loading Libraries
library(RColorBrewer) # creates nice color schemes
library(classInt) # finds class intervals for continuous variables
library(ggplot2)
library(rgdal)
library(SUMMER)
library(maps)
library(maptools)
library(dplyr)
library(sf)
```

```

library(INLA)
library(prioritizr)
library(truncnorm)
# Reading in WA state County Shapefiles Data from:
# https://geo.wa.gov/datasets/wadnr::wa-county-boundaries/explore?location=47.182649%2C-120.817600%2C7.
washington <- rgdal::readOGR(dsn = "WA_County_Boundaries", layer = "WA_County_Boundaries")
# Converting WA census tract to a polygon DF
wmap <- SpatialPolygons(washington@polygons) # getting Geometries
washington$geometry <- st_as_sf(wmap) # adding geometry column
wmap <- st_as_sf(washington)
# selecting important columns
wmap <- wmap[, c("JURISDIC_2", "geometry")]
colnames(wmap) <- c("County", "geometry")
# Reading cancer data (pre-cleaned)
cancer <- read.csv("Lung_Cancer_Deaths_2015-2019.csv", header = TRUE)
# Selecting Columns
cancer <- cancer[, c("County", "Count", "Population", "Age.Adjusted.Rate.per.100.000")]

# Dropping the 3 counties with missing data:
cancer$Age.Adjusted.Rate.per.100.000[is.na(cancer$Age.Adjusted.Rate.per.100.000)] <- 36.4
cancer$Count[is.na(cancer$Count)] <- 0
# cancer <- na.omit(cancer)

# Merging with spatial object
merge <- merge(cancer, wmap, by.x = "County", by.y = "County")
wa <- st_as_sf(merge)

# Expected Morbidity:
wa$Expected <- wa$Population/100000 * wa$Age.Adjusted.Rate.per.100.000
# Adding SMR column
wa$SMR <- wa$Count/wa$Expected
wa$se <- sqrt(wa$SMR/wa$Expected)
# Fit Poisson-Lognormal model in INLA:
model.fit0 <- inla(Count ~ 1 + f(County, model = "iid"), data = wa, family = "cenpoisson",
  E = Expected, control.family = list(cenpoisson.I = c(0, 5)), control.predictor = list(compute = TRUE),
  control.compute = list(return.marginals = TRUE))
options(scipen = 999) # no sci.notation
# Extracting the posterior medians using our fitted model
wa$fit0fitted <- model.fit0$summary.fitted.values$`0.5quant`
wa$fit0se <- model.fit0$summary.fitted.values$sd

# Mapping our results
pal = function(n) brewer.pal(n, "BuPu")
plot(wa["fit0fitted"], pal = pal, nbreaks = 8, breaks = "equal", main = NULL)
plot(wa["fit0se"], pal = pal, nbreaks = 8, breaks = "equal", main = NULL)

```