# hpam7660 Cancer Alley Analytic Data File

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#### 2024-02-22

```
library(readr)
la_mort <-</pre>
  read_csv("https://www.dropbox.com/scl/fi/fzsnhfd3lq80v2o3sag6c/la_mort.csv?rlkey=h1vyjm2b8ppgejgsg3e8
## Rows: 642696 Columns: 29
## -- Column specification -----
## Delimiter: ","
## chr (7): stocr, strsd, stbrth, brthr, sex, marstat, ucod
## dbl (22): restatus, cntyocr, popcntyocr, cntyrsd, popcntyresd, educ1989, edu...
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
la_mort$cancer_parish <- ifelse(la_mort$cntyrsd %in% c(5, 33, 47, 51, 71, 89, 93, 95, 121), 1, 0)
la_mort$cancer39 <- ifelse(la_mort$ucr39 %in% c(5:15), 1, 0)</pre>
table(la_mort$cancer_parish)
##
##
## 445138 197558
table(la_mort$cntyrsd[la_mort$cancer_parish == 1])
##
                  47
                        51
                              71
                                           93
       5
            33
                                    89
                                                 95
                                                      121
## 10217 55300 4761 61822 47752 5963 2946 5844 2953
library(dplyr)
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
```

```
## The following objects are masked from 'package:base':
##
##
       intersect, setdiff, setequal, union
la_mort_age <- la_mort %>%
  filter(age != 9999)
la mort age$age <- ifelse(la mort age$age < 2000, la mort age$age - 1000, 0)
age_breaks <- c(0, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, Inf)
age_labels <- c("0_4", "5_9", "10_14", "15_19", "20_24", "25_29", "30_34", "35_39",
                "40 44", "45_49", "50_54", "55_59", "60_64", "65_69", "70_74",
                "75_79", "80_84", "85+")
la_mort_age$agegrp <- as.character(cut(la_mort_age$age, breaks = age_breaks, labels = age_labels, right</pre>
parish_count <- la_mort %>%
  group_by(cntyrsd, cancer_parish, year) %>%
  summarize(cancer39 = sum(cancer39, na.rm = TRUE))
## 'summarise()' has grouped output by 'cntyrsd', 'cancer_parish'. You can
## override using the '.groups' argument.
parish_count_age <- la_mort_age %>%
  group_by(cntyrsd, cancer_parish, agegrp, year) %>%
  summarize(cancer39 = sum(cancer39, na.rm = TRUE))
## 'summarise()' has grouped output by 'cntyrsd', 'cancer_parish', 'agegrp'. You
## can override using the '.groups' argument.
la_pop <-
read_csv("https://www.dropbox.com/scl/fi/650k1obpczky6bwa19ex6/la_county_pop.csv?rlkey=0aokd9m76q7mxw
## Rows: 24320 Columns: 23
## -- Column specification ---
## Delimiter: ","
## chr (3): stname, ctyname, agegrp
## dbl (20): state, county, year, tot_pop, tot_male, tot_female, wa_male, wa_fe...
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
# Check column names in both datasets
colnames(parish_count)
## [1] "cntyrsd"
                       "cancer_parish" "year"
                                                       "cancer39"
colnames(la_pop)
## [1] "state"
                                  "stname"
                                                            "year"
                     "county"
                                               "ctyname"
                                  "tot_male"
## [6] "agegrp"
                     "tot_pop"
                                               "tot female" "wa male"
## [11] "wa_female" "ba_male"
                                  "ba_female" "ia_male"
                                                            "ia_female"
## [16] "aa male"
                     "aa_female" "na_male"
                                               "na_female" "tom_male"
## [21] "tom_female" "h_male"
                                  "h female"
```

```
library(dplyr)
# Correct join operation without renaming columns
la_joined <- parish_count %>%
  inner_join(la_pop, by = c("cancer_parish" = "county", "year"))
## Warning in inner_join(., la_pop, by = c(cancer_parish = "county", "year")): Detected an unexpected m
## i Row 31 of 'x' matches multiple rows in 'y'.
## i Row 77 of 'y' matches multiple rows in 'x'.
## i If a many-to-many relationship is expected, set 'relationship =
   "many-to-many" to silence this warning.
la_joined <- parish_count_age %>%
 inner_join(la_pop, by = c("cntyrsd" = "county", "year", "agegrp"))
stnrd_pop <-
  read_csv("https://www.dropbox.com/scl/fi/xzd2o5lza237so6vamqwb/stnrd_pop.csv?rlkey=zp90au2tuq6eptvi1y
## Rows: 18 Columns: 2
## -- Column specification -----
## Delimiter: ","
## chr (1): agegrp
## dbl (1): stnrd_pop
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
la joined stnrd <- la joined %>%
  inner_join(stnrd_pop, by = "agegrp")
la_joined_stnrd$stnrd_pop_weight <- (la_joined_stnrd$stnrd_pop) / (sum(stnrd_pop$stnrd_pop))</pre>
la_joined_stnrd$cancer_rate_adj <- ((la_joined_stnrd$cancer39) / (la_joined_stnrd$tot_pop / 100000)) *</pre>
parish_rates <- la_joined_stnrd %>%
  group_by(cntyrsd, cancer_parish, year) %>%
  summarize(cancer_rate_adj = sum(cancer_rate_adj, na.rm = TRUE), cancer39 = sum(cancer39), tot_pop =
              sum(tot_pop))
## 'summarise()' has grouped output by 'cntyrsd', 'cancer_parish'. You can
## override using the '.groups' argument.
parish_rates$cancer_rate_crude <- (parish_rates$cancer39) / (parish_rates$tot_pop / 100000)
la_joined_all <- parish_count %>%
inner_join(la_pop, by = c("cancer_parish" = "county", "year"))
## Warning in inner_join(., la_pop, by = c(cancer_parish = "county", "year")): Detected an unexpected m
## i Row 31 of 'x' matches multiple rows in 'y'.
## i Row 77 of 'y' matches multiple rows in 'x'.
## i If a many-to-many relationship is expected, set 'relationship =
   "many-to-many" 'to silence this warning.
```

```
# Assuming la_joined_all exists and contains the correct data
parish_cancer_2019 <- subset(la_joined_all, year == 2019)</pre>
```

## library(knitr)

# Adjust the column names to those that exist in your dataframe
kable(parish\_cancer\_2019[, c("cancer\_parish", "cancer39")])

cancer_	_parish	cancer39
	1	162
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cancer_	_parish	cancer39
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cancer_	_parish	cancer39
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$\operatorname{cancer}_{\_}$	_parish	cancer39
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```
library(knitr)

# Adjusting the code to use existing columns
kable(parish_cancer_2019[, c("cancer_parish", "cancer39")])
```

cancer_parish	cancer39
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cancer_	_parish	cancer39
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```
parish_cancer_2019 <- subset(parish_rates, year == 2019)
kable(parish_cancer_2019[, c("cntyrsd", "cancer_rate_crude", "cancer_rate_adj")])</pre>
```

cntyrsd	cancer_	_rate_	_crude	cancer_	_rate_	_adj
1		22	5.0551		182.5	5548
3			4.8501		181.6	
5			7.7623		131.1	
7			7.7050		186.3	
9			9.1405		188.7	
11			6.6296		195.5	
13		29	7.9484		168.9	
15		17	8.9962		156.0	769
17		23	2.0832		175.2	2182
19		20	9.7648		179.7	7991
21		36	5.1767		183.9	9878
23		36	0.5375		106.0	)562
25		29	3.9555		119.8	3748
27		24	7.8402		145.5	5867
29		33	2.9065		205.5	5863
31		31	6.2555		171.0	0102
33		16	7.8479		149.8	3723
35		54	1.2157		327.0	)177
37		34	3.6641		202.1	1083
39		25	0.9007		188.6	3733
41		31	8.8496		182.7	7571
43		24	4.4855		164.9	9050
45		23	9.6932		189.9	9145
47		24	2.3203		157.6	6160
49		41	1.5865		227.1	
51		21	0.7829		159.7	7797
53		28	2.8387		193.3	3757
55			7.0765		154.7	
57		23	5.3096		173.2	
59			1.3268		170.4	
61			3.6131		157.6	
63			7.5293		145.9	
65			1.3761		226.4	
67			0.4252		192.7	
69			7.3315		187.3	
71			6.8743		157.3	
73			4.9008		188.9	
75			5.4104		144.(	
77			2.6880		168.8	
79			1.8490		160.3	
81			3.4590		204.9	
83			2.5399		155.2	
85			1.3429		192.7	
87			7.5550		122.1	
89			9.9838		176.4	
91			8.3294		162.7	
93			7.8892		138.3	
95 07			1.0904		161.9	
97			9.9795		209.0 157.1	
99 101			0.8799		191.4	
101 103			1.5519 $6.2739$		161.6	
109		∠0	0.4139		101.(	1010

cntyrsd	$cancer\_rate\_crude$	cancer_rate_adj
105	204.6794	183.3851
107	575.6857	190.4850
109	246.3126	193.8026
111	377.7371	187.6486
113	244.1977	153.0439
115	228.4710	225.5663
117	275.1419	207.0287
119	250.5023	171.7850
121	178.1911	138.3193
123	270.4108	159.7352
125	232.8080	128.8255
127	476.4318	234.1971

```
parish_rates$pop_weight <- (parish_rates$cancer_rate_adj) * (parish_rates$tot_pop)
cancer_alley_rates <- parish_rates %>%
  group_by(cancer_parish, year) %>%
  summarize(cancer_rate_adj_wt = sum(pop_weight) / sum(tot_pop))
```

## 'summarise()' has grouped output by 'cancer\_parish'. You can override using the
## '.groups' argument.

## kable(cancer\_alley\_rates)

year	$cancer\_rate\_adj\_wt$
2005	215.9012
2006	211.1969
2007	199.2163
2008	210.5785
2009	202.7788
2010	198.5223
2011	194.5824
2012	194.9155
2013	191.4183
2014	188.3508
2015	186.8605
2016	178.2077
2017	181.0797
2018	176.0163
2019	174.1137
2005	197.2898
2006	198.7948
2007	199.3910
2008	196.7380
2009	190.6874
2010	191.1738
2011	189.7244
2012	180.9129
2013	181.2483
2014	181.1850
	2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2006 2007 2008 2009 2010 2011 2012 2013

cancer_parish	year	cancer_rate_adj_wt
1	2015	166.3009
1	2016	157.8499
1	2017	161.2732
1	2018	153.9050
1	2019	153.9429

```
cancer_alley <-
    subset(cancer_alley_rates, cancer_parish == 1, select = c(cancer_rate_adj_wt, year)) %>%
    rename(cancer_alley_rate = cancer_rate_adj_wt)

no_cancer_alley <-
    subset(cancer_alley_rates, cancer_parish == 0, select = c(cancer_rate_adj_wt, year)) %>%
    rename(no_cancer_alley_rate = cancer_rate_adj_wt)

cancer_alley_table <- cancer_alley %>%
    inner_join(no_cancer_alley, by = "year")

cancer_alley_table <- cancer_alley_table[,c("year", "cancer_alley_rate", "no_cancer_alley_rate")]

kable(cancer_alley_table)</pre>
```

year	cancer_alley_rate	no_cancer_alley_rate
2005	197.2898	215.9012
2006	198.7948	211.1969
2007	199.3910	199.2163
2008	196.7380	210.5785
2009	190.6874	202.7788
2010	191.1738	198.5223
2011	189.7244	194.5824
2012	180.9129	194.9155
2013	181.2483	191.4183
2014	181.1850	188.3508
2015	166.3009	186.8605
2016	157.8499	178.2077
2017	161.2732	181.0797
2018	153.9050	176.0163
2019	153.9429	174.1137