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Advanced Features

Source: vignettes/4_advanced.Rmd

Note: This article is a work in progress

EXAMPLES OF FILES & TEST DATA EJAM CAN IMPORT OR OUTPUT

Sample spreadsheets & shapefiles for trying the web app

Examples of .xlsx files and shapefiles are installed locally with EJAM, as input files you can use to try out EJAM functions or the web app, or to see what an input file should look like.

Local folders with sample files

The best, simplest way to see all these files is the function called testdata()

```
testdata()
```

For more details, you might find the following useful, but testdata() will probably provide what you are looking for.

Another way to see a list of local folders (where EJAM is installed locally) with files that can be uploaded to the EJAM web app or provided as inputs to EJAM functions (as examples or for testing):

```
x <- list.dirs(system.file("testdata/", package = "EJAM"), r

cbind(`Local folders with installed file examples` = x, Subf
```

To see a list of the files available locally as installed sample/test data:

```
for (example_type in x) {
    cat("\n", basename(example_type), "\n\n")
    these = matrix(list.files(example_type))
    colnames(these) <- paste0("Examples Installed in /testda
```

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```
#>  address
#>
#>      Examples Installed in /testdata/address/
#> [1,] "street_address_9.xlsx"
#> [2,] "test_address_table.xlsx"
#> [3,] "test_address_table_9.xlsx"
#> [4,] "test_address_table_goodnames.xlsx"
#> [5,] "test_address_table_withfull.xlsx"
#>
#>  ejscreenapi
#>
#>      Examples Installed in /testdata/ejscreenapi/
#> [1,] "datafile_apiv2.3_output_example.pjson"
#> [2,] "datafile_apiv2.3_output_example_json.R"
#>
#>  examples_of_output
#>
#>       Examples Installed in /testdata/examples_of_output/
#>  [1,] "community_report_100.html"
#>  [2,] "testoutput_doaggregate_1000pts_1miles.xlsx"
#>  [3,] "testoutput_doaggregate_1000pts_1miles_ejam2excel.x
#>  [4,] "testoutput_doaggregate_100pts_1miles.xlsx"
#>  [5,] "testoutput_doaggregate_100pts_1miles_ejam2excel.xl
#>  [6,] "testoutput_doaggregate_10pts_1miles.xlsx"
#>  [7,] "testoutput_doaggregate_10pts_1miles_ejam2excel.xls
#>  [8,] "testoutput_ejamit_1000pts_1miles.xlsx"
#>  [9,] "testoutput_ejamit_100pts_1miles.xlsx"
#> [10,] "testoutput_ejamit_10pts_1miles.xlsx"
#>
#>  fips
#>
#>       Examples Installed in /testdata/fips/
#>  [1,] "cities_2.xlsx"
#>  [2,] "counties_in_AL_detailed.xlsx"
#>  [3,] "counties_in_Alabama.xlsx"
#>  [4,] "counties_in_Delaware.xlsx"
#>  [5,] "counties_in_Delaware_invalid.xlsx"
#>  [6,] "county_10.xlsx"
#>  [7,] "county_100.xlsx"
#>  [8,] "county_1000.xlsx"
#>  [9,] "county_state_300.xlsx"
#> [10,] "state_10.xlsx"
#> [11,] "state_50.xlsx"
```

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```
#> [15,] "tract_1000.csv"
#> [16,] "tract_state_285.xlsx"
#>
#>  latlon
#>
#>       Examples Installed in /testdata/latlon/
#>  [1,] "3points.xlsx"
#>  [2,] "testpoints_02.xlsx"
#>  [3,] "testpoints_10.xlsx"
#>  [4,] "testpoints_100.xlsx"
#>  [5,] "testpoints_100_sites_with_signif_violations_NAICS_
#>  [6,] "testpoints_1000.xlsx"
#>  [7,] "testpoints_1000_Latitude_LONG.xlsx"
#>  [8,] "testpoints_10000.xlsx"
#>  [9,] "testpoints_100000.xlsx"
#> [10,] "testpoints_2.xlsx"
#> [11,] "testpoints_207_sites_with_signif_violations_NAICS_
#> [12,] "testpoints_5.xlsx"
#> [13,] "testpoints_50.xlsx"
#> [14,] "testpoints_500.xlsx"
#> [15,] "testpoints_bad.xlsx"
#> [16,] "testpoints_invalid_latlon.xlsx"
#> [17,] "testpoints_invalid_latlon_more_cases.xlsx"
#> [18,] "testpoints_overlap3.xlsx"
#> [19,] "testpoints_PR_GU_AS_VI_MP.xlsx"
#>
#>  program_type
#>
#>      Examples Installed in /testdata/program_type/
#> [1,] "program_name_only_3.xlsx"
#>
#>  programid
#>
#>      Examples Installed in /testdata/programid/
#> [1,] "program_test_data_10.csv"
#> [2,] "program_test_data_10.xlsx"
#> [3,] "program_test_data_100.csv"
#> [4,] "program_test_data_1000.csv"
#> [5,] "program_test_data_10000.csv"
#> [6,] "test_pgm_sys_id_1000.xlsx"
#>
#>  registryid
#>
```

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```
#>  [3,] "FRS_example_data.xlsx"
#>  [4,] "frs_test_regid_8.xlsx"
#>  [5,] "frs_testpoints_10.csv"
#>  [6,] "frs_testpoints_10.xlsx"
#>  [7,] "frs_testpoints_100.csv"
#>  [8,] "frs_testpoints_100.xlsx"
#>  [9,] "frs_testpoints_1000.csv"
#> [10,] "frs_testpoints_1000.xlsx"
#> [11,] "frs_testpoints_10000.csv"
#> [12,] "frs_testpoints_10000.xlsx"
#> [13,] "frs_testpoints_100000.csv"
#> [14,] "frs_testpoints_100000.xlsx"
#> [15,] "frs_testpoints_3_duplicated_id.xlsx"
#> [16,] "testids_registry_id_8.xlsx"
#>
#>  shapes
#>
#>       Examples Installed in /testdata/shapes/
#>  [1,] "portland.gdb"
#>  [2,] "portland.gdb.zip"
#>  [3,] "portland.json"
#>  [4,] "portland_folder_shp"
#>  [5,] "portland_folder_shp.zip"
#>  [6,] "portland_shp.zip"
#>  [7,] "stations.zip"
#>  [8,] "stations_shp.zip"
#>  [9,] "testshapes_2.zip"
```

You can try uploading these kinds of files in the web app, for example, by finding them in these local folders where you installed the package:

- / `EJAM/testdata/latlon/testpoints_100.xlsx`
- / `EJAM/testdata/shapes/portland_shp.zip`
- etc.

To open the locally installed “testdata” folders (in Windows File Explorer, or MacOS Finder)

```
browseURL(system.file("testdata", package = "EJAM"))
```

Example of using a file in EJAM

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```
  full.names = T
  )
testpoint_files

latlon_from_anything(testpoint_files[2])
```

Sample R data objects: Examples of inputs & outputs of EJAM functions

The package has a number of data objects, installed as part of EJAM and related packages, that are examples of inputs or intermediate data objects that you can use to try out EJAM functions, or you may just want to see what the outputs and inputs look like, or you could use them for testing purposes.

For documentation on each input or output item (R object), see https://usepa.github.io/EJAM/reference/index.html#test-data

This code snippet provides a useful list of test/ sample data objects in EJAM and related packages:

POINT DATA (LAT/LON COORDINATES) for testing ejamit(), mapfast(), ejscreenit(), getblocksnearby(), etc.

```
x <- EJAM:::datapack(simple = FALSE)
x <- x[order(x$Package, x$Item), !grepl("size", names(x))]
```

```
x[grepl("^testp", x$Item), ]
#>     Package                Item
#> 102    EJAM       testpoints_10
#> 124    EJAM      testpoints_100
#> 122    EJAM   testpoints_100_dt
#> 127    EJAM     testpoints_1000
#> 156    EJAM    testpoints_10000
#> 110    EJAM        testpoints_5
#> 120    EJAM       testpoints_50
#> 137    EJAM      testpoints_500
#> 111    EJAM      testpoints_bad
#> 103    EJAM testpoints_overlap3
#>                                                          Ti
#> 102 test points data.frame with columns sitenumber, lat,
#> 124 test points data.frame with columns sitenumber, lat,
```

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```
#> 110 test points data.frame with columns sitenumber, lat,
#> 120 test points data.frame with columns sitenumber, lat,
#> 137 test points data.frame with columns sitenumber, lat,
#> 111       test points data.frame with columns note, lat,
#> 103       test points data.frame with columns note, lat,
```

STREET ADDRESSES for testing geocoding in latlon_from_address() etc.

```
x[grepl("^test_", x$Item), ]
#>     Package                          Item
#> 100    EJAM          test_address_parts1
#> 107    EJAM           test_address_table
#> 121    EJAM         test_address_table_9
#> 108    EJAM test_address_table_goodnames
#> 109    EJAM  test_address_table_withfull
#> 101    EJAM             test_addresses_9
#> 45     EJAM              test_addresses2
#> 3      EJAM                   test_regid
#> 4      EJAM                   test_xtrac
#>
#> 100                     datasets for trying address-rela
#> 107                     datasets for trying address-rela
#> 121                     datasets for trying address-rela
#> 108                     datasets for trying address-rela
#> 109                     datasets for trying address-rela
#> 101                     datasets for trying address-rela
#> 45                      datasets for trying address-rela
#> 3   test_regid (DATA) test data, vector of EPA FRS Regist
#> 4                                                      for
cat("\n\n")
```

FACILITY REGISTRY IDs for testing latlon_from_regid() etc.

```
x[grepl("^test[^op_]", x$Item), ]
#>     Package                   Item
#> 9      EJAM testids_program_sys_id
#> 5      EJAM    testids_registry_id
#> 126    EJAM           testshapes_2
#>
#> 9   test data, string vector of EPA FRS Program System ID
#> 5                test data, vector of EPA FRS Registry ID
```

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EXAMPLES OF OUTPUTS from ejamit(), ejscreenit(), getblocksnearby(), etc., you can use as inputs to ejam2report(), ejam2excel(), ejam2ratios(), ejam2barplot(), doaggregate(), etc.

```
x[grepl("^testout", x$Item), ]
#>     Package                                      Item
#> 165    EJAM     testoutput_doaggregate_1000pts_1miles
#> 157    EJAM      testoutput_doaggregate_100pts_1miles
#> 148    EJAM       testoutput_doaggregate_10pts_1miles
#> 166    EJAM          testoutput_ejamit_1000pts_1miles
#> 158    EJAM           testoutput_ejamit_100pts_1miles
#> 151    EJAM            testoutput_ejamit_10pts_1miles
#> 134    EJAM        testoutput_ejscreenapi_1pts_1miles
#> 140    EJAM             testoutput_ejscreenapi_plus_5
#> 146    EJAM        testoutput_ejscreenit_10pts_1miles
#> 144    EJAM                    testoutput_ejscreenit_5
#> 152    EJAM                   testoutput_ejscreenit_50
#> 162    EJAM                  testoutput_ejscreenit_500
#> 129    EJAM testoutput_ejscreenRESTbroker_1pts_1miles
#> 161    EJAM testoutput_getblocksnearby_1000pts_1miles
#> 149    EJAM  testoutput_getblocksnearby_100pts_1miles
#> 139    EJAM   testoutput_getblocksnearby_10pts_1miles
#>
#> 165
#> 157
#> 148
#> 166
#> 158
#> 151
#> 134                                                 test
#> 140 test data examples of output from 'ejscreenapi_plus()
#> 146                                    test output of ejsc
#> 144       test data examples of output from 'ejscreenit()
#> 152      test data examples of output from 'ejscreenit()'
#> 162     test data examples of output from 'ejscreenit()'
#> 129                                                 test
#> 161                   test output of getblocksnearby(),
#> 149                   test output of getblocksnearby(),
#> 139                   test output of getblocksnearby(),
cat("\n\n")
```

LARGE DATASETS USED BY THE PACKAGE

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blocks, the facility datasets with info about EPA-regulated sites, and the blockgroup-related datasets with EJScreen indicators.

Some datasets get downloaded by the package at installation or launch or as needed. Datasets may include for example: [blockwts], [blockpoints], [quaddata], [blockid2fips], [frs], [frs_by_programid], [frs_by_naics], [frs_by_sic], and [frs_by_mact].

Blockgroup-related datasets incude [blockgroupstats], [bgpts], [bgej], [usastats], [statestats], [bgid2fips], and [bg_cenpop2020]. For more info see https://usepa.github.io/EJAM/reference/index.html#datasets-with-indicators-etc-

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USING NAICS AND SIC CODES TO LOCATE FACILITIES BY INDUSTRY

EJAM helps select regulated sites based on industrial classification, using NAICS or SIC code. Finding the right NAICS and finding all the right sites by NAICS is complicated. Doing so requires understanding the NAICS system and the FRS dataset, and the functions in EJAM that help find or use NAICS codes.

NAICS/SIC categories can be explored in a few ways: - NAICS.com website with extensive information about NAICS and SIC - Key EJAM functions for using NAICS/SIC - EPA FRS Facility Industrial Classification Search tool where you can find facilities based on NAICS or SIC. - EPA APIs exist that can be used for similar queries.

Some key EJAM functions include [regid_from_naics()], [latlon_from_naics()], [frs_from_naics()], [naics_findwebscrape()], and [naics_categories()]. These functions can help find EPA FRS sites based on naics codes or titles. They rely on [frs_by_naics] (a data.table), and [naics_from_any()] for querying by code or title of category.

Important points:

- Note that a very large fraction of all FRS sites (as obtained for use in EJAM) lack NAICS code!

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- Note that NAICS.com reports many more businesses for a given 6-digit category than the FRS shows, which might be due to FRS only including EPA-regulated sites but also due to data gaps.
- Note the difference between children = TRUE and children = FALSE in EJAM functions like latlon_from_naics()
- Note that searching on a 6-digit code misses parent categories you may want. The FRS data on NAICS by site is inconsistent in how many digits are reported for the NAICS (explained below).

A given site might be listed in the FRS as being under one or more NAICS codes of various lengths, such as only a parent code (large grouping), only a detailed code (6-digit), or some combination of codes and their subcategories.

And the same title, like “Petroleum Refineries,” may be assigned by the NAICS system to the category but also a subcategory, as with codes 32411 and 324110. The function [naics_from_any()] shows what codes and title exist in the NAICS system.

Also, certain terms appear in the online description of a NAICS but not in the title of the NAICS – the function [naics_findwebscrape()] helps with those cases, e.g., compare these:

```
naics_findwebscrape("cement")

naics_from_any("cement")
```

Compare also these:

```
naics_findwebscrape("refiner")

naics_from_any("refiner")
```

`naics_findwebscrape("refiner")` reports “324110” (Petroleum Refineries) and other related industries, but not the 5-digit “32411” (also Petroleum Refineries).

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Using `naics_findwebscrape()` finds only the 6-digit codes that match on title or description, so it would find some codes not found by [naics_from_any()] which does not query description, but could lead to missing some facilities in the sense that the 6-digit code does not cover the sites listed in FRS under only the 5-digit code for Petroleum Refineries (not the 6-digit).

It is important to note that searching on a 6-digit code misses parent categories that may include sites you expect to find:

`frs_from_naics("324110", children = F)[,1:5]` finds a few hundred sites, but it fails to find some sites you would find using `frs_from_naics("32411", children = F)[,1:5]`

The code example below shows that the FRS dataset has some facilities listed under the 5-digit "32411" code only, some with the 6-digit "324110" code only, and some with both codes:

```
hasboth = intersect(
  frs_from_naics("32411",  children = F)[,1:5]$REGISTRY_ID,
  frs_from_naics("324110", children = F)[,1:5]$REGISTRY_ID
  )
hasonly6digit = setdiff(
  frs_from_naics("32411",  children = F)[,1:5]$REGISTRY_ID,
  frs_from_naics("324110", children = F)[,1:5]$REGISTRY_ID
  )
hasonly5digit = setdiff(
  frs_from_naics("324110", children = F)[,1:5]$REGISTRY_ID,
  frs_from_naics("32411",  children = F)[,1:5]$REGISTRY_ID
  )

length(hasonly5digit)  # Most of the FRS sites here
#> [1] 362
length(hasonly6digit)
#> [1] 12
length(hasboth)
#> [1] 12
```

Examples of some NAICS/SIC functions

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```
 naics_from_code(211)
 naicstable[code==211,]
 naics_subcodes_from_code(211)
 naics_from_code(211,  children = TRUE)
 naicstable[n3==211,]
 NAICS[211][1:3] # wrong
 NAICS[NAICS == 211]
 NAICS["211 - Oil and Gas Extraction"]

naics_from_any("plastics and rubber")[,.(name,code)]
naics_from_any(326)
naics_from_any(326, children = T)[,.(code,name)]
naics_from_any("plastics", children=T)[,unique(n3)]
naics_from_any("pig")
naics_from_any("pig ") # space after g

# naics_from_any("copper smelting")
# naics_from_any("copper smelting", website_scrape=TRUE)
# browseURL(naics_from_any("copper smelting", website_url=T

a = naics_from_any("plastics")
b = naics_from_any("rubber")
fintersect(a,b)[,.(name,code)] #  a AND b
funion(a,b)[,.(name,code)]     #  a OR  b
naics_subcodes_from_code(funion(a,b)[,code])[,.(name,code)]
naics_from_any(funion(a,b)[,code], children=T)[,.(name,code

NROW(naics_from_any(325))
#[1] 1
NROW(naics_from_any(325, children = T))
#[1] 54
NROW(naics_from_any("chem"))
#[1] 20
NROW(naics_from_any("chem", children = T))
# [1] 104
```

HOW TO ANALYZE PROXIMITY USING EJAM

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in selecting radius.

DEMOGRAPHICS BY DISTANCE AT BLOCK GROUP RESOLUTION

It is easiest to analyze distance increments based on each block-group's average resident here. Block resolution is covered in a later section.

WITHIN ONE RADIUS

Overall list of sites

At the *OVERALL LIST of sites* as a whole, which groups are *overrepresented* within X mile radius vs Statewide?

```
out <- ejamit(testpoints_100, radius = 3.1)
```

```
ejam2ratios(out)
#>
#>
#> Average Resident in Place(s) Analyzed vs US or State
#>                       Ratio_to_US_avg Ratio_to_State_avg
#> Demog.Ind.                        1.2                1.2
#> Suppl Demog.Ind.                  1.0                1.1
#> %Low-inc.                         1.0                1.1
#> %Limited English                  1.8                1.4
#> %Unemployed                       1.2                1.1
#> %< High School                    1.2                1.2
#> %< age 5                          1.1                1.1
#> %> age 64                         0.9                0.9
#> %POC                              1.5                1.3
#> %Hispanic                         1.6                1.3
#> %Black NHA                        1.2                1.5
#> %Asian NHA                        2.1                1.3
#> %AmerIndian/AK NHA                0.4                0.8
#> %Hawaiian/PI NHA                  0.9                1.2
#> %Other race NHA                   1.6                1.2
#> %multirace NH                     1.0                1.0
#> %White NHA                        0.7                0.8
#> PM2.5                             1.1                1.0
#> Ozone                             1.1                1.0
#> NO2                               1.6                1.3
#> Diesel PM                         2.2                1.6
```

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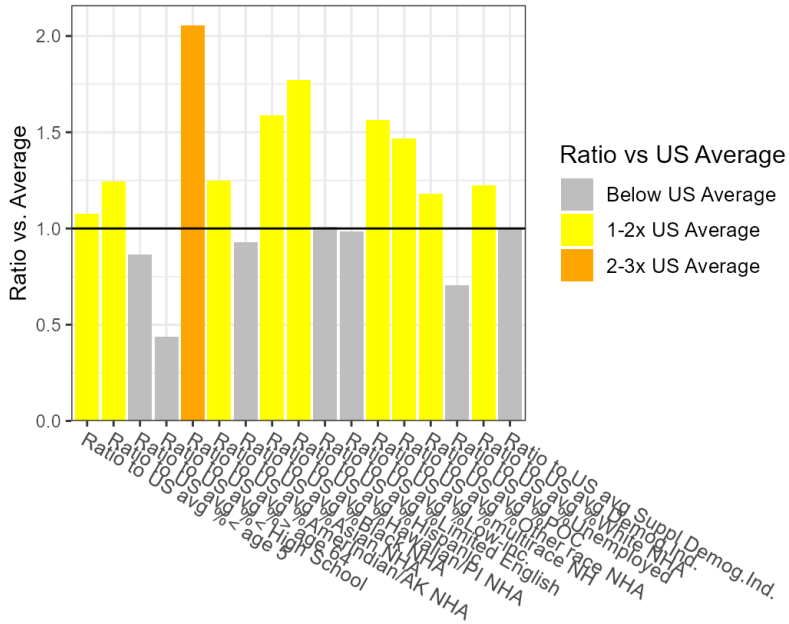
```
#> NPL                2.8                1.5
#> RMP                1.2                1.3
#> TSDF               3.6                1.9
#> UST                3.2                2.0
#> NPDES              0.0                0.7
#> Drinking           1.8                1.6
```

```
ejam2barplot(out)
```

raphics at the Analyzed Locations Compared to US Overall



Example of ejam2barplot() showing percent Asian among residents within 5 km of these 100 sites is more than two times the US rate overall

Just one site

At *JUST ONE SITE*, which groups are *overrepresented* within X mile radius vs Statewide?

```
out1 <- ejamit(testpoints_100[2, ], radius = 3.1)
ejam2ratios(out1)
```

```
ejam2barplot(out1)
```

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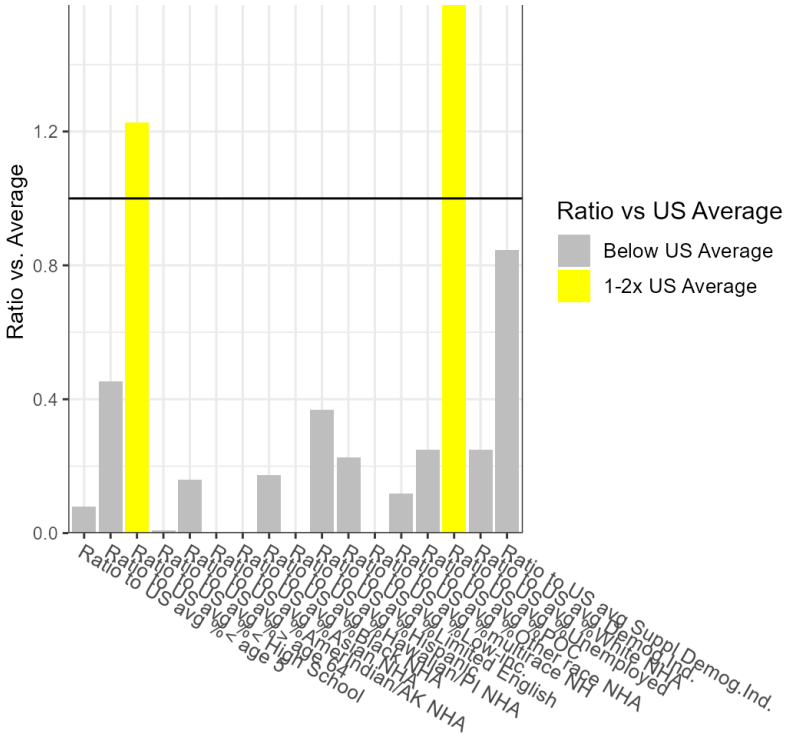

Example of ejam2barplot() showing percent non-Hispanic White Alone among residents within 5 km of this one site is about 1.6 times the US rate overall

Site by site comparison

Which groups are *overrepresented* at *EACH SITE*, within X mile radius vs Statewide

```
out <- testoutput_ejamit_10pts_1miles
x = round(data.frame(out$results_bysite)[, c("ratio.to.state
names(x) = fixcolnames(names(x),"r","shortlabel")
x = data.frame(sitenumber = 1:NROW(x), x)
x
#>    sitenumber Ratio.to.State.avg..Low.inc. Ratio.to.State
#> 1           1                         0.97
#> 2           2                         1.08
#> 3           3                         0.57
#> 4           4                         0.33
#> 5           5                         2.12
#> 6           6                         2.22
#> 7           7                         0.97
#> 8           8                         0.68
```

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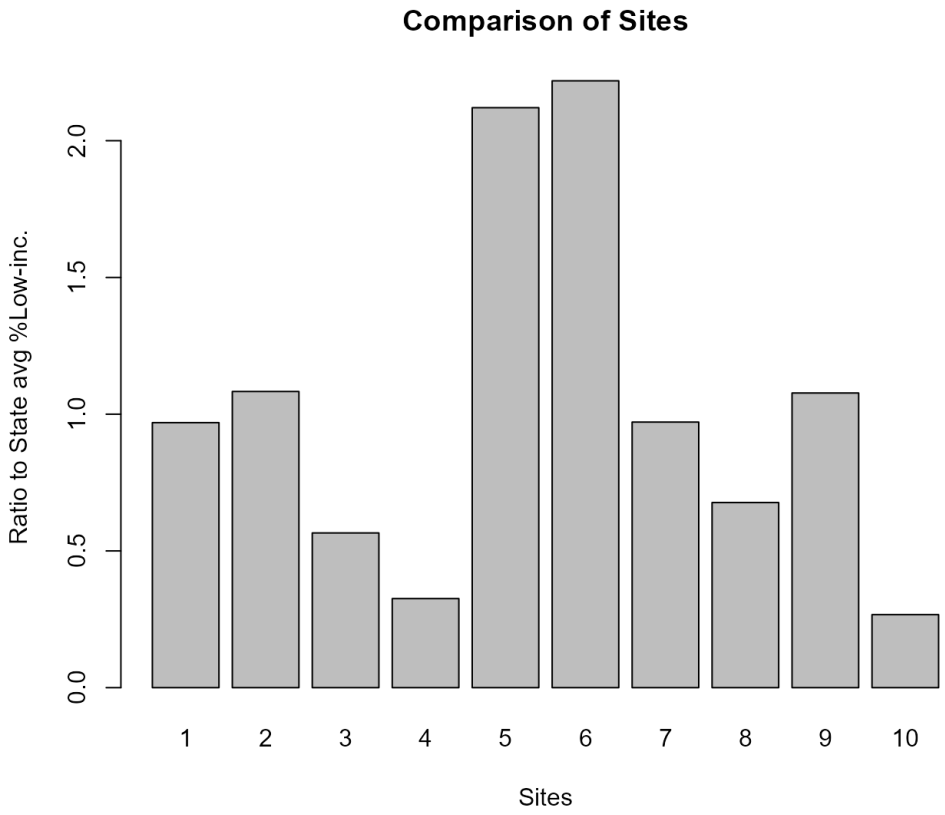
Plot to compare sites, for just one demographic indicator

This plot shows that % low income among residents at sites 5 and 6 is more than twice the relevant State average. It is near average at several other sites, and is less than half the State average at sites 4 and 10.

```
ejam2barplot_sites(out, "ratio.to.state.avg.pctlowinc", topr
```



Example of ejam2barplot_sites()

```
## For raw values at key sites:
# ejam2barplot_sites(out, "pctlowinc")
```

WITHIN MULTIPLE DISTANCES - COMPARING RADIUS CHOICES

Overall list of sites

At the *OVERALL LIST of sites* as a whole, which groups are *overrepresented* within X mile radius vs Statewide?

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```
pts <- testpoints_100[10:12, ]
```

See just the table

```
x <- ejamit_compare_distances(pts, radii = radii, quiet = TR
```

```
#> Analyzing 3 points, radius of 1 miles around each.
#> Analyzing 3 points, radius of 2 miles around each.
#> Analyzing 3 points, radius of 3 miles around each.
#> Analyzing 3 points, radius of 10 miles around each.
#>
#>                                        1   2   3  10
#> Ratio to State avg %Hispanic         2.5 2.3 2.3 1.8
#> Ratio to State avg %Black NHA        0.4 0.2 0.2 1.2
#> Ratio to State avg %Asian NHA        0.1 0.4 0.5 1.0
#> Ratio to State avg %AmerIndian/AK NHA 0.3 0.2 0.2 0.5
#> Ratio to State avg %Hawaiian/PI NHA  0.0 0.0 0.1 0.6
#> Ratio to State avg %Other race NHA   0.7 1.1 0.7 0.8
#> Ratio to State avg %multirace NH     0.1 0.1 0.1 0.4
#> Ratio to State avg %White NHA        0.2 0.3 0.2 0.3
```

See the plot

```
# x <- ejamit_compare_distances(pts, radii = radii, quiet =
# or
ejamit_compare_distances2plot(x)
#>
#> Indicators that increase the most as you get closer:
```

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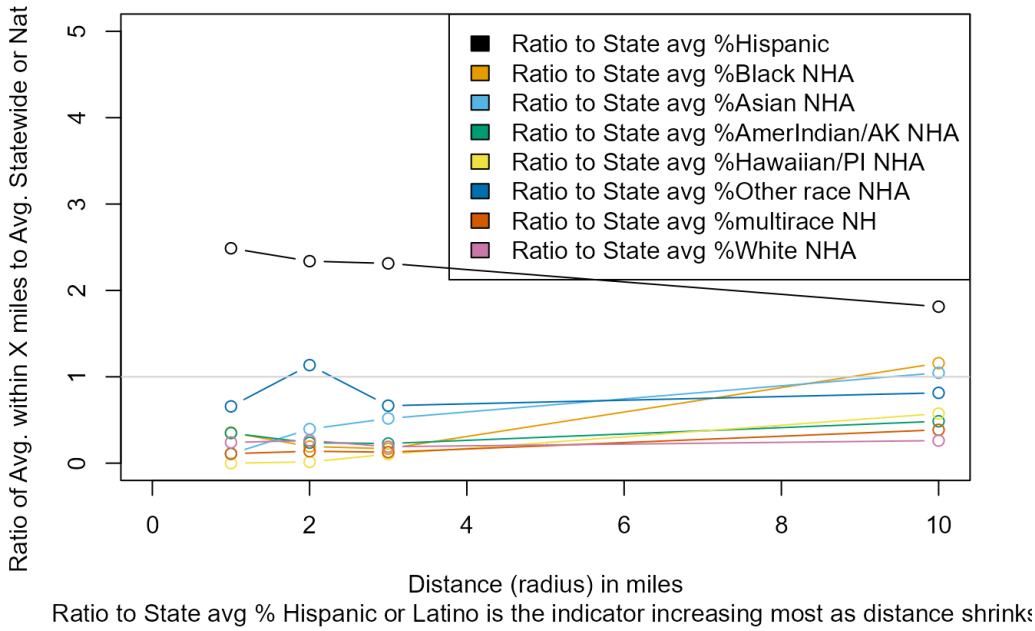


Example of using ejamit_compare_distances2plot()

```
#> [1] "Ratio to State avg % Hispanic or Latino"
```

DEMOGRAPHICS AT BLOCK GROUP RESOLUTION

Most of the EJAM functions use distance to the average resident of a block group, which is calculated from the distance to each block's internal point and uses the approximation that within a block the average resident and all residents are as far as that internal point. For typical distances analyzed in EJAM (e.g., 3 mile radius, or about 5 km) that is a good approximation, since only about 2% of all US blocks are larger than 1 square mile.

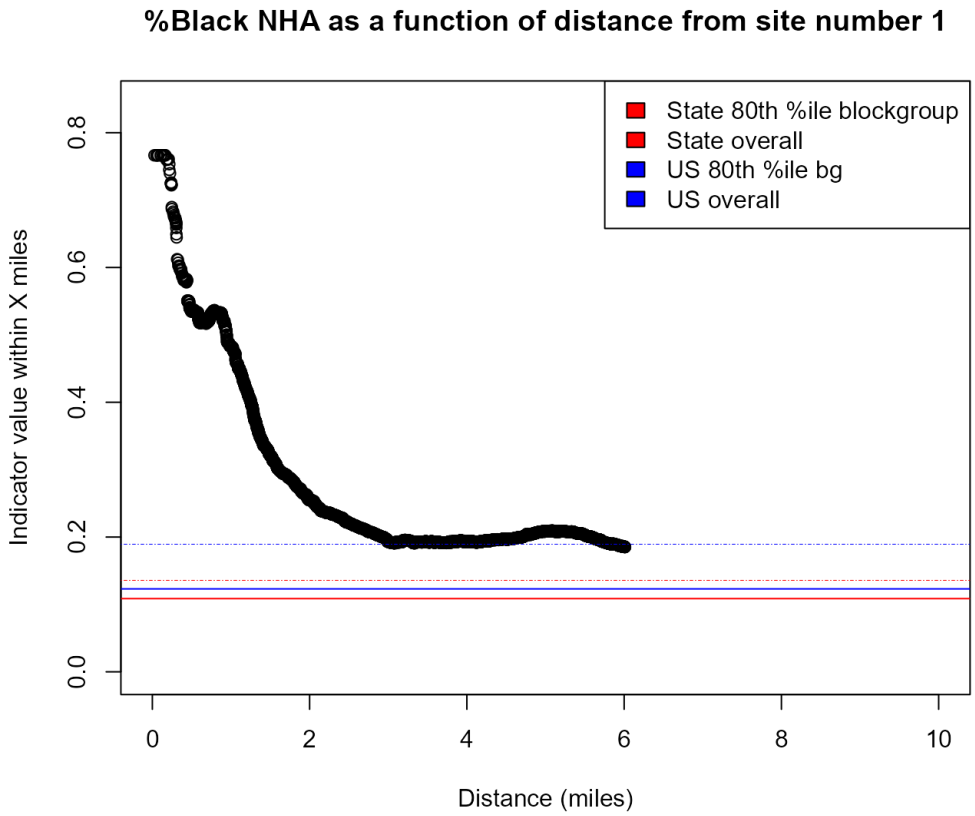
If you need high spatial resolution (block by block) plots of an indicator as a function of distance, you can directly work with getblocksnearby() or just use the function plot_distance_by_pctd(). It uses the distance from the site to each block's internal point (like a centroid) rather than just the distance to the average resident in each block group.

How demographics at *ONE SITE* vary as *a continuous function of distance*

Example of area where %Black is very high within 1 mile but drops by 3 miles away

EJAM 2.32.0

```
  getblocksnearby(pts, radius = 10, quiet = T),
  score_colname = "pctnhba",
  sitenumber = 1)
#> Analyzing 1 points, radius of 10 miles around each.
```



Example of using plot_distance_by_pctd()

```
#browseURL(url_ejscreen_report(lat = pts$lat, lon = pts$lon,
#browseURL(url_ejscreen_report(lat = pts$lat, lon = pts$lon,
```

Example of area that has higher %Hispanic as you go 10 to 30 miles away from this specific point

```
pts <- data.table::data.table(lat = 45.75464, lon = -94.3679

y <- plot_distance_by_pctd(pts,
                           sitenumber = 1, score_colname = "pcthi
#> Analyzing 1 points, radius of 30 miles around each.
```

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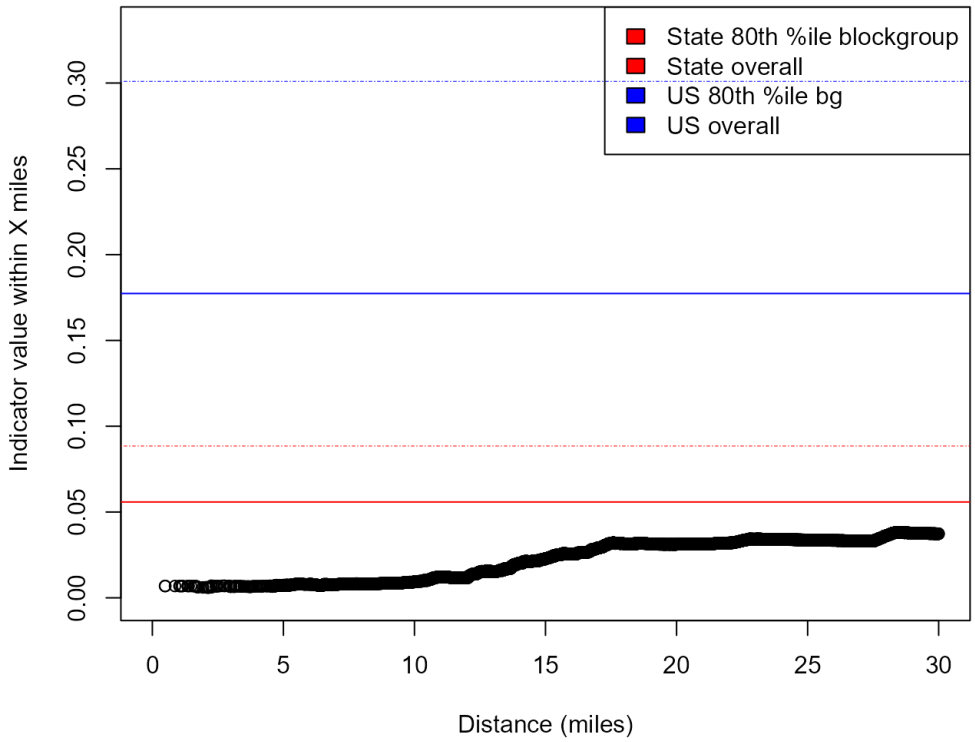


Example of using plot_distance_by_pctd()

```
# browseURL(url_ejscreen_report(lat = pts$lat, lon = pts$lor
# browseURL(url_ejscreen_report(lat = pts$lat, lon = pts$lor
```

Step through all the sites to see an indicator versus distance at each

Examples of sites analyzed here show some conclusions are very sensitive to the radius used. The choice of radius in proximity analysis for some sites will lead to a very different conclusion depending on the radius analyzed, if only a single distance is checked or reported on. The relationship between distance X and percent demographics within X miles can be positive, negative, or roughly flat, etc., depending on the site and group. The percent demographics may be above or below the US average or the State average within a given distance of the site.

For the ten sites analyzed in this example, a wide range of patterns is found:

- At site 5, % low income is extremely high very close to the site and falls sharply with distance but it remains quite high (still above 80th percentile of US or State) even within 4 miles.

percentile within about 1 mile, but then it falls to below State and then US average within around 2 and then 3 miles of the site.

- At site 7, it is below average until about 8 miles, but is above US and State averages within 10 miles.
- At site 9, it can be above or below average in State and/or in US, depending on the distance, but it is never as high as the 80th percentiles.
- At sites 2, 3, 4, and 10, % low income is far below US and State averages within any distance shown here.

```
pts <- testpoints_10
s2b <- getblocksnearby(pts, radius = 10, quiet = T)
for (i in 1:NROW(pts)) {
  plot_distance_by_pctd(s2b, sitenumber = i, score_colname =
  readline() # hit any key to step through the plots
}
```

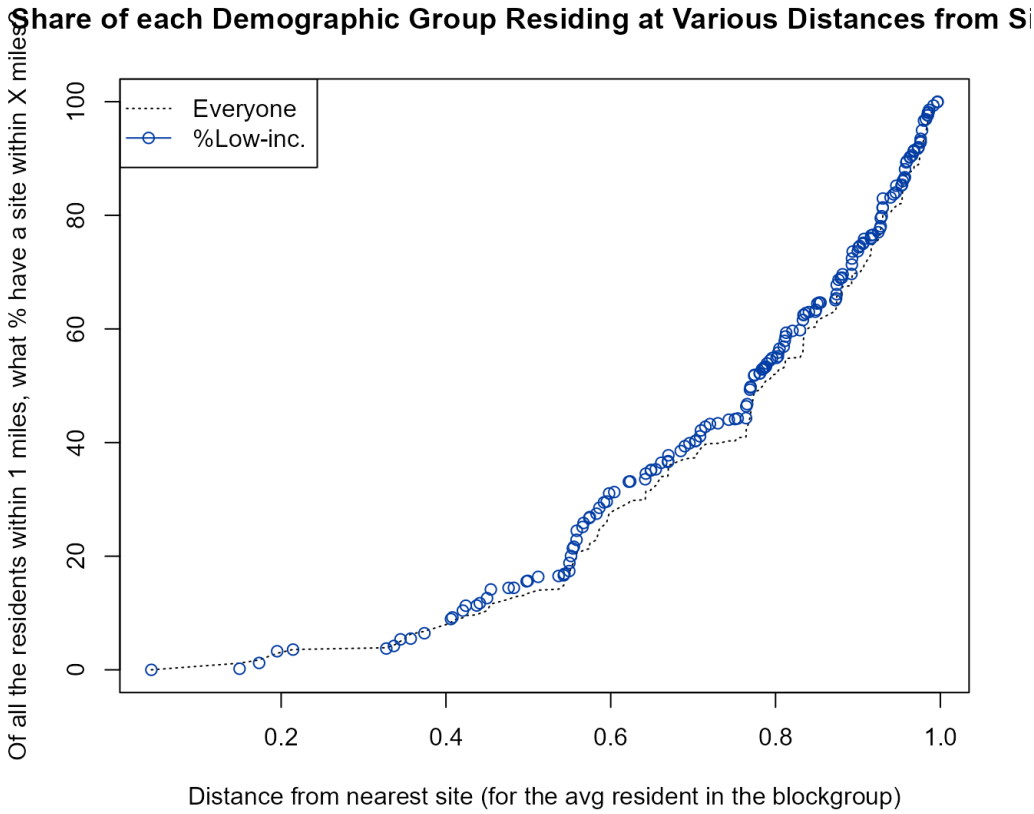
Block by block details are also easy to view in a map of all the nearby blocks, as shown in the section on [plotblocksnearby()] and details of blocks near one site.

Cumulative Distribution plots of groups as *a continuous function of distance*

Out of all the residents within the area analyzed, see how some are mostly nearby and others are further away, as a CDF plot. This shows the share of each demographic group residing at various distances from sites, with distance from nearest site on the x axis and the cumulative share of each group on the y axis (of all residents within 10 miles, what percent have a site within X miles?). It compares everyone nearby to just those who are among the percent low income, and shows that, for example, a larger share of all the low income population within 10 miles actually live within about 6 miles than is the case for everyone within 10 miles. In other words, within the 10 mile radius circles, more of the low income residents are closer to a site than are the non-low income residents or all residents.

```
 # out <- ejamit(testpoints_10, radius = 10)
distance_by_group_plot(
```

EJAM 2.32.0



Example of using distance_by_group_plot()

MEAN DISTANCE BY DEMOGRAPHIC GROUP

The analysis described above looks at demographics as a function of distance. Another perspective is provided by looking at distance as a function of demographic group. This means looking at the average distance or the whole distribution of distances (or proximities) among all the residents within a single demographic group, one group at a time, and comparing these groups.

Overall list of sites

Mean distance of each group, at the *OVERALL LIST of sites* as a whole

To see a table of demographic indicators, showing the mean distance for each group, compared to distance for those not in that demographic group:

```
out <- testoutput_ejamit_1000pts_1miles
```

EJAM 2.32.0

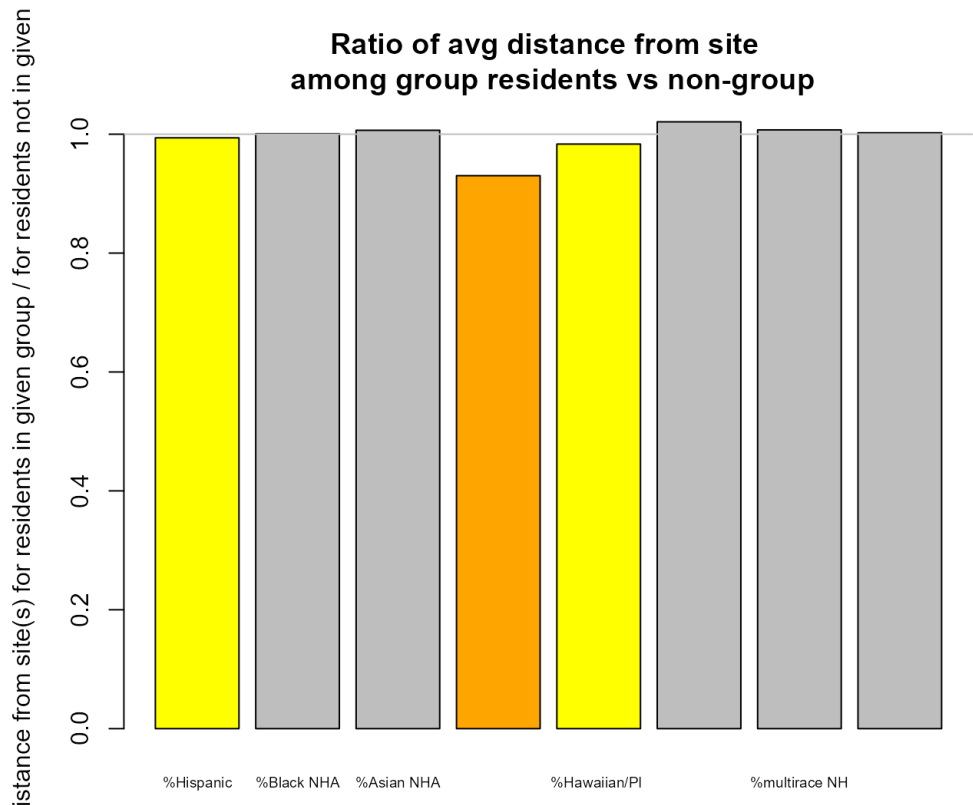
```
# see a table of demog indicators
distance_mean_by_group(out$results_bybg_people)
#>                              group nearest nearer ratio
#> Demog.Ind.              Demog.Index   FALSE  FALSE 1.010
#> Suppl Demog.Ind.   Demog.Index.Supp   FALSE  FALSE 1.010
#> %Low-inc.                 pctlowinc   FALSE   TRUE 0.984
#> %Limited English         pctlingiso   FALSE   TRUE 0.987
#> %Unemployed           pctunemployed   FALSE   TRUE 0.990
#> %< High School              pctlths   FALSE   TRUE 0.986
#> %< age 5                  pctunder5   FALSE  FALSE 1.004
#> %> age 64                 pctover64   FALSE  FALSE 1.002
#> %POC                         pctmin   FALSE   TRUE 0.998
#> %Hispanic                   pcthisp   FALSE   TRUE 0.994
#> %Black NHA                  pctnhba   FALSE  FALSE 1.001
#> %Asian NHA                  pctnhaa   FALSE  FALSE 1.007
#> %AmerIndian/AK NHA       pctnhaiana    TRUE   TRUE 0.930
#> %Hawaiian/PI NHA         pctnhnhpia   FALSE   TRUE 0.983
#> %Other race NHA     pctnhotheralone   FALSE  FALSE 1.021
#> %multirace NH            pctnhmulti   FALSE  FALSE 1.007
#> %White NHA                  pctnhwa   FALSE  FALSE 1.002
#>                   avg_distance_for_nongroup
#> Demog.Ind.                             0.68
#> Suppl Demog.Ind.                       0.68
#> %Low-inc.                              0.69
#> %Limited English                       0.69
#> %Unemployed                            0.69
#> %< High School                         0.69
#> %< age 5                               0.69
#> %> age 64                              0.69
#> %POC                                   0.69
#> %Hispanic                              0.69
#> %Black NHA                             0.69
#> %Asian NHA                             0.69
#> %AmerIndian/AK NHA                     0.69
#> %Hawaiian/PI NHA                       0.69
#> %Other race NHA                        0.69
#> %multirace NH                          0.69
#> %White NHA                             0.69

# for just 1 indicator
print(distance_mean_by_group(
  out$results_bybg_people,
  demogvarname = 'pctlowinc', demoglabel = 'Low Income'))
```

EJAM 2.32.0

```
#> Low Income                        0.69
```

To see a barplot, comparing just race/ethnicity groups:

```
plot_distance_mean_by_group(out$results_bybg_people,
                        demogvarname = names_d_subgroups,
                        demoglabel = fixcolnames(names_d_subg
                        )
```



are highlighted, with closest in orange (%AmerIndian/AK NHA is only 93% as far as everyone el

Example of using plot_distance_mean_by_group()

```
#>                              group nearest nearer ratio a
#> %Hispanic                  pcthisp   FALSE   TRUE 0.994
#> %Black NHA                 pctnhba   FALSE  FALSE 1.001
#> %Asian NHA                 pctnhaa   FALSE  FALSE 1.007
#> %AmerIndian/AK NHA      pctnhaiana    TRUE   TRUE 0.930
#> %Hawaiian/PI NHA        pctnhnhpia   FALSE   TRUE 0.983
#> %Other race NHA    pctnhotheralone   FALSE  FALSE 1.021
#> %multirace NH           pctnhmulti   FALSE  FALSE 1.007
#> %White NHA                 pctnhwa   FALSE  FALSE 1.002
#>                    avg_distance_for_nongroup
```

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```
#> %AmerIndian/AK NHA                    0.69
#> %Hawaiian/PI NHA                      0.69
#> %Other race NHA                       0.69
#> %multirace NH                         0.69
#> %White NHA                            0.69
```

Site by site comparison

Mean distance of each group, at *EACH SITE*, as ratio to mean of everyone else nearby

Ratios at each site, of avg dist of group / avg dist of everyone else near site:

```
out <- testoutput_ejamit_10pts_1miles
## But try a larger radius to reveal more information:
# out <- ejamit(testpoints_10, radius = 31)

x = distance_by_group_by_site(out$results_bybg_people)
x

# summary of closest group at each site and by how much
data.frame(site = colnames(x),
           closestgroup = rownames(x)[sapply(x, which.min)],
           their_avg_distance_as_pct_of_everyone_elses = rou
)
```

BACKGROUND AND OVERVIEW OF ISSUES IN PROXIMITY, DISTANCE, OR RADIUS

Distance from a potential source of environmental risk is often used as a simple proxy for actual exposure or risk, when data are limited. Proximity analysis uses distance (how far away) from a site, which is just the opposite of proximity (how near) to a site.

Conclusions can be sensitive to the choice of radius, if only one radius is reported on, as shown in [Step through all the sites to see an indicator versus distance at each].

Demographics-by-distance or distance-by-demographic group?

demographics:

1. Demographics as a function of risk (or proximity): Many proximity analyses report percent demographics by distance or risk bin, such as % low income within 3 miles of a point. This expresses demographics as a function of proximity or risk. Sometimes other distance or risk bins are used, such as areas with risk above some cutoff. And sometimes instead of a continuous measure of % demographics, the demographic data are used to categorize places in bins, such as areas in the top quartile of poverty rates.

2. Risk (or proximity) as a function of demographics: A different way to present this information is to report distance or risk as a function of demographic group – this expresses distance within each demographic group, such as the average distance by group or the full distribution of risk within each group.

Radius, radii, or continuous distance?

Proximity or distance as binary, categorical, or continuous metrics: Proximity analysis has often relied on picking a single distance, a radius, and analyzing conditions within that radius, such as all residents who live within 3 miles of a point where a regulated facility is located. Sometimes an analysis will look at two or even three distances. In some more sophisticated analyses, distance is treated as a continuous measure. Some tools like EJScreen use a proximity metric based on the inverse of distance (1/d) to provide a proximity score that gets higher as distance gets smaller. But many EJ analyses still use a single distance and analyze conditions within that distance.

EJAM makes it easier to do any of these types of analysis, because conclusions can be sensitive to the choice of a single radius, and metrics and methods provide different perspectives and reveal a richer picture of where people actually live in relation to potential sources of exposure or risk.

Comparisons within what distances or to what reference area(s)?

This is a tricky issue in proximity analysis: There is a subtle but vital difference between proximity analysis using a single radius (binary distance) and analysis using continuous distance. One way to think of this

(radius) from a single facility point (or a whole set of facilities). These two ways of summarizing proximity are complementary:

1. Which groups tend to live nearby in the sense of being **within the radius versus outside the radius** selected? In other words, which groups are "overrepresented" within X miles of the site? This treats proximity as a yes/no, binomial question – **a resident is nearby or not**. It would focus on whether someone is anywhere within 3 miles, say, and ignore the differences between being 1, 2, or 3 miles away. Most proximity analysis has tended to look at this type of summary.

2. Among the residents within X miles of the site, which groups live especially close to the facility? This question recognizes proximity is a continuous variable, and focuses on the difference between 1 mile, 1.5 miles, etc. However, it only looks at residents within the X miles radius area analyzed, so it fails to recognize that some groups tend to live more than 3 miles away, for example. This perspective does not take into account which groups are overrepresented within the original total radius near a site.

Some functions like distance_mean_by_group() or distance_by_group_by_site() do the second of these two types of analysis. They report, only among those anywhere inside the radius, which groups are closer to the site.

In a specific location, for example, one demographic group could be underrepresented within 3 miles, but those few who are in the group still might live right next to the facility in which case their average distance would be higher than that of any other group because this function only counts those within the radius analyzed.

In some other location, the opposite could occur – if one group is overrepresented within 3 miles, they still might all live in a community about 2.9 miles away from the site – that would mean their distance from the site on average is greater (or their proximity score is lower) than other groups within 3 miles of the site.

The question of whether to compare to Statewide or Nationwide or urban/rural or other reference averages or percentiles is related to this

demographics within 1 mile, 2 miles, etc. all the way out until one was looking at the county overall, the state overall, and eventually the nation overall. Selecting a single radius or selecting a single reference area should be done with a recognition of what questions one is actually trying to answer, and an understanding of how impacts vary with distance from a particular type of facility or source of potential risk.

If one is comparing demographic groups in terms of distance (or risk level), or if one is comparing % demographics at each distance (or risk level), the implicit assumption is that there is some "expected" rate, and/or some "equitable" or "proportionate" % or ratio or risk.

CHOICE OF RADIUS AND UNCERTAINTY DUE TO A SMALL RADIUS WHERE BLOCKS ARE LARGE

Choosing a radius (or polygon) that is small relative to local Census blocks can lead to significant uncertainty in EJAM/EJScreen estimates, so it is important to understand the details if one wants to use a small radius especially in rural (low population density) areas.

To help consider this uncertainty, EJAM reports how many block centroids were found inside each area (inside a circular buffer defined by the selected radius, or inside a polygon that is from a shapefile). That count of blocks is found in a column of the spreadsheet output provided by the web app and also the table called results_bysite that is one output of the ejamit() function.

You could also Map all sites with popup at each saying how many blocks were found nearby and therefore might have more uncertainty in counts nearby.

```
# out <- ejamit(testpoints_1000, radius = 1)
# out$results_bysite$blockcount_near_site
out <- testoutput_ejamit_1000pts_1miles

barplot(
  table(cut(
    out$results_bysite$blockcount_near_site,
    c(-1, 9, 29, 100, 1000)
  )),
  names.arg = c("< 10 blocks", "10-29", "30-100", "> 100 blo
  main = "How many blocks are within 1 mile of these 1,000 t
```

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For more details about distance adjustments, overlaps of circles, etc.

This function prints a very large amount of diagnostic information, and provides a barplot histogram showing in this case that almost none of the 1000 sites have zero blocks within a mile but roughly 10-15% have under 10 blocks nearby and a similar share have only 10-29 blocks nearby.

```
# (Printed information is lengthy)

  getblocks_diagnostics(
  testoutput_getblocksnearby_1000pts_1miles,
  # getblocksnearby(testpoints_1000, radius = 1, quiet = T),
  detailed = T, see_pctiles = T
  )
```

Suggestions on radius and uncertainty

Here are some suggestions about how to consider the radius in relation to uncertainty where blocks are large:

- A closer look at uncertainty and care in communicating uncertainty may be needed where a circle or polygon contains fewer than about 30 block centroids. That is especially important if it contains fewer than about 10, and essential if it contains only 1 or zero block centroids.
- Using a radius of 5 miles or more does not raise these issues in 99% of US locations where EPA-regulated facilities are found.
- A radius of 3 miles might need a closer look for about 1% to 5% of typical sites in the US.
- A radius of 1 mile or less requires caution and understanding of the issues at a significant share of locations in the US (about 1 in 4 locations might need a closer look to check for uncertainties).
- A 0.5 mile radius should not be used without cautious interpretation or offline analysis in most locations where EPA-regulated facilities are located.
- A 0.25 mile radius should only be used on a case-by-case basis where each location is examined individually and other methods are likely more suited for the analysis of those sites.

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Demographic counts and percentages of environmental indicators are calculated from block group demographic and environmental indicators and an estimate of what fraction of each block group is inside each site. For proximity analysis that means a circle is drawn around a point using a radius, and for shapefiles a similar approach is used. In either case, the fraction of the block group counted as inside the area analyzed is based on which block centroids (each is technically called a block "internal point") are inside the circle or polygon. All the residents of a block are assumed to be inside if the block centroid is inside. This is exactly true unless a block is on the edge of the circle or polygon. Even for the ones on the edge, some centroids are just outside and some just inside the shape, so the contributions of some blocks are overcounted and other undercounted, but those tend to cancel each other out in the sense that it is unlikely they would all be undercounted, for example. Still, when a large share of the block points in circle or polygon are from blocks not entirely inside, uncertainty is higher than when the vast majority of blocks are entirely inside. In other words, if the circle or polygon has a very large number of blocks in it, uncertainty is lower because only a small fraction are along the edge and bisected. If a radius of 3 miles is used, the area is 28 square miles. If the blocks in that location are only about 0.28 square miles each, the circle might contain or partly contain about 100 blocks.

The dataset used by EJAM called blockwts has a column called block_radius_miles that is what the radius would be if the block were circular, and it was created based on area = pi * block_radius_miles^2 or block_radius_miles = sqrt(area / pi) where area is in square miles.

Details on the blocks found near one site

Table of distances between each site and each block

Use `getblocksnearby()` to quickly find residents/blocks that are within a specified distance, as a table of distances between sites and nearby blocks.

```
sitepoints <- testpoints_10[1:2, ]

sites2blocks <- getblocksnearby(
  sitepoints = sitepoints,
  radius = 3.1
)
```

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```
#> min distance before adjustment:  0.06504053
#> max distance before adjustment:  4.670403
head(sites2blocks)
#> Key: <blockid>
#>    ejam_uniq_id blockid distance    blockwt  bgid distanc
#>           <int>   <int>    <num>      <num> <int>
#> 1:            2     296 2.946818 0.00000000    15
#> 2:            2     297 3.040476 0.00000000    15
#> 3:            2     773 2.925869 0.07083906    32
#> 4:            2     780 2.873082 0.03576341    32
#> 5:            2     781 2.739460 0.05249885    32
#> 6:            2     786 3.077032 0.03163686    32
```

Detailed stats on blocks found near site(s)

```
x <- getblocks_diagnostics(sites2blocks)
#>
#>    DISTANCES FROM BLOCKS (AND RESIDENTS) TO SITES (AND FC
#>
#> 3.097412 miles is max. distance to block internal point (
#> 3.097412 miles is max. distance to average resident in bl
#> 0.06504053 miles is shortest distance to block internal p
#> 0.06504053 miles is shortest distance to average resident
#> 0 block distances were adjusted (these stats may count sc
#>   0 block distances were adjusted up (reported dist to av
#>   0 block distances were adjusted down (reported < unadju
#> 0 unique sites had one or more block distances adjusted c
#>
#>   BLOCK COUNTS PER SITE (FEWER MEANS HIGHER UNCERTAINTY A
#>
#> 362 blocks are near the avg site or in avg buffer
#> (based on their block internal point, like a centroid)
#>
#>   sites    blocks_per_site
#> 1     0         Not even 1
#> 2     0       some but <10
#> 3     0              10-29
#> 4     2 at least 30 blocks
#>
#>   BLOCK COUNTS TOTAL AND IN OVERLAPS OF AREAS (MULTIPLE S
#>
#> 723 actual unique blocks total
#> 723 blocks including doublecounting in overlaps,
#>              in final row count (block-to-site pairs tabl
```

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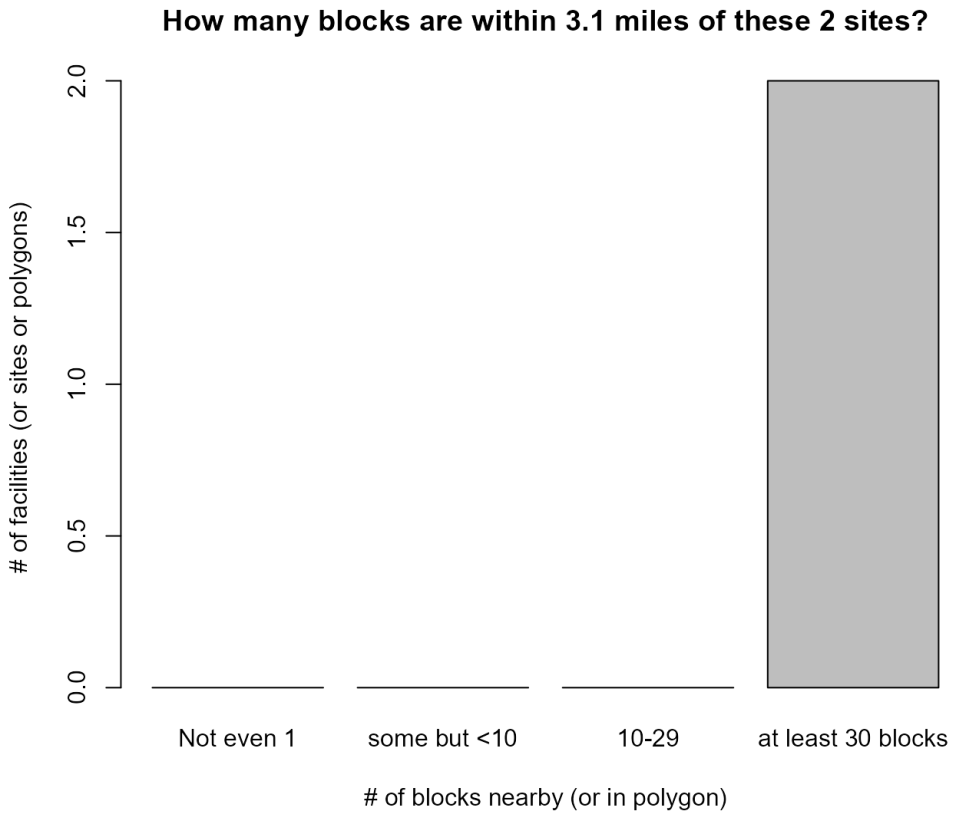
```
#>              (assuming they live at the block internal po
#>
#>   SITE COUNTS TOTAL AND IN OVERLAPS OF AREAS (MULTIPLE SI
#>
#> 2 unique output sites
#>
#> 723 blocks (and their residents) have exactly 1 site near
#> 0 blocks (and their residents) have exactly 2 sites nearb
#> 0 blocks (and their residents) have exactly 3 sites nearb
```



Example of getblocks_diagnostics() to see tables and histogram barplot of how many blocks are within 3.1 miles of these 2 sites

```
# x <- getblocks_summarize_blocks_per_site(sites2blocks)
# print(x) shows more info returned invisibly
```

Map 1 site to inspect the blocks nearby

Clicking on a block point provides a popup window showing information such as this:

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```
blocklat: 30.9913730000001
blocklon: -83.3753460999999
distance: 1.03614020347595
distance_unadjusted: 1.03614020347595
blockwt: 0
blockpop: 0
pop_nearby: 6237
bgpop: 1281
bgfips: 131850102031
bgid: 64286
ejam_uniq_id: 1
blockcount_near_site: 219
```

```
x <- plotblocksnearby(testpoints_10[1, ], radius = 3, returr
#> Analyzing 1 points, radius of 3 miles around each.
#> Finding Census blocks with internal point within  3  mile
#> Stats via getblocks_diagnostics(), but NOT ADJUSTING UP F
#> min distance before adjustment:  0.2321264
#> max distance before adjustment:  4.412158
# Set returnmap= TRUE to actually return a leaflet map
```

POPULATION DENSITY – WHY THE AVG SITE AND AVG RESIDENT ARE SO DIFFERENT

Reporting EJAM information summarized for the average site gives very different answers than reporting on the average resident near any one or more of those sites. The average site and average resident are completely different because most of the residents live near just a few of the sites – the ones with higher population density – when one is using a fixed radius at all sites, such as 3 miles from each site. Taking the average of sites gives equal weight to each site, even the ones with very few residents around them. Taking the average of all residents near all the sites gives equal weight to each person, so conditions near certain sites affect more people and have more influence on that average.

Sites vary widely in count of blocks nearby, depending on population density (which is closely related to block area in square miles)

- what blocks are near each site
- how far are they

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- how many sites are near a block (residents with > 1 site nearby)

```
out <- testoutput_ejamit_100pts_1miles
cat("  ", popshare_p_lives_at_what_pct(out$results_bysite$pc
#>    6% of places account for 50% of the total population (
cat("  ", popshare_at_top_n(out$results_bysite$pop, c(1, 5,
#>    1, 5, 10 places account for 17%, 46%, 58% of the total
```

Find all blocks nearby each site

```
radius <- 3
sitepoints <- testpoints_100
sites2blocks <- getblocksnearby(sitepoints, radius, quadtree
#> Analyzing 100 points, radius of 3 miles around each.
# testoutput_getblocksnearby_10pts_1miles is also available
names(sites2blocks)
#> [1] "ejam_uniq_id"        "blockid"             "distance
#> [4] "blockwt"             "bgid"                "distance
```

Very few blocks are within a radius of 1/4 mile.

Hundreds are often within 1 mile, but sometimes there are only a handful or even zero.

```
s2b_stats <- sites2blocks[ , .(
  avgDistance = round(mean(distance), 2),
  blocksfound = .N,
  blocks_within_1mile = sum(distance <= 1),
  blocks_within_0.75   = sum(distance <= 0.75),
  blocks_within_0.25  = sum(distance <= 0.25)
), by = 'ejam_uniq_id'][order(blocksfound), ]
setorder(s2b_stats, ejam_uniq_id)
head(s2b_stats)
#>    ejam_uniq_id avgDistance blocksfound blocks_within_1mi
#>           <int>       <num>       <int>              <in
#> 1:            1        1.66         341
#> 2:            2        2.13          56
#> 3:            3        1.50        2111                6
#> 4:            4        1.65         735                2
#> 5:            5        0.90         405                2
#> 6:            6        2.00          48
```

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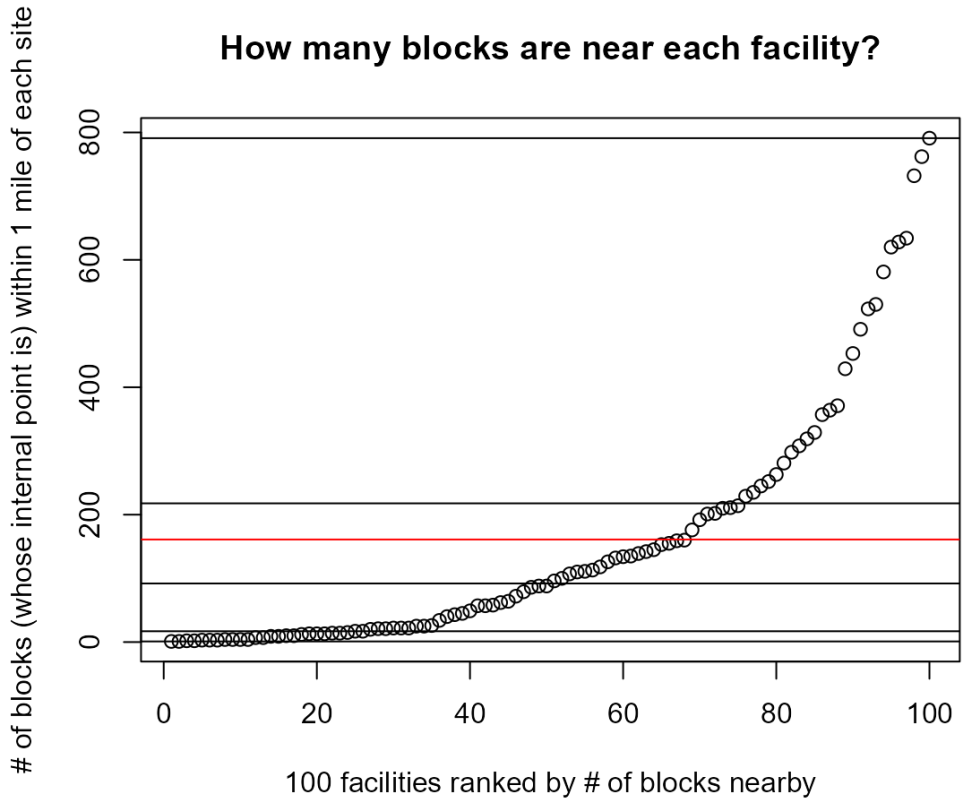
```
#> 2:                  0
#> 3:                 36
#> 4:                 12
#> 5:                 50
#> 6:                  0
```

CDF of how many blocks are nearby a site



How many blocks are near each of these 100 facilities?

Histogram and table showing how many blocks are nearby a site

```
hist(sites2blocks[,.N, by = "ejam_uniq_id"][, N], 20,
     xlab = "How many blocks are nearby?",
     ylab = "Frequency (# of sites)",
     main = "A given site may have zero to hundreds of block
     sub = "A typical site in this example has about 100 blo
```

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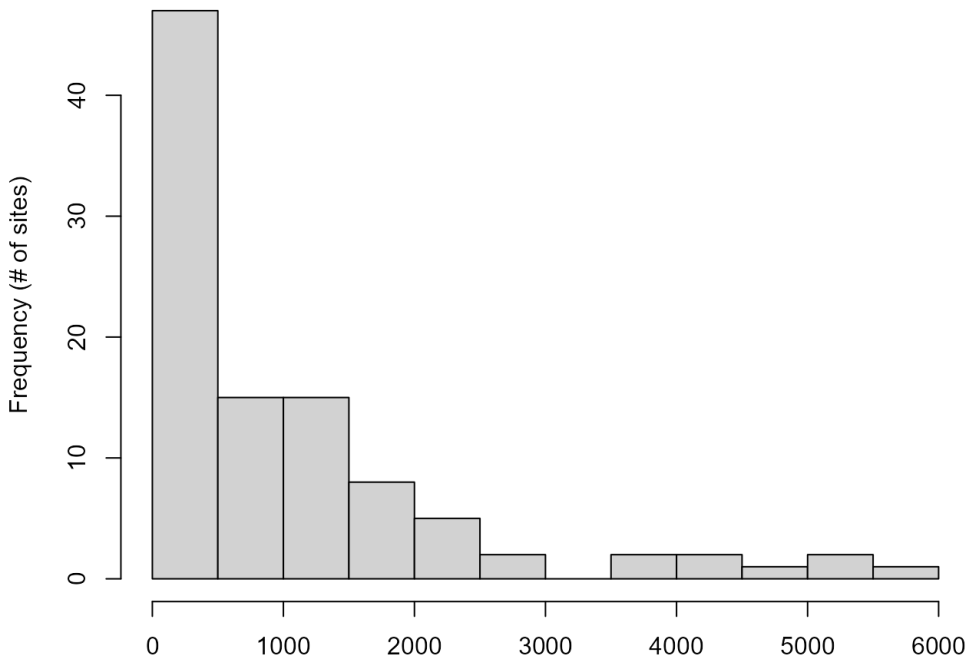

Example of Histogram and table showing how many blocks are within 3 miles of a site

```
DT::datatable(s2b_stats,  rownames = FALSE)
# more summaries showing there may be only 1 block or hundre
```

Summary stats on how many blocks are within each radius

```
# Just within 1 mile
summary(sites2blocks[distance <= 1, .N, by = "ejam_uniq_id"]
# or
quantile(s2b_stats$blocks_within_1mile, probs = (0:4) * 0.25

# Within each distance
summary(s2b_stats)
# t(summary(s2b_stats))
```

Map all sites with popup at each saying how many blocks were found nearby

```
## done previously:
# radius <- 3
# sitepoints <- testpoints_100

out <- ejamit(sitepoints = sitepoints,
```

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```
#> Aggregating at each site and overall.
#> Warning in batch.summarize(sitestats = data.frame(out$res
#> quiet, : specified threshnames not all found in sitestats
#> defaults

few <- out$results_bysite$blockcount_near_site < 30

mapthis <- cbind(
  sitepoints,
  out$results_bysite[, c(
    "pop", "bgcount_near_site", "blockcount_near_site"
    )],
  NOTE = ifelse(few, "< 30 blocks here", "")
  )

# Show in red the sites with very few blocks nearby, suggest

mm <- mapfast(mapthis, radius = radius, color = 'navy')
mm |> leaflet::addCircles(
    lng = mapthis$lon[few],
    lat = mapthis$lat[few],
    color = "red", radius = radius * 2 * meters_per_mile,
    popup = popup_from_any(mapthis[few, ])
)
```

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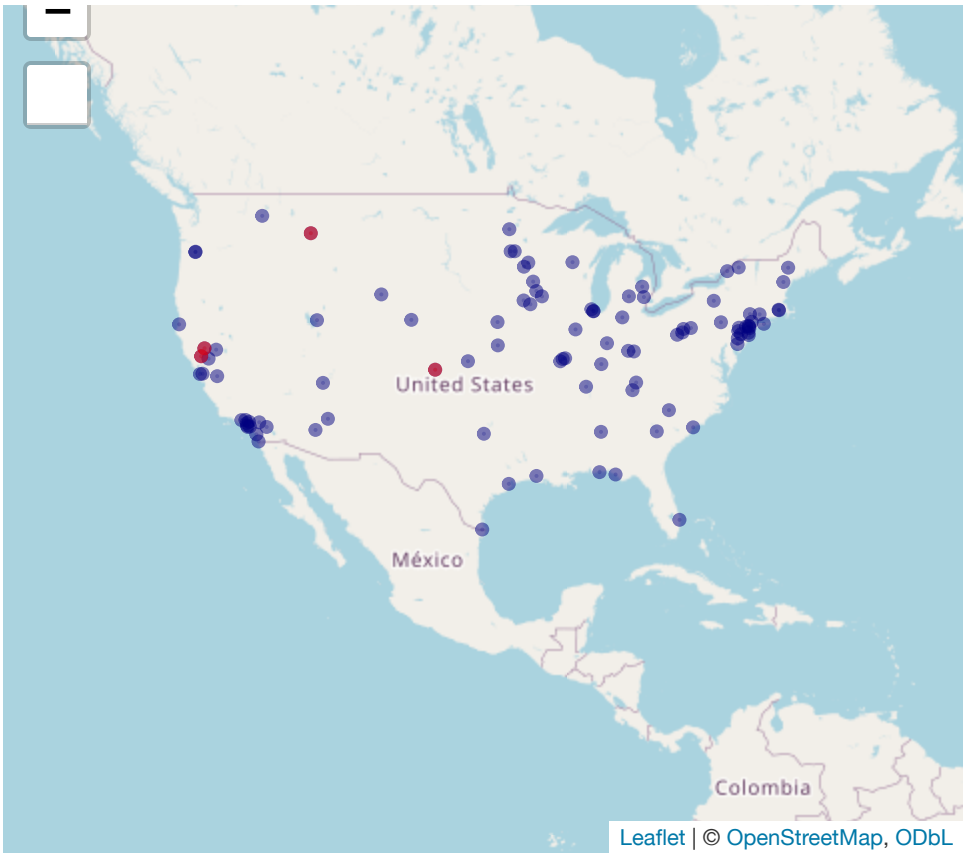

Example of mapfast() for seeing how many blocks are at each site

Some places have very few – if any – blocks within 1 mile

```
tail(s2b_stats[order(s2b_stats$blocks_within_1mile, decreasi
               c('ejam_uniq_id', 'blocks_within_1mile')], 3)
#>    ejam_uniq_id blocks_within_1mile
#>           <int>               <int>
#> 1:           68                   2
#> 2:           14                   1
#> 3:           19                   1
```

Some places have hundreds nearby: a 1 mile radius is huge within a dense urban area

```
head(s2b_stats[order(s2b_stats$blocks_within_1mile, decreasi
               c('ejam_uniq_id', 'blocks_within_1mile')], 3)
#>    ejam_uniq_id blocks_within_1mile
#>           <int>               <int>
#> 1:           57                 791
#> 2:           42                 762
#> 3:           21                 732
```

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```
leastdense <- s2b_stats$ejam_uniq_id[order(
    s2b_stats$blocks_within_1mile, decreasing = F)][1]
```

```
#> Analyzing 1 points, radius of 3 miles around each.
#> Finding Census blocks with internal point within  3  mile
#> Stats via getblocks_diagnostics(), but NOT ADJUSTING UP F
#> min distance before adjustment:  0.02342987
#> max distance before adjustment:  6.646285
```

```
plotblocksnearby(sitepoints = sitepoints[densest, ])
```

```
#> Analyzing 1 points, radius of 3 miles around each.
#> Finding Census blocks with internal point within  3  mile
#> Stats via getblocks_diagnostics(), but NOT ADJUSTING UP F
#> min distance before adjustment:  0.5222611
#> max distance before adjustment:  5.281615
```

```
plotblocksnearby(sitepoints = sitepoints[ leastdense, ])
```

Within a 1 mile radius, the blocks found tend to be about 2/3 of a mile from the site at the center.

```
summary(s2b_stats$avgDistance)
#>    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
#>   0.900   1.765   1.930   1.853   2.033   2.500
```

On this page

EXAMPLES OF FILES & TEST DATA EJAM CAN IMPORT OR OUTPUT

USING NAICS AND SIC CODES TO LOCATE FACILITIES BY INDUSTRY

HOW TO ANALYZE PROXIMITY USING EJAM

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