TADA Cybertown Workshop June 2025

TADA Team

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Accessing vignette

A vignette is a long-form guide to a package often written as a R Markdown document, such as this one. It provides detailed explanations of functions and showcases an example workflow. This vignette can be created as an html document or other format using the knit option on the top of the RStudio toolbar. Users can also access this vignette on the EPATADA Github page found (here).

Install

First, install and load the remotes package specifying the repo. This is needed before installing the *EPATADA* R package because it is only available on GitHub.

```r
install.packages("remotes", repos = "http://cran.us.r-project.org")
library(remotes)
```

Next, install (or update) the *EPATADA* R package using the *remotes* R package. Additional dependency R packages that are used within *EPATADA* will be downloaded automatically. You may be prompted in the console to update dependency packages that have more recent versions available. If you see this prompt, it is recommended to update all of them (enter 1 into the console). Our team is actively developing *EPATADA*, therefore we highly recommend that you update the package (and all of its dependencies) each time you use it.

```r
remotes::install_github("USEPA/EPATADA", ref = "develop", dependencies = TRUE
)
```

Load the EPATADA R Package.

```r
library(EPATADA)
```

Record start time

```r
start.time <- Sys.time()
```

Retrieve

Query the WQP using TADA_DataRetrieval. TADA_AutoClean is a powerful function that runs as part of TADA_DataRetrieval when applyautoclean = TRUE. It performs a variety of tasks, for example:

1. creating new “TADA” prefixed columns and and capitalizing their contents to reduce case sensitivity issues,
2. converts special characters in value columns,
3. converts latitude and longitude values to numeric,
4. replaces “meters” with “m”,
5. replaces deprecated characteristic names with current WQX names,
6. harmonizes result and detection limit units,
7. converts depths to meters, and
8. creates the column TADA.ComparableDataIdentifier by concatenating characteristic name, result sample fraction, method speciation, and result measure unit.

In this example, we will first leverage EPA’s How’s My Waterway (HMW) application to discover an ATTAINS Assessment Unit of interest (example waterbody report). Then, we will use the Assessment Unit ID to query ATTAINS geospatial services for the associated shapefile (polygon area of the Assessment Unit). Now we can use this shapefile (only works for polygons for now) as our input for the new aoi_sf query option included in TADA_DataRetrieval. This allows us to download WQP data within the Assessment Unit (our area of interest/AOI).

```
query.params <- list(
  where = "assessmentunitidentifier IN ('CT6400-00-1-L5_01')",
  outFields = "*",
  f = "geojson"
)

url <- "https://gispub.epa.gov/arcgis/rest/services/OW/ATTAINS_Assessment/Map
Server/2/query?"

poly.response <- httr::GET(url, query = query.params)

poly.geojson <- httr::content(poly.response, as = "text", encoding = "UTF-8")

poly.sf <- sf::st_read(poly.geojson, quiet = TRUE)

WQP_raw <- TADA_DataRetrieval(
  startDate = "null",
  endDate = "null",
  aoi_sf = poly.sf,
  countrycode = "null",
  countycode = "null",
  huc = "null",
  siteid = "null",
  siteType = "null",
  tribal_area_type = "null",
  tribe_name_parcel = "null",
  characteristicName = "null",
  characteristicType = "null",
  sampleMedia = "null",
  statecode = "null",
  organization = "null",
  project = "null",
  providers = "null",
  bBox = "null",
  maxrecs = 350000,
  ask = FALSE,
  applyautoclean = TRUE
)
```

```
## [1] "Downloading WQP query results. This may take some time depending upon
the query size."
## list()
## [1] "Data successfully downloaded. Running TADA_AutoClean function."
## [1] "TADA_Autoclean: creating TADA-specific columns."
## [1] "TADA_Autoclean: harmonizing dissolved oxygen characterisic name to DI
SSOLVED OXYGEN SATURATION if unit is % or % SATURATN."
## [1] "TADA_Autoclean: handling special characters and coverting TADA.Result
MeasureValue and TADA.DetectionQuantitationLimitMeasure.MeasureValue value fi
elds to numeric."
## [1] "TADA_Autoclean: converting TADA.LatitudeMeasure and TADA.LongitudeMea
sure fields to numeric."
## [1] "TADA_Autoclean: harmonizing synonymous unit names (m and meters) to m
."
## [1] "TADA_Autoclean: updating deprecated (i.e. retired) characteristic nam
es."
## [1] "No deprecated characteristic names found in dataset."
## [1] "TADA_Autoclean: harmonizing result and depth units."
## [1] "TADA_Autoclean: creating TADA.ComparableDataIdentifier field for use
when generating visualizations and analyses."
## [1] "NOTE: This version of the TADA package is designed to work with numer
ic data with media name: 'WATER'. TADA_AutoClean does not currently remove (f
ilter) data with non-water media types. If desired, the user must make this s
pecification on their own outside of package functions. Example: dplyr::filte
r(.data, TADA.ActivityMediaName == 'WATER')"
```

```
# # For demo purposes, we pre-downloaded this example data
# WQP_raw <- cybertown
```

Remove intermediate variables in R by using ‘rm()’.

```
rm(poly.response, poly.sf, query.params, poly.geojson, url)
```

Flag, clean, and visualize

Now, let's use EPATADA functions to review, visualize, and whittle the returned WQP data down to include only results that are applicable to our water quality analysis and area of interest.

TADA is primarily designed to accommodate water data from the WQP. Let's see what activity media types are represented in the data set. Are there any media type that are not water in our data frame?

```
# Create table with count for each ActivityMediaName
TADA_FieldValuesTable(
  WQP_raw,
  field = "ActivityMediaName",
  characteristicName = "null"
  )

##   Value Count
## 1 Water   990
```

The **TADA_AnalysisDataFilter** function can assist in identifying and filtering surface water, groundwater, and sediment results. If you set clean = FALSE, this function will categorize and flag (but not remove) rows in a new *TADA.UseForAnalysis.Flag* column for review. However, the default functionality (clean = TRUE) is to include surface water and exclude groundwater and sediment results. For this example, we will choose to exclude any results that have been explicitly identified as groundwater or sediment if any results were found. Our data set does not contain any ground water or sediment results to remove.

```
WQP_flag <- TADA_AnalysisDataFilter(
  WQP_raw,
  clean = FALSE,
  surface_water = TRUE,
  ground_water = FALSE,
  sediment = FALSE
)

## [1] "TADA_AnalysisDataFilter: Identifying groundwater results."
## [1] "TADA_AnalysisDataFilter: Flagging surface water results to include in
assessments."
## [1] "TADA_AnalysisDataFilter: Flagging groundwater results to exclude from
assessments."
## [1] "TADA_AnalysisDataFilter: Flagging sediment results to exclude from as
sessments."
## [1] "TADA_AnalysisDataFilter: Returning all results with TADA.UseForAnalys
is.Flag column indicating if result should be used for assessments."

# Review unique flags
unique(WQP_flag$TADA.UseForAnalysis.Flag)

## [1] "Yes - SURFACE WATER" "No - NA"
```

```r
# Keep rows that are NOT flagged as sediment (keep SW and NA)
WQP_clean <- WQP_flag %>%
  dplyr::filter(TADA.UseForAnalysis.Flag != "No - SEDIMENT")
```

Create an overview map.

```r
TADA_OverviewMap(WQP_clean)
```

Let's take a quick look at all unique values in the MonitoringLocationIdentifier column and see how how many results are associated with each.

```r
# use TADA_FieldValuesTable to create a table of the number of results per Mo
nitoringLocationIdentifier
sites <- TADA_FieldValuesTable(
  WQP_clean,
  field = "MonitoringLocationIdentifier",
  characteristicName = "null"
  )

DT::datatable(sites, fillContainer = TRUE)
```

Are there sites located within 100 meters of each other?

```r
WQP_clean <- TADA_FindNearbySites(
  WQP_clean,
  dist_buffer = 100,
  nhd_res = "Hi",
  org_hierarchy = "none",
  meta_select = "random"
  )

## [1] "TADA_FindNearbySites: No org_hierarchy supplied by user. Organization
will not be taken into account during metadata selection."

TADA_NearbySitesMap(WQP_clean)
```

Now let's review all unique values in the TADA.ComparableDataIdentifier column and see how how many results are associated with each. TADA.ComparableDataIdentifier concatenates TADA.CharacteristicName, TADA.ResultSampleFractionText, TADA.MethodSpeciationName, and TADA.ResultMeasure.MeasureUnitCode.

```r
# use TADA_FieldValuesTable to create a table of the number of results per TA
DA.ComparableDataIdentifier
chars <- TADA_FieldValuesTable(
  WQP_clean,
  field = "TADA.ComparableDataIdentifier",
  characteristicName = "null"
  )

DT::datatable(chars, fillContainer = TRUE)
```

Remove intermediate variables in R by using ‘rm()’.

```
rm(chars, sites, WQP_flag_review, WQP_flag)
```

Next, let’s check if the dataset contains potential duplicate results from within a single organization or from within multiple organizations (such as when two or more organizations monitor the same location and may submit duplicate results).

If you would like to prioritize results from one organization over another, this can be done using the org_hierarchy argument in `TADA_FindPotentialDuplicatesMultipleOrgs`.

```
# find duplicates from single org
WQP_flag <- TADA_FindPotentialDuplicatesSingleOrg(WQP_clean)

## [1] "TADA_FindPotentialDuplicatesSingleOrg: 69 groups of potentially dupli
cated results found in dataset. These have been placed into duplicate groups
in the TADA.SingleOrgDupGroupID column and the function randomly selected one
result from each group to represent a single, unduplicated value. Selected va
lues are indicated in the TADA.SingleOrgDup.Flag as 'Unique', while duplicate
s are flagged as 'Duplicate' for easy filtering."

# Review organizations. You can select one to prioritize in TADA_FindPotentia
lDuplicatesMultipleOrgs
unique(WQP_flag$OrganizationIdentifier)

## [1] "USGS-CT"  "CT_DEP01" "NALMS"    "CTVOLMON"

unique(WQP_flag$OrganizationFormalName)

## [1] "USGS Connecticut Water Science Center"
## [2] "Connecticut Dept. of Environmental Protection"
## [3] "North American Lake Management Society"
## [4] "CT DEEP Volunteer Water Monitoring Program (Volunteer)"

# find duplicates across multiple orgs
WQP_flag <- TADA_FindPotentialDuplicatesMultipleOrgs(
  WQP_flag,
  org_hierarchy = c("CT_DEP01", "USGS-CT", "CTVOLMON", "NALMS")
)

## [1] "No duplicate results detected. Returning input dataframe with duplica
te flagging columns set to 'N'."
```

Let’s review the duplicates:

```
WQP_flag_review <- WQP_flag %>%
  dplyr::select(
    MonitoringLocationName,
    TADA.MonitoringLocationIdentifier,
    # TADA.MultipleOrgDuplicate,
    # TADA.MultipleOrgDupGroupID,
    # TADA.ResultSelectedMultipleOrgs,
    TADA.SingleOrgDupGroupID,
    TADA.SingleOrgDup.Flag,
    TADA.ComparableDataIdentifier,
    ResultMeasureValue,
    TADA.ResultMeasure.MeasureUnitCode,
    TADA.MonitoringLocationName,
    TADA.NearbySites.Flag,
    TADA.NearbySiteGroup,
    OrganizationIdentifier
  ) %>%
  dplyr::filter(TADA.SingleOrgDupGroupID != "Not a duplicate") %>%
  dplyr::distinct()
```

We will select to keep only unique samples from `TADA_FindPotentialDuplicatesSingleOrg` by filtering for TADA.SingleOrgDup.Flag equals “Unique”.

There are no multiple org duplicates from `TADA_FindPotentialDuplicatesMultipleOrgs` in this example, but if there were, duplicates can by removed by filtering for TADA.ResultSelectedMultipleOrgs equals “Y”.

```
WQP_clean <- WQP_flag %>%
  dplyr::filter(TADA.SingleOrgDup.Flag == "Unique") %>%
  dplyr::filter(TADA.ResultSelectedMultipleOrgs == "Y")
```

Remove intermediate variables in R by using ‘rm()’. In the remainder of this workshop, we will work with the clean data set.

```
rm(WQP_flag, WQP_flag_review)
```

Censored data are measurements for which the true value is not known, but we can estimate the value based on known lower or upper detection conditions and limit types. TADA fills missing *TADA.ResultMeasureValue* and *TADA.ResultMeasure.MeasureUnitCode* values with values and units from *TADA.DetectionQuantitationLimitMeasure.MeasureValue* and *TADA.DetectionQuantitationLimitMeasure.MeasureUnitCode*, respectively, using the `TADA_AutoClean` function.

The TADA package currently has functions that summarize censored data incidence in the dataset and perform simple substitutions of censored data values, including x times the detection limit and random selection of a value between 0 and the detection limit. The user may specify the methods used for non-detects and over-detects separately in the input to the `TADA_SimpleCensoredMethods` function. The next step we take in this example is to perform simple conversions to the censored data in the dataset: we keep over-detects as is (no conversion made) and convert non-detect values to 0.5 times the detection limit (half the detection limit).

```
WQP_clean <- TADA_SimpleCensoredMethods(
  WQP_clean,
  nd_method = "multiplier",
  nd_multiplier = 0.5,
  od_method = "as-is",
  od_multiplier = "null"
)
```

```
## [1] "Dataframe does not include any information (all NA's) in MeasureQuali
fierCode."
## [1] "TADA_IDCensoredData: No censored data detected in your dataframe. Ret
urning input dataframe with new column TADA.CensoredData.Flag set to Uncensor
ed"
## [1] "Cannot apply simple censored methods to dataframe with no censored da
ta results. Returning input dataframe."
```

`TADA_AutoFilter` removes rows where the result value is not numeric to prepare a dataframe for quantitative analyses. Specifically, this function removes rows with "Text" and "NA - Not Available" in the TADA.ResultMeasureValueDataTypes.Flag column, or NA in the TADA.ResultMeasureValue column. In addition, this function removes results with QA/QC ActivityTypeCode's. This function also removes any columns not required for TADA workflow where all values are equal to NA.

```
WQP_clean <- TADA_AutoFilter(WQP_clean)
```

```
## [1] "Quality control samples have been removed or were not present in the
input dataframe. Returning dataframe with TADA.ActivityType.Flag column for t
racking."
## [1] "TADA_Autofilter: removing columns not required for TADA workflow if t
hey contain only NAs."
## [1] "The following column(s) were removed as they contained only NAs: Acti
vityDepthAltitudeReferencePointText, ActivityEndDate, ActivityEndTime.Time, A
ctivityEndTime.TimeZoneCode, SampleAquifer, ResultTemperatureBasisText, Binar
yObjectFileName, BinaryObjectFileTypeCode, AnalysisStartDate, ResultDetection
QuantitationLimitUrl, LabSamplePreparationUrl, SourceMapScaleNumeric, Vertica
lAccuracyMeasure.MeasureValue, VerticalAccuracyMeasure.MeasureUnitCode, Verti
calCollectionMethodName, FormationTypeText, ProjectMonitoringLocationWeightin
gUrl, DrainageAreaMeasure.MeasureValue, DrainageAreaMeasure.MeasureUnitCode,
ContributingDrainageAreaMeasure.MeasureValue and ContributingDrainageAreaMeas
ure.MeasureUnitCode."
## [1] "TADA_Autofilter: checking required columns for non-NA values."
## [1] "TADA Required column(s) SubjectTaxonomicName, SampleTissueAnatomyName
, MethodSpeciationName, TADA.MethodSpeciationName, ResultDetectionConditionTe
xt, DetectionQuantitationLimitTypeName, DetectionQuantitationLimitMeasure.Mea
sureValue, DetectionQuantitationLimitMeasure.MeasureUnitCode, TADA.DetectionQ
uantitationLimitMeasure.MeasureValue, TADA.DetectionQuantitationLimitMeasure.
MeasureUnitCode, ResultDepthAltitudeReferencePointText, ActivityRelativeDepth
Name, ActivityDepthHeightMeasure.MeasureValue, TADA.ActivityDepthHeightMeasur
e.MeasureValue, ActivityDepthHeightMeasure.MeasureUnitCode, TADA.ActivityDept
hHeightMeasure.MeasureUnitCode, ActivityTopDepthHeightMeasure.MeasureValue, T
ADA.ActivityTopDepthHeightMeasure.MeasureValue, ActivityTopDepthHeightMeasure
.MeasureUnitCode, TADA.ActivityTopDepthHeightMeasure.MeasureUnitCode, Activit
```

```
yBottomDepthHeightMeasure.MeasureValue, TADA.ActivityBottomDepthHeightMeasure
.MeasureValue, ActivityBottomDepthHeightMeasure.MeasureUnitCode, TADA.Activit
yBottomDepthHeightMeasure.MeasureUnitCode, ResultTimeBasisText, StatisticalBa
seCode, ResultFileUrl, ResultAnalyticalMethod.MethodName, ResultAnalyticalMet
hod.MethodDescriptionText, ResultAnalyticalMethod.MethodUrl, MeasureQualifier
Code, DataQuality.PrecisionValue, DataQuality.BiasValue, DataQuality.Confiden
ceIntervalValue, DataQuality.UpperConfidenceLimitValue, DataQuality.LowerConf
idenceLimitValue, LaboratoryName, ResultLaboratoryCommentText, ProjectFileUrl
, AquiferName, AquiferTypeName, LocalAqfrName, ConstructionDateText, WellDept
hMeasure.MeasureValue, WellDepthMeasure.MeasureUnitCode, WellHoleDepthMeasure
.MeasureValue and WellHoleDepthMeasure.MeasureUnitCode contain only NA values
. This may impact other TADA functions."
## [1] "Function removed 189 results. These results are either text or NA and
cannot be plotted or represent quality control activities (not routine sample
s or measurements)."
```

TADA_RunKeyFlagFunctions is a shortcut function to run important TADA flagging functions. See ?function documentation for TADA_FlagResultUnit, TADA_FlagFraction, TADA_FindQCActivities, TADA_FlagMeasureQualifierCode, and TADA_FlagSpeciation for more information.

```
WQP_clean <- TADA_RunKeyFlagFunctions(
  WQP_clean,
  clean = TRUE
)

## [1] "Quality control samples have been removed or were not present in the
input dataframe. Returning dataframe with TADA.ActivityType.Flag column for t
racking."
## [1] "Dataframe does not include any information (all NA's) in MeasureQuali
fierCode."
```

Another set of TADA flagging functions, `TADA_FlagAboveThreshold` and `TADA_FlagBelowThreshold`, can be used to check results against national lower and upper thresholds. For these, we will set clean = FALSE and flaggedonly = TRUE so that it returns only flagged results in the review dataframe returned. We will keep these in our “clean” dataframe for now.

```
WQP_flag_reviewabove <- TADA_FlagAboveThreshold(WQP_clean, clean = FALSE, fla
ggedonly = TRUE)

WQP_flag_reviewbelow <- TADA_FlagBelowThreshold(WQP_clean, clean = FALSE, fla
ggedonly = TRUE)

## [1] "This dataframe is empty because no data below the WQX Lower Threshold
was found in your dataframe"
```

Remove intermediate variables.

```
rm(WQP_flag_reviewabove, WQP_flag_reviewbelow)
```

Let’s take another look at all unique values in the TADA.ComparableDataIdentifier column and see how how many results are associated with each. TADA.ComparableDataIdentifier concatenates TADA.CharacteristicName, TADA.ResultSampleFractionText, TADA.MethodSpeciationName, and TADA.ResultMeasure.MeasureUnitCode.

```
# use TADA_FieldValuesTable to create a table of the number of results per TA
DA.ComparableDataIdentifier
chars <- TADA_FieldValuesTable(
  WQP_clean,
  field = "TADA.ComparableDataIdentifier",
  characteristicName = "null"
  )

chars_before <- unique(WQP_clean$TADA.ComparableDataIdentifier)

DT::datatable(chars, fillContainer = TRUE)
```

Scroll through the table and check to see if there any synonyms. It may be possible that some of these can be automatically harmonized using `TADA_HarmonizeSynonyms` so their results can be directly compared.

Let’s give it a try.

```
WQP_clean <- TADA_HarmonizeSynonyms(WQP_clean)
```

How many unique TADA.ComparableDataIdentifier’s do we have now? In this example, there were no synonyms.

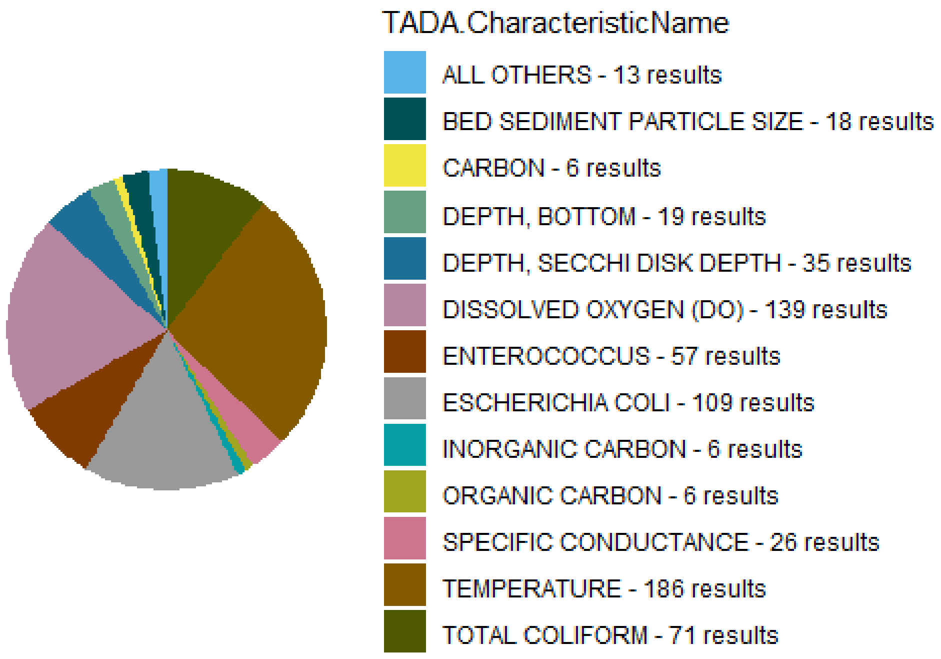
```
chars_after <- unique(WQP_clean$TADA.ComparableDataIdentifier)
```

Remove intermediate variables.

```
rm(chars_before, chars_after)
```

Create a pie chart.

```
TADA_FieldValuesPie(
  WQP_clean,
  field = "TADA.CharacteristicName",
  characteristicName = "null"
  )
```



Select characteristic

Let's filter the data and focus on a one characteristic of interest.

```
# Select characteristics of interest
WQP_clean_subset <- WQP_clean %>%
  dplyr::filter(TADA.CharacteristicName %in% "ESCHERICHIA COLI")
```

Remove intermediate variables. We will focus on the subset from now on.

```
rm(WQP_clean, chars)
```

Integrate ATTAINS and map

In this section, we will associate geospatial data from **ATTAINS** with the **WQP** data. Our initial WQP data pull was done using a shapefile for Assessment Unit CT6400-00-1-L5_01. TADA functions can pull in additional ATTAINS meta data for this assessment unit. We can also generate a new table to give us some information about the individual monitoring locations within this assessment unit.

- TADA_GetATTAINS() automates matching of WQP monitoring locations with ATTAINS assessment units that fall within (intersect) the same NHDPlus catchment (details)

- The function uses high resolution NHDPlus catchments by default because 80% of state submitted assessment units in ATTAINS were developed based on high res NHD; users can select med-res if applicable to their use case

```
WQP_clean_subset_spatial <- TADA_GetATTAINS(
  WQP_clean_subset,
  return_nearest = TRUE,
  fill_catchments = FALSE,
  resolution = "Hi",
  return_sf = TRUE
)

# Adds ATTAINS info to df
WQP_clean_subset <- WQP_clean_subset_spatial$TADA_with_ATTAINS
```

View catchments and assessment units on map

```
ATTAINS_map <- TADA_ViewATTAINS(WQP_clean_subset_spatial)

ATTAINS_map
```

Remove intermediate variables:

```
rm(ATTAINS_map)
```

Create table of monitoring location identifiers and AUs.

```
ML_AU_crosswalk <- WQP_clean_subset %>%
  dplyr::select(TADA.MonitoringLocationIdentifier, ATTAINS.assessmentunitiden
tifier, ATTAINS.assessmentunitname, TADA.CharacteristicName) %>%
  dplyr::distinct()
```

Remove intermediate variables. Let's keep going with WQP_clean_subset.

```
rm(ML_AU_crosswalk, WQP_clean_subset_spatial)
```

`TADA_RetainRequired` removes all duplicate columns where TADA has created a new column with a TADA prefix. It retains all TADA prefixed columns as well as other original fields that are either required by other TADA functions or are commonly used filters.

```
WQP_clean_subset <- TADA_RetainRequired(WQP_clean_subset)

## [1] "TADA_RetainRequired: removing columns not required for TADA workflow
including original columns that have been replaced with TADA prefix duplicate
s."
## [1] "The following non-required columns were removed: ActivityConductingOr
ganizationText, ActivityLocation.LatitudeMeasure, ActivityLocation.LongitudeM
easure, ResultWeightBasisText, ResultParticleSizeBasisText, USGSPCode, Activi
tyStartTime.TimeZoneCode_offset, HorizontalAccuracyMeasure.MeasureValue, Hori
zontalAccuracyMeasure.MeasureUnitCode, HorizontalCollectionMethodName, Vertic
alMeasure.MeasureValue, VerticalMeasure.MeasureUnitCode, VerticalCoordinateRe
ferenceSystemDatumName, ProviderName and LastUpdated."
```

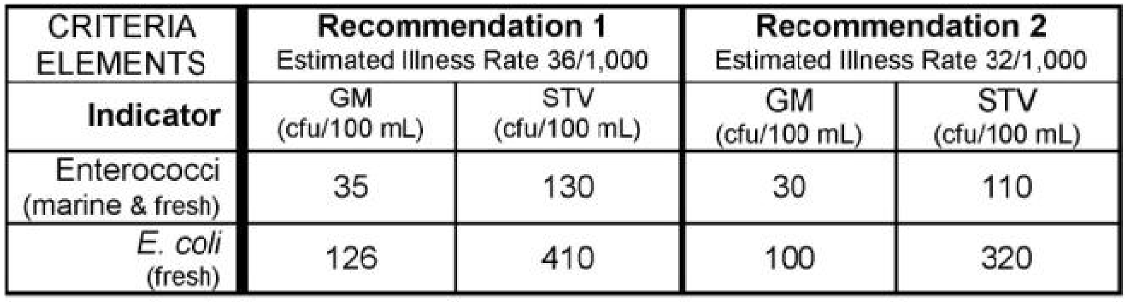
Exploratory analysis

Review unique TADA.ComparableDataIdentifier’s

```
unique(WQP_clean_subset$TADA.ComparableDataIdentifier)

## [1] "ESCHERICHIA COLI_NA_NA_CFU/100ML"
```

Let’s check if any results are above the EPA 304A recommended maximum criteria magnitude (see: 2012 Recreational Water Quality Criteria Fact Sheet).



CRITERIA ELEMENTS	Recommendation 1 Estimated Illness Rate 36/1,000		Recommendation 2 Estimated Illness Rate 32/1,000	
Indicator	GM (cfu/100 mL)	STV (cfu/100 mL)	GM (cfu/100 mL)	STV (cfu/100 mL)
Enterococci (marine & fresh)	35	130	30	110
E. coli (fresh)	126	410	100	320

If interested, you can find other state, tribal, and EPA 304A criteria in EPA’s Criteria Search Tool.

Let’s check if any individual results exceed 320 CFU/100mL (the magnitude component of the EPA recommendation 2 criteria for ESCHERICHIA COLI).

```
# add column with comparison to criteria mag (excursions)
WQP_clean_subset <- WQP_clean_subset %>%
  sf::st_drop_geometry() %>%
  dplyr::mutate(meets_criteria_mag = ifelse(TADA.ResultMeasureValue <= 320, "
Yes", "No"))

# review
WQP_clean_subset_review <- WQP_clean_subset %>%
  dplyr::select(
    MonitoringLocationIdentifier, OrganizationFormalName, ActivityStartDate,
TADA.ResultMeasureValue,
    meets_criteria_mag
  )

DT::datatable(WQP_clean_subset_review, fillContainer = TRUE)
```

Generate stats table. Review percentiles. Less than 5% of results fall above 10 CFU/100mL, and over 98% of results fall below 265.2 CFU/100m.

```
WQP_clean_subset_stats <- WQP_clean_subset %>%
  sf::st_drop_geometry() %>%
  TADA_Stats()
```

Generate a scatterplot. One result value is above the threshold.

```r
TADA_Scatterplot(WQP_clean_subset, id_cols = "TADA.ComparableDataIdentifier")
%>%
  plotly::add_lines(
    y = 320,
    x = c(min(WQP_clean_subset$ActivityStartDate), max(WQP_clean_subset$Activ
ityStartDate)),
    inherit = FALSE,
    showlegend = FALSE,
    line = list(color = "red"),
    hoverinfo = "none"
  )
```

Generate a histogram.

```r
TADA_Histogram(WQP_clean_subset, id_cols = "TADA.ComparableDataIdentifier")
```

TADA_Boxplot can be useful for identifying skewness and percentiles.

```r
TADA_Boxplot(WQP_clean_subset, id_cols = "TADA.ComparableDataIdentifier")
```

Record end time

```r
end.time <- Sys.time()

end.time - start.time

## Time difference of 39.14603 secs
```

Reproducible and Documented

This workflow is reproducible and the decisions at each step are well documented. This means that it is easy to go back and review every step, understand the decisions that were made, make changes as necessary, and run it again.