

```

# source ("C:/data/program/R/NMMP_WMA_web.R")
#-----
DateStamp <- function(typ) {
  Copyright.statement <- "Please acknowledge source: Resource Quality Information Services, Department of Water and
  Author <- c("Michael Silberbauer")
  # File.description comment
  program.purpose <-
    "Summarise _Escherichia coli_, faecal coliform and turbidity data from the national microbiological monitoring program
  program.inputs <- "The national water quality database, WMS"
  program.outputs <-
    "Tables, time series plots and maps for each Water Management Area, showing (E. coli || faecal coliforms) && turbidity
  ver <- 0.1 # 2011-06-03 Michael Silberbauer and Willie Geldenhuys - ODBC connection to wmsdb
  ver <- 1.0 # 2011-07-13 Michael Silberbauer plot NMMP data by WMS
  ver <- 1.1 # 2011-07-26 Deon van Zyl monster SQL query
  ver <- 1.11 # 2011-08-19 Michael Silberbauer - fix error in link to image file: basename() saves the day!
  ver <- 1.2 # 2011-08-19 Michael Silberbauer - make key table more compact, add town names
  ver <- 1.3 # 2011-09-23 Michael Silberbauer - add links to googleVis time series plots
  ver <- 1.31 # 2011-09-26 Michael Silberbauer - change 'Home' to index.asp
  ver <- 1.4 # 2011-10-18 Michael Silberbauer - add Google Analytics tracker script
  ver <- 1.5 # 2011-10-18 Michael Silberbauer - add risk legend to E. coli plot
  ver <- 1.6 # 2011-10-21 Michael Silberbauer - add versioning
  ver <- 2.01 # 2011-11-18 Michael Silberbauer - add layer of 'year' index files http://www.dwa.gov.za/iwqs/microbio/rep
  ver <- 2.02 # 2011-11-30 Michael Silberbauer - fix swapped temperature and turbidity columns noted by Kevin Murray
  ver <- 2.03 # 2011-12-02 Michael Silberbauer - add link to KMZ files created by NMMP_KML_balloons.R
  ver <- 2.04 # 2011-12-05 Michael Silberbauer - rowspan and colspan to insert "Risk" header
  ver <- 2.1 # 2012-02-10 Michael Silberbauer - fade out lines connecting points on two-month plots, because the data
  ver <- 2.11 # 2012-02-10 Michael Silberbauer - changed lowest permitted value for E. coli to 0.5 to avoid crashing log
  ver <- 2.12 # 2012-02-13 Michael Silberbauer - fix leap year use in file name for 'fil.nx'
  ver <- 2.13 # 2012-03-07 Michael Silberbauer - round E. coli value in table, so that '0.5' reverts to zero
  ver <- 2.14 # 2012-03-15 Michael Silberbauer - add link to PNG full record time series plots
  ver <- 2.15 # 2012-04-05 Michael Silberbauer - no change: added TODO to flag multiple records for same day, usually
  ver <- 2.16 # 2012-05-10 Michael Silberbauer - no change: altered name of script to NMMP_WMA_web.R from RODB
  ver <- 3.0 # 2012-05-23 Michael Silberbauer - change selection of sites in WMA to use the nms_wms-geo.shp file cre
  ver <- 3.1 # 2012-05-25 Michael Silberbauer - remove some bugs introduced in version 3.0
  ver <- 3.2 # 2012-05-28 Michael Silberbauer - remove more bugs introduced in version 3.0, related to selection of site
  ver <- 3.3 # 2012-05-31 Michael Silberbauer - fix selection of NMMP sites from stn shapefile
  ver <- 3.4 # 2012-07-20 Michael Silberbauer - make selection of NMMP sites by WMA from stn shapefile more robust
  ver <- 3.41 # 2012-08-07 Michael Silberbauer - 2012-08-07 year2 <- as.numeric(substr(Sys.time(),1,4)) # current year
  ver <- 3.5 # 2012-09-04 Michael Silberbauer - fix high risk from full or partial contact to be 400 not 2000 in map and g
  ver <- 3.51 # 2012-10-26 Michael Silberbauer - add , rows_at_time = 1 to sqlQuery statements
  ver <- 4.0 # 2013-06-20 Michael Silberbauer - include faecal coliform data
  ver <- 4.1 # 2013-06-21 Michael Silberbauer - minor improvements to graph legend, including key to E. coli or faecal
  ver <- 4.11 # 2013-07-26 Michael Silberbauer - minor debug: if (file.exists(fil.fpng) )
  ver <- 4.12 # 2013-07-29 Michael Silberbauer - minor text change from "Risk based on E. coli where present" to "Risk
  ver <- 4.2 # 2013-09-10 Michael Silberbauer - use common toTitle()
  ver <- 4.3 # 2014-05-02 Michael Silberbauer - create a new index.asp file during each run
  ver <- 4.4 # 2014-07-02 Michael Silberbauer - source the auxiliary scripts automatically, if auto.xtras is TRUE
  ver <- 4.5 # 2014-07-07 Michael Silberbauer - fix erroneous http://www.dwa.gov.za/iwqs/ in DateStamp()
  ver <- 4.51 # 2014-08-07 Michael Silberbauer - checked whether map legend should be part of map itself - decided a
  ver <- 4.6 # 2014-10-28 Michael Silberbauer - change settings for https server by making html references relative to /
  #
    - update names of department and directorate
  ver <- 4.7 # 2014-10-28 Michael Silberbauer - embed miniplot in table
  ver <- 5.0 # 2014-12-09 Michael Silberbauer - update all WMA references and maps - use separate 2004, 2012 web p
  ver <- 5.1 # 2014-12-11 Michael Silberbauer - deal with the plague of bugs emanating from separate 2004, 2012 web
  ver <- 5.2 # 2014-12-12 Michael Silberbauer - move index file fil.html into 2004, 2012 directories
  ver <- 5.3 # 2014-12-17 Michael Silberbauer - change "pathogenic bacteria" to "microbial pathogens"; add favicon to
  ver <- 5.3 # 2014-12-23 Michael Silberbauer - fix link to NMMP_notes.htm; remove style from index.asp table

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TODO : think how to deal with very high turbidity on time series plots, e.g. log y or cutoff with ^
 # TODO : differentiate between active and inactive sites as suggested by Deon:
 # : ps.sample_term_ind = 0 AND ----- slegs aktiewe samples
 # TODO : extract all required data from WMS into a table at the start, then query the table thereafter?
 # TODO : create a single legend to include at the bottom of the HTML file next to <td><img src=\"loc_\", pf.wman,\".png

```
scr.ver <- paste("NMMP_WMA_web.R ver", ver)
if (typ=="txt") DateStamp <-
  paste("Data from the NMMP programme. Plotted at Resource Quality Information Services, Department of Water and Sanitation, c",
    format(Sys.time(), "%Y-%m-%d %H:%M:%S"), " using ", scr.ver, " under ", R.version.string, sep="")
if (typ=="htm") DateStamp <-
  paste("<hr /><br /><small>",
    "Data from the Water Management System, <a href=\"iwqs/microbio/nmmp.html\">NMMP</a> programme. ",
    "Plotted at <a href=\"iwqs/\">Resource Quality Information Services</a>, Department of Water and Sanitation, c",
    format(Sys.time(), "%Y-%m-%d %H:%M:%S"), "\nusing the script ", scr.ver, " under ", R.version.string,
    "</small>", sep="")
return(DateStamp)
}
#-----
WmsCheck <- function(queryresult) {
  if("ERROR:" %in% unlist(strsplit(as.character(queryresult), split=" "))) {
    print(noquote(queryresult))
    print(noquote(DateStamp("txt")))
    stop("error in result of query")
  }
}
#-----
HTMLIndex <- function(yr1, yr2, fil.html) {
  write("<!--#include virtual=\"iwqs/Includes/bighead.inc\" -->", file=fil.html)
  write(" <table width=\"100%\" border=\"0\" cellpadding=\"0\" cellspacing=\"0\">", file=fil.html, append=TRUE)
  write(" <tr>", file=fil.html, append=TRUE)
  write(" <!-- left column = main menu -->", file=fil.html, append=TRUE)

  write(" <td width=\"12%\" rowspan=\"3\" align=\"left\" valign=\"top\">", file=fil.html, append=TRUE)
  write(" background=\"http://www.dwa.gov.za/images/menubg_06b.gif\">", file=fil.html, append=TRUE)
  write(" bgcolor=\"#F0F6F3\">", file=fil.html, append=TRUE)
  #write(" <!-- #include virtual=\"IWQS/Includes/leftmenu.inc\" -->", file=fil.html, append=TRUE)# obsolete
  write(" </td>", file=fil.html, append=TRUE)
  write(" <!-- spacer column -->", file=fil.html, append=TRUE)

  write(" <td width=\"1%\" height=\"100%\" rowspan=\"3\" align=\"left\">", file=fil.html, append=TRUE)
  write(" valign=\"top\">", file=fil.html, append=TRUE)
  write(" </td>", file=fil.html, append=TRUE)
  write(" <!-- middle column = main text -->", file=fil.html, append=TRUE)

  write(" <td width=\"64%\" rowspan=\"3\" valign=\"top\">", file=fil.html, append=TRUE)
  write(" <table cellspacing=\"0\" cellpadding=\"0\" width=\"100%\">", file=fil.html, append=TRUE)
  write(" border=\"0\">", file=fil.html, append=TRUE)
  write(" <tbody>", file=fil.html, append=TRUE)
  write(" <!-- spacer row -->", file=fil.html, append=TRUE)

  write(" <tr>", file=fil.html, append=TRUE)
  write(" <td height=\"9\" valign=\"middle\">", file=fil.html, append=TRUE)
  write(" </td>", file=fil.html, append=TRUE)

  write(" <td height=\"9\">", file=fil.html, append=TRUE)
  write(" </td>", file=fil.html, append=TRUE)
  write(" </tr>", file=fil.html, append=TRUE)
```

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write("        <!-- heading row ==-->", file=fil.html, append=TRUE)

write("        <tr>", file=fil.html, append=TRUE)
write("        <td valign=\"middle\"><img height=\"11\" alt=\"bullet\"", file=fil.html, append=TRUE)
write("        src=\"", file=fil.html, append=TRUE)
write("        \"/iwqs/images/goldTriangleBig.gif\"", file=fil.html, append=TRUE)
write("        width=\"6\" align=\"right\"></td>", file=fil.html, append=TRUE)

write("        <td width=\"100%\">", file=fil.html, append=TRUE)
write("        <h1>National Microbiological Monitoring Programme Bi-monthly Assessments</h1>",
      file=fil.html, append=TRUE)
write("        </td>", file=fil.html, append=TRUE)
write("        </tr>", file=fil.html, append=TRUE)
write("        <!-- content row ==-->", file=fil.html, append=TRUE)

write("        <tr>", file=fil.html, append=TRUE)
write("        <td colspan=\"2\">", file=fil.html, append=TRUE)
write("        <table cellspacing=\"0\" cellpadding=\"2\" width=\"", file=fil.html, append=TRUE)
write("        \"96%\" align=\"center\" border=\"0\">", file=fil.html, append=TRUE)
write("        <tbody>", file=fil.html, append=TRUE)
write("        <!-- spacer row --->", file=fil.html, append=TRUE)

write("        <tr>", file=fil.html, append=TRUE)
write("        <td colspan=\"2\" height=\"10\">", file=fil.html, append=TRUE)
write("        </td>", file=fil.html, append=TRUE)
write("        </tr>", file=fil.html, append=TRUE)

write("        <tr>", file=fil.html, append=TRUE)
write("        <!-- content row ==-->", file=fil.html, append=TRUE)
write("        <td valign=\"top\" colspan=\"2\">", file=fil.html, append=TRUE)
write("        <h2> ", file=fil.html, append=TRUE)
write("        <img src=\"/iwqs/images/blueTriangle.gif\"", file=fil.html, append=TRUE)
write("        width=\"5\" height=\"9\"> The ", file=fil.html, append=TRUE)
write("        <a href=\"/iwqs/microbio/nmmp.html\">NMMP</a> bi-monthly assessments",
      file=fil.html, append=TRUE)
write("        are available at the links below, grouped by WMA version", version.wma)
write("        file=fil.html, append=TRUE)
write("        </h2> ", file=fil.html, append=TRUE)

# for(year in yr2 : yr1) {
#   write(
#     paste("
#       <a href=\"NMMPkey_\", year, \".html\">", year, "</a><br />", sep=""),
#     file=fil.html, append=TRUE)
# }
# replace with table layout:
write(paste(
  "#<table id=\"hor-minimalist-b\" border summary=\"NMMP year list\", # makes an ugly table!
  "<table border=\"0\" summary=\"NMMP year list \"",
  yr1, " ", yr2, "\">", sep=""), file=fil.html, append=TRUE)
write(paste(
  "<tr><th>Year</th></tr>", sep=""), file=fil.html, append=TRUE)
for(year in yr2 : yr1) {
  write(
    paste("
      #<tr><td><a href=\"wma\", version.wma, \"/NMMPkey_\", year, \".html\">", year, "</a></td></tr>", sep=""
      "<tr><td><a href=\"NMMPkey_\", year, \".html\">", year, "</a></td></tr>", sep=""
    ),
  )
}

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    file=fil.html, append=TRUE)
}
write(paste(
  "</table>", sep=""), file=fil.html, append=TRUE)

write("          <br /><br /><p><small>Last update of this page ",
      file=fil.html, append=TRUE)
write(paste("          <!-- datestamp:begin -->",
  Sys.time(), "<!-- datestamp:end -->"), file=fil.html, append=TRUE)
write("          </small></p>", file=fil.html, append=TRUE)

write("          </td>", file=fil.html, append=TRUE)
write("          ", file=fil.html, append=TRUE)
write("        </tr>", file=fil.html, append=TRUE)
write("      </tbody>", file=fil.html, append=TRUE)
write("    </table>", file=fil.html, append=TRUE)
write("  </td>", file=fil.html, append=TRUE)
write("  </tr>", file=fil.html, append=TRUE)
write("  </tbody>", file=fil.html, append=TRUE)
write("  </table>", file=fil.html, append=TRUE)
write("  </td>", file=fil.html, append=TRUE)
write("  <!-- spacer column right --->", file=fil.html, append=TRUE)

write("    <td width=\"1%\" rowspan=\"3\" align=\"left\" valign=\"top\">", file=fil.html, append=TRUE)
write("    </td>", file=fil.html, append=TRUE)
write("    <!-- right column = date row --->", file=fil.html, append=TRUE)

write("    <td height=\"100%\" align=\"right\" valign=\"top\" bgcolor=", file=fil.html, append=TRUE)
write("    \"#F0F6F3\" class=\"captionblue\">", file=fil.html, append=TRUE)
write("    </td>", file=fil.html, append=TRUE)
write("  </tr>", file=fil.html, append=TRUE)

write("  <tr>", file=fil.html, append=TRUE)
write("  <!-- right column = right menu --->", file=fil.html, append=TRUE)

write("    <td width=\"20%\" align=\"left\" valign=\"top\" bgcolor=", file=fil.html, append=TRUE)
write("    \"#F0F6F3\">", file=fil.html, append=TRUE)
write("    <!--#include virtual=\"/iwqs/Includes/rightmenu_nmmp.inc\" -->", file=fil.html, append=TRUE)
write("    </td>", file=fil.html, append=TRUE)
write("  </tr>", file=fil.html, append=TRUE)
write("  <!-- right column = 'top' row --->", file=fil.html, append=TRUE)

write("  <tr>", file=fil.html, append=TRUE)
write("  <td style=\"padding-right:5px; padding-bottom:5px;\" align=", file=fil.html, append=TRUE)
write("  \"right\" valign=\"bottom\" bgcolor=\"#F0F6F3\" class=\"top\"><a", file=fil.html, append=TRUE)
write("  href=\"#\" style=\"color:#0C4F7A\">top</a></td>", file=fil.html, append=TRUE)
write("  </tr>", file=fil.html, append=TRUE)
write("  </table>", file=fil.html, append=TRUE)
write("  <!--#include virtual=\"/iwqs/Includes/bigfoot.inc\" -->", file=fil.html, append=TRUE)
write("  </table>", file=fil.html, append=TRUE)
}
#-----
HTMLhead <- function(htmtitle, fil.html) {
  write("<!DOCTYPE html PUBLIC \"-//W3C//DTD XHTML 1.0 Transitional//EN\" \"http://www.w3.org/TR/xhtml1/DTD/xhtml1-
  write("<html>\n<head>", file=fil.html, append=TRUE)
  write("<style type=\"text/css\">\n<!--\n @import url(\"../style_wms_nmmp.css\");\n-->\n</style>\n", file=fil.html, append=TRUE)
  write(paste("<title>", htmtitle, "</title>\n"), file=fil.html, append=TRUE)
  write(paste("<link rel=\"shortcut icon\" href=\"/iwqs/images/favicon.ico\" />\n"), file=fil.html, append=TRUE)
}

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write(paste("</head>\n<body>\n"), file=fil.htme, append=TRUE)
write(paste("<h2>", htmtitle, "</h2>"), file=fil.htme, append=TRUE)
}
#-----
cap <- function(s) {
  paste(toupper(substring(s,1,1)), tolower(substring(s,2)), sep="")
}

#-----
leapyear <- function(year) {
  leapyear=FALSE
  if(year%%4==0) {
    leapyear=TRUE
    if(year%%100==0&&year%%400!=0) leapyear=FALSE
  }
  return(leapyear)
}
#-----
fil.pr <- function(year, yr1, yr2, bim, Bm1, Bm2, nmmfil.pr, wdir, pf.wman) {
  fil.pr <- nmmfil.pr # jump to index file when in doubt
  if(year == yr1 && bim == 1) return(fil.pr)
  if(bim == 1) {
    d1 <- as.Date(paste(year - 1, Bm1[6], sep=""))
    d2 <- as.Date(paste(year - 1, Bm2[6], sep=""))
  }
  if(bim > 1) {
    d1 <- as.Date(paste(year, Bm1[bim - 1], sep=""))
    d2 <- as.Date(paste(year, Bm2[bim - 1], sep=""))
  }
  fil.pr <- paste(wdir, "coli_", pf.wman, "_", "NMMP", "_", d1, "_", d2, ".htm",
    sep="")
  return(fil.pr)
}
#-----
fil.nx <- function(year, yr1, yr2, bim, Bm1, Bm2, fil.nmmp, wdir, pf.wman) {
  fil.nx <- fil.nmmp # jump to index file when in doubt
  if(year == yr2 && bim == 6) return(fil.nx)
  if(bim == 6) {
    Bm2[1] <- "-02-28"
    if(leapyear(year + 1)) Bm2[1] <- "-02-29" # how these leap years jump out and catch you!
    print(noquote(paste("Year", year, "Bm2[1]", Bm2[1],
      "leapyear(year+1)", leapyear(year + 1),
      "Output in", wdir, "and", wdr0)
    )
  )
  d1 <- as.Date(paste(year + 1, Bm1[1], sep=""))
  d2 <- as.Date(paste(year + 1, Bm2[1], sep=""))
}
if(bim<6) {
  d1 <- as.Date(paste(year, Bm1[bim + 1], sep=""))
  d2 <- as.Date(paste(year, Bm2[bim + 1], sep=""))
}
fil.nx <- paste(wdir, "coli_", pf.wman, "_", "NMMP", "_", d1, "_", d2, ".htm",
  sep="")
return(fil.nx)
}
#-----
classtext <- function(glclassn, glrange, ecoli_max) {

```

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classtext <- paste("<=10",glclassn[1])
for(i in 1:length(glrange)) {
  #print(paste(i,glrange[i],glclassn[i]))
  if(i%%2==0) {sepa="\n"} else {sepa="; "}
  if(ecoli_max>=glrange[i]) classtext <- paste(classtext,sepa,">",glrange[i], " ",glclassn[i+1],sep="")
}
return(classtext)
}
#-----Main program -

require(RODBC)
require(maptools)
require(stringr)
# use standard totitle function
if (!exists("toTitle", mode="function")) source("C:/data/program/R/toTitle.R")

db <- "wmsdb"
channel <- odbcConnect(db)
db_unlock <- "set isolation dirty read"
sqlQuery(channel, db_unlock)

vars <- sqlQuery(channel,"select * from monitorng_variable")
vars$mon_variable_name <- str_trim(vars$mon_variable_name) # remove trailing blanks
#mv <- "E.COLI"
#varid <- subset(vars$mon_variable_id,grep(mv,vars$mon_variable_abbr))
auto.xtras <- TRUE # run the auxiliary scripts for plots, miniplots, KMLs
version.wma <- 2004 # use the old 19 Water Management Areas
#version.wma <- 2012 # use the newer 9 Water Management Areas
mvc <- c("ESCHERICHIA COLI", "FAECAL COLIFORM COUNT")
mve <- c("ESCHERICHIA COLI")
mvf <- c("FAECAL COLIFORM COUNT")
varidc <- vars$mon_variable_id[vars$mon_variable_name %in% mvc]
varide <- vars$mon_variable_id[vars$mon_variable_name %in% mve]
varidf <- vars$mon_variable_id[vars$mon_variable_name %in% mvf]

wdir <- paste0("C:/tmp/nmmp/WMA", version.wma, "/") # WMA dir for NMMP
wdr0 <- paste0("C:/tmp/nmmp/") # root dir for NMMP
#yr1 <- 1994
yr1 <- 1990
yr2 <- as.numeric(substr(Sys.time(), 1, 4)) # current year
#fil.html <- paste(wdr0, "indexwma", version.wma, ".asp", sep="") # causes complications
fil.html <- paste(wdir, "index.asp", sep="")
HTMLIndex(yr1, yr2, fil.html)

readGIS <- TRUE # skip reading GIS data during testing
if (readGIS) {
  print("Define and read geographical data...")
  #pris <- "C:/data_large/av/drainage/hca_1_simpler.shp"
  stns <- "C:/data_large/av/nms_wms_geo.shp"
  stn <- readShapePoints(stns, proj4string=CRS("+proj=longlat +datum=WGS84"))
  pris <- "C:/data_large/av/drainage/hca_1geo.shp" # polygon version
  pri <- readShapePoly(pris, proj4string=CRS("+proj=longlat +datum=WGS84"))
  #pri <- readShapeLines(pris, proj4string=CRS("+proj=longlat +datum=WGS84"))
  ters <- "C:/data_large/av/drainage/hca3geo.shp"
  ter <- readShapePoly(ters, proj4string=CRS("+proj=longlat +datum=WGS84"))
  if(version.wma == 2004) {
    wmas <- "C:/data_large/av/drainage/hrg_2004_geo_polygon.shp"
    wmargin <- readShapePoly(wmas, proj4string=CRS("+proj=longlat +datum=WGS84"))
  }
}

```

```

}
if(version.wma == 2012) {
  wmas <- "C:/data_large/av/drainage/wma2012_simple.shp"
  wmargin <- readShapePoly(wmas, proj4string=CRS("+proj=longlat +datum=WGS84"))
  names(wmargin)[which(names(wmargin) == "WMA_ID")] <- "NUMBER"
  names(wmargin)[which(names(wmargin) == "WMA_NAME")] <- "NAME"
  names(stn)[which(names(stn) == "WMANUM")] <- "WMA1NUM"
  names(stn)[which(names(stn) == "WMANAME")] <- "WMA1NAME"
  names(stn)[which(names(stn) == "WMA2NUM")] <- "WMANUM"
  names(stn)[which(names(stn) == "WMA2NAME")] <- "WMANAME"
}
#prip <- "C:/data_large/av/drainage/hca_1geo.shp" # polygon version
#prip <- readShapePoly(prip, proj4string=CRS("+proj=longlat +datum=WGS84"))
rvr <- "C:/data_large/av/drainage/wriall500_SimplifyLine_500m.shp"
rv <- readShapeLines(rvr, proj4string=CRS("+proj=longlat +datum=WGS84"))
lakes <- "C:/data_large/av/drainage/wla500g.shp"
lak <- readShapePoly(lakes, proj4string=CRS("+proj=longlat +datum=WGS84"))
towns <- "C:/data_large/av/drainage/smu_500g_simpl_pr_100m.shp"
town <- readShapePoly(towns, proj4string=CRS("+proj=longlat +datum=WGS84"))
twm <- town[!is.na(town$NAMETAG),]
twm_big <- twm[twm$AREA > quantile(twm$AREA, 97/100, type=1, na.rm=TRUE),]
twm_big <- twm_big[!duplicated(twm_big$NAMETAG),]
} else print("Assuming GIS data already in memory")

```

this step is required if selecting by an attribute that has NAs
st <- (stn[!is.na(stn\$LOC_TYPE),])

```

glcol <- c("mediumblue", "seagreen", "gold3", "red", "darkmagenta", "mediumvioletred")
glcols <- c("#0000CD", "#2E8B57", "#CDAD00", "#FF0000", "#8B008B", "#C71585")
glcol <- paste(glcols, "AA", sep="") # slight transparency for overlapping symbols
glcolpastel <- c("honeydew3", "lemonchiffon", "thistle1", "lightpink")
#glcolpastel <- c("#F0FFF0", "#FFFACD", "#FFE1FF", "#FFB6C1")
glcolpastel <- c("#C1CDC1", "#FFFACD", "#FFE1FF", "#FFB6C1")

```

```

glclassn <- c("low-med risk",
  "high risk when drinking untreated water",
  "high risk from full or partial contact",
  "high risk when irrigating crops that are eaten raw",
  "high risk when drinking after only limited treatment")
glrange <- c(10, 400, 4000, 20000)

```

Guidelines for assessing the potential health risk for the four water uses

E.coli _or_ faecal coliforms /100mL

Low High Sensitive Water Use Narrative Identifier Abbreviated Identifier

1 10 1 Drinking untreated water Guideline: >10 = high risk when drinking untreated water Untreated

200 400 2 Full or partial contact Guideline: >400 = high risk from full or partial contact Contact

1000 4000 3 Irrigation of crops eaten raw Guideline: >4 000 = high risk when irrigating crops that are eaten raw

2000 20000 4 Drinking after limited treatment Guideline: >20 000 = high risk when drinking after only limited treatment

```

gl.risk.untreated <- c(1, 10)
gl.risk.lim_treat <- c(2000, 20000)
gl.risk.irrigation <- c(1000, 4000)
gl.risk.contact <- c(200, 400)

```

```

Qn1 <- c("-01-01", "-04-01", "-07-01", "-10-01")
Qn2 <- c("-03-31", "-06-30", "-09-30", "-12-31")
Bm1 <- c("-01-01", "-03-01", "-05-01", "-07-01", "-09-01", "-11-01")
Bm2 <- c("-02-28", "-04-30", "-06-30", "-08-31", "-10-31", "-12-31")

```

```

gsizsize <- c(1.0, 1.5, 2.1, 2.5, 3.0)
gsizsize <- 2 * gsizsize

xr <- c(16.5, 33)
yr <- c(-35, -21)
xpixels <- 800
ypixels <- 600

programme.n <- 135
q <- paste("SELECT UNIQUE mon_program_id, mon_feature_id ",
  "FROM programme_sample WHERE mon_program_id = ", programme.n, sep="")
sites.nmmp <- sqlQuery(channel, q)
st <- (stn[stn$FEAT_ID %in% sites.nmmp$mon_feature_id, ])

for (year in yr1:yr2) {
  fil.nmmp <- paste(wdir, "NMMPkey_", year, ".htm", sep="")
  HTMLhead(paste("NMMP bimonthly reports for", year, "with WMA ver.", version.wma), fil.nmmp)
  write("<hr />", file=fil.nmmp, append=TRUE)
  write(paste("<a href='\"index.asp\"'>Home</a>|", sep=""), file=fil.nmmp, append=TRUE)
  write(paste("<a href='\"../NMMP_notes.html\"'>Notes</a>", sep=""), file=fil.nmmp, append=TRUE)
  write("<hr />", file=fil.nmmp, append=TRUE)
  for (bim in 1:6) {
    Bm2 <- c("-02-28", "-04-30", "-06-30", "-08-31", "-10-31", "-12-31")
    if(leapyear(year)) Bm2[1] <- "-02-29"
    Date1 <- as.Date(paste(year, Bm1[bim], sep=""))
    Date2 <- as.Date(paste(year, Bm2[bim], sep=""))
    write(paste(
      "<table id='\"hor-minimalist-b\"' border summary='\"NMMP bimonthly reports \"",
      Date1, " ", Date2, "\">", sep=""), file=fil.nmmp, append=TRUE)
    nwmas=0
    for (p in wmarg$NUMBER[wmarg$NUMBER != 0]) {
      rgn.wma <- wmarg$NAME[wmarg$NUMBER == p]
      print(paste(rgn.wma, Date1, "to", Date2))

      # Replaced the WMA parts of this query with one that uses nms_wms-geo.shp.
      if(p %in% unique(st$WMANUM)) {
        st.label <- st[st$WMANUM == p, ]
        n.label <- nrow(st.label)
      } else {
        st.label <- NA
        n.label <- 0
      }
      print (paste("Found", n.label, "sites in WMA", p, rgn.wma))

      if(n.label > 0) {
        st.list <- unlist(strsplit(as.character(st.label$FEAT_ID), split=" "))
        q <- paste(
          "SELECT UNIQUE ",
          "ps.mon_program_id, p.program_abbr, p.program_name, ",
          "ps.mon_feature_id, mp.mon_feature_name, ",
          "mp.point_latitude, mp.point_longitude, ",
          "mp.loc_feature_name, mp.loc_type, ",
          "mp.drain_region_name, mp.mon_active_ind ",
          "FROM ",
          "programme_sample ps, ",
          "mon_programme p, ",
          "monfeat_sample_sum mp ",
          "WHERE ",

```

```

"ps.mon_feature_id = mp.mon_feature_id AND ",
"ps.mon_program_id = p.mon_program_id AND ",
# "ps.sample_term_ind = 0 AND",
"ps.mon_program_id = ", programme.n, " AND ",
"ps.mon_feature_id IN (", paste(unlist(st.list), collapse=" ", ", " ) ,
"ORDER BY ps.mon_feature_id",
sep="")
# "ps.sample_term_ind = 0 AND ----- slegs aktiewe samples: Deon (actually we need to differentiate between
sites <- sqlQuery(channel, q)
WmsCheck(sites)
ids <- sites$mon_feature_id
} else {
  sites <- NULL
}
# check if any data for this combination of site, date and WMA:
is.data <- FALSE

if (is.null(sites) || nrow(sites) == 0) {
  print (paste("No data for", rgn.wma, Date1, "to", Date2))
} else {
  for (nf in 1:length(ids)) {
    featid <- sites$mon_feature_id[nf]
    name <- sites$mon_feature_name[nf]

    # this is a query for a combination of E. coli and faecal coliforms:
    qs <- paste(
      "SELECT mon_feature_id, sample_begin_date, sample_begin_time,",
      " sample_begin_depth,",
      " result_num_value FROM released_result",
      " WHERE mon_variable_id IN (", paste(unlist(varidc), collapse=" ", ", " ) ,
      " AND mon_feature_id = ", featid,
      " AND sample_begin_date >= \"", Date1, "\",",
      " AND sample_begin_date <= \"", Date2, "\",",
      sep="")
    ccolis <- sqlQuery(channel, qs, rows_at_time = 1)
    print(noquote(paste("First check:", featid, "has", nrow(ccolis),
      " E. coli or faecal coliform samples from", Date1, "to", Date2)))
    if (nrow(ccolis) > 0) {
      is.data=TRUE
    }
  }
}

pf.wman <- gsub(" ", "", rgn.wma)
pf.wman <- gsub("/", "", pf.wman)
fil.htm <- paste(wdir, "coli_", pf.wman, "_", "NMMP", "_", Date1, "_", Date2,
  ".htm", sep="")
#htmfi <- paste(mv, "_", pf.wman, "_", "NMMP", "_", Date1, "_", Date2, ".htm", sep="")

if(nwmas == 0) write(paste(
  "<tr><td rowspan=\\"5\\><h4>", Date1, " to<br />", Date2, "</h4></td>",
  sep=""), file=fil.nmmp, append=TRUE)
else if(nwmas %% 4 == 0) write("</tr><tr>", file=fil.nmmp, append=TRUE)
nwmas <- nwmas + 1

if (is.data) {
  write(paste(
    "<td><a href=\\"", basename(fil.htm), "\">", rgn.wma, "</a></td>",
    sep=""), file=fil.nmmp, append=TRUE)

```

```

cmnt <- ""
} else {
  write(paste("<td>", gsub("_", " ", rgn.wma), "</td>", sep=""), file=fil.nmmp, append=TRUE)
  cmnt <- "(no data)"
}
fil.p <- paste(wdir, "coli_", pf.wman, "_", "NMMP", "_", Date1, "_", Date2,
  "_map.png", sep="")
fi.p <- basename(fil.p)

```

```

HTMLhead (paste("NMMP", gsub("_", " ", rgn.wma), Date1, "to", Date2, cmnt, "- WMA ver.", version.wma), fil.htm)
write("<hr />", file=fil.htm, append=TRUE)
write("<a href='\"index.asp\"'>Home</a>|", file=fil.htm, append=TRUE)
write(paste("<a href='\"", basename(fil.nmmp), "\">Report list</a>|", sep=""),
  file=fil.htm, append=TRUE)
write("<a href='\"../NMMP_notes.html\"'>Notes</a>|", file=fil.htm, append=TRUE)

```

Previous and Next navigation

```

hfil.prev <- fil.pr(year, yr1, yr2, bim, Bm1, Bm2, fil.nmmp, wdir, pf.wman)
hfil.next <- fil.nx(year, yr1, yr2, bim, Bm1, Bm2, fil.nmmp, wdir, pf.wman)
write(paste("<a href='\"", basename(hfil.prev),
  "\"><b>&laquo;Prev</b></a>|<a href='\"", basename(hfil.next),
  "\"><b>Next&rarr;</b></a>", sep=""),
  file=fil.htm, append=TRUE)
write("<hr />", file=fil.htm, append=TRUE)

```

```

if (is.data) {

```

Note use of rowspan and colspan to split heading rows and columns:

```

write(paste("<table id='\"hor-minimalist-b\"' border summary='\"', feaid, '\">", sep=""), file=fil.htm, append=TRUE)
write("<tr>", file=fil.htm, append=TRUE)
write("<th rowspan='\"2\"'>&#8470;</th>", file=fil.htm, append=TRUE)
write("<th rowspan='\"2\"'>Site<br />Follow ID link to locate site in Google Earth</th>", file=fil.htm, append=TRUE)
write("<th rowspan='\"2\"' align='\"center\"'>Plot all data</th>", file=fil.htm, append=TRUE)
write("<th rowspan='\"2\"' align='\"center\"'>Date</th>", file=fil.htm, append=TRUE)
write("<th colspan='\"2\"' align='\"center\"'>MPN / 100mL<br /></th>", file=fil.htm, append=TRUE)
write("<th rowspan='\"2\"' align='\"center\"'>Turb.<br />NTU</th>", file=fil.htm, append=TRUE)
write("<th rowspan='\"2\"' align='\"center\"'>pH</th>", file=fil.htm, append=TRUE)
write("<th rowspan='\"2\"' align='\"center\"'>Temp.<br /><sup>o</sup>C</th>", file=fil.htm, append=TRUE)
write("<th colspan='\"4\"' align='\"center\"'>Risk based on <i>E. coli</i> if recorded, otherwise on faecal coliforms</th>",
  file=fil.htm, append=TRUE)
write("<tr>", file=fil.htm, append=TRUE)
write("<th align='\"center\"'><i>E. coli</i></th>", file=fil.htm, append=TRUE)
write("<th align='\"center\"'>faecal coli&shy;forms</th>", file=fil.htm, append=TRUE)
write("<th align='\"center\"'>drinking-<br />no treat&shy;ment</th>", file=fil.htm, append=TRUE)
write("<th align='\"center\"'>drinking-<br />limited treat&shy;ment</th>", file=fil.htm, append=TRUE)
write("<th align='\"center\"'>full or<br />partial<br />contact</th>", file=fil.htm, append=TRUE)
write("<th align='\"center\"'>irrigation-<br />crops eaten raw</th>", file=fil.htm, append=TRUE)
write("</tr>", file=fil.htm, append=TRUE)
n.site=0

```

this is a query for E. coli only:

```

qs <- paste(
  "SELECT mon_feature_id, sample_begin_date, sample_begin_time,",
  " sample_begin_depth, result_num_value",
  " FROM released_result",
  " WHERE mon_variable_id IN (", paste(unlist(varide), collapse=","), ")",
  " AND mon_feature_id IN (", paste(unlist(ids), collapse=","), ")",
  " AND sample_begin_date >= \"", Date1, "\"",
  " AND sample_begin_date <= \"", Date2, "\"",

```

```

    sep=""
  )
  ecolis.a <- sqlQuery(channel, qs, rows_at_time = 1)
  WmsCheck(ecolis.a)
  ecolis.a <- na.omit(ecolis.a)
  print(paste(paste(unlist(ids), collapse=" + "), "Number of E. coli samples =", nrow(ecolis.a)))

# this is a query for faecal coliforms only:
  qs <- paste(
    "SELECT mon_feature_id, sample_begin_date, sample_begin_time,",
    " sample_begin_depth, result_num_value",
    " FROM released_result",
    " WHERE mon_variable_id IN (", paste(unlist(varidf), collapse=","), ")",
    " AND mon_feature_id IN (", paste(unlist(ids), collapse=","), ")",
    " AND sample_begin_date >= \'", Date1, "\'",
    " AND sample_begin_date <= \'", Date2, "\'",
    sep=""
  )
  fcolis.a <- sqlQuery(channel, qs, rows_at_time = 1)
  WmsCheck(fcolis.a)
  fcolis.a <- na.omit(fcolis.a)
  print(paste(paste(unlist(ids), collapse=" + "), "Number of faecal coliform samples =", nrow(fcolis.a)))

# combine the query results into a single data frame:
  efcolis.a <- merge(ecolis.a, fcolis.a,
    by=c("mon_feature_id", "sample_begin_date",
        "sample_begin_time", "sample_begin_depth"
    ),
    all=TRUE)
  names(ecolis.a)[5] <- "ecoli"
  names(ecolis.a)[6] <- "fcoli"
  # TODO : flag records with ecoli > fcoli

  if (nrow(ecolis.a) > 0) {

    # Decide which data to use and put into a new column, ccoli -
    # prefer E. coli, arbitrarily, and replace missing E. coli with faecal coliforms
    # - add a ctype column with the symbol for plotting
    efcolis.a$ccoli <- as.numeric(ecolis.a$ecoli)
    efcolis.a$type <- with(ecolis.a, 16)
    for (ci in 1:nrow(ecolis.a)) {
      if (is.na(ecolis.a$ccoli[ci])) {
        efcolis.a$ccoli[ci] <- as.numeric(ecolis.a$fcoli[ci])
        efcolis.a$type[ci] <- 1
        if (is.na(ecolis.a$ccoli[ci])) efcolis.a$type[ci] <- 4
      }
    }
  }

  for (nf in 1:length(ids)) {
    featid <- sites$mon_feature_id[nf]
    name <- sites$mon_feature_name[nf]

    efcolis <- efcolis.a[efcolis.a$mon_feature_id == featid, ]

    if (nrow(ecolis) > 0) {

```

```

fil.pl <- paste(wdir, "coli_", featid, "_", "NMMP",
               "_", Date1, "_", Date2, "_plot.png", sep="")
is.data <- TRUE
n.site <- n.site + 1
efcolis$Date <- as.Date(efcolis$sample_begin_date, "%Y-%m-%d")

# Wolda, H. and Marek, J. (1994). Measuring variation in abundance,
# the problem with zeros. European Journal of Entomology, 91(2):145-161:

if(min(efcolis$ccoli, na.rm=TRUE) < 0.5)
  efcolis$ccoli[efcolis$ccoli < 0.5] <- 0.5

efcoli_max <- max(efcolis$ccoli, na.rm=TRUE)

# plot coli and turbidity data

png(filename=fil.pl, width=800, height=600)
layout(1:2)
plot(efcolis$Date, efcolis$ccoli,
     xlim=c(as.numeric(Date1), as.numeric(Date2)),
     ylim=c(0.1, efcoli_max),
     xlab="", ylab="/100mL", xaxt="n", yaxt="n", type="n", log="y")
title(
  main=paste(year, ":", gsub("_", " ", rgn.wma), "WMA," "site", featid, "\n",
             "showing high risk guidelines for indicators of microbial pathogens.")
)
title(
  sub=paste(Date1, "to", Date2, "\n", toTitle(name), "\n",
            classtext(glclassn, glrange, efcoli_max)),
  cex.sub=0.8, line=4.0
)

axis.Date(1, at=seq(Date1, Date2, "days"), labels=FALSE, tcl=-0.1)
axis.Date(1, at=seq(Date1, Date2, "weeks"), tcl=-0.2, cex.axis=0.8, padj=-1.6)
rect(par("usr")[1], 10^par("usr")[3], par("usr")[2], 10^par("usr")[4], col="lightsteelblue3") # grey85
rect(par("usr")[1], glrange[1], par("usr")[2], glrange[2], border=NA, col=glcolpastel[1])
rect(par("usr")[1], glrange[2], par("usr")[2], glrange[3], border=NA, col=glcolpastel[2])
rect(par("usr")[1], glrange[3], par("usr")[2], glrange[4], border=NA, col=glcolpastel[3])
rect(par("usr")[1], glrange[4], par("usr")[2], 10^par("usr")[4], border=NA, col=glcolpastel[4])
for (ny in c(0:10)) segments(par("usr")[1], 10^ny, par("usr")[2], 10^ny, col="white")
for (nx in c(0, 7, 14, 21, 28, 35, 42, 49, 56, 63))
  segments(Date1+nx, 10^par("usr")[3], Date1+nx, 10^par("usr")[4], col="white")
for (nx in c(0, 28, 56))
  segments(Date1+nx, 10^par("usr")[3], Date1+nx, 10^par("usr")[4], col="white", lwd=2)
lines(efcolis$Date, efcolis$ccoli, col="grey90", lwd=2)

# make the symbol solid for E. coli and hollow for faecal coliforms
points(efcolis$Date, efcolis$ccoli, pch=efcolis$type, col="grey20", cex=1.2)
pointLabel(efcolis$Date, efcolis$ccoli,
           labels=as.character(round(efcolis$ccoli)), cex=0.7, pos=1)
if(efcoli_max < 10000) {
  axis(2, c(1, 10, 100, 1000), c("1", "10", "100", "1000"), cex.axis=0.75, las=1)
} else {
  axis(2, c(1, 1000, 100000, 1000000), c("1", "1000", "100000", "1000000"), cex.axis=0.75, las=1)
}
legend("bottomright",
      legend=c(expression(italic("Eschericia coli")), "faecal coliforms"),
      bg="#ffffff", col="grey20", pch=c(16, 1),

```

```

inset=c(0.001, 0.01), box.col="grey", horiz=TRUE, cex=0.7)
rect(par("usr")[1], 10^par("usr")[3], par("usr")[2], 10^par("usr")[4], border="grey60")

# get turbidity data:
qs <- paste("SELECT mon_feature_id, sample_begin_date, sample_begin_time, sample_begin_depth, ",
            "result_num_value FROM released_result WHERE mon_variable_id = ", 66,
            " AND mon_feature_id = ", featid,
            " AND sample_begin_date >= \'", Date1, "\'",
            " AND sample_begin_date <= \'", Date2, "\'",
            sep="")
turbidity <- sqlQuery(channel, qs, rows_at_time = 1)
WmsCheck(turbidity)

turbidity$Date <- as.Date(turbidity$sample_begin_date,"%Y-%m-%d")
if (nrow(turbidity) > 0) {
  plot(turbidity$Date, turbidity$result_num_value, xlim=c(as.numeric(Date1), as.numeric(Date2)),
       main="Turbidity",
       sub=DateStamp("txt"), cex.sub=0.7,
       xlab="", xaxt="n", ylab="NTU", type="n", pch=16, las=1, col="grey60",
       ylim=c(0, max(turbidity$result_num_value, na.rm=TRUE)))
  axis.Date(1, at=seq(Date1, Date2, "days"), labels=FALSE, tcl=-0.1)
  axis.Date(1, at=seq(Date1, Date2, "weeks"), tcl=-0.2, cex.axis=0.8)
  rect(par("usr")[1], par("usr")[3], par("usr")[2], par("usr")[4], col="lightsteelblue3") # grey85
  rect(par("usr")[1], 10, par("usr")[2], par("usr")[4], border=NA, col=glcolpastel[3])
  for (nx in c(0, 7, 14, 21, 28, 35, 42, 49, 56, 63))
    segments(Date1 + nx, par("usr")[3], Date1 + nx, par("usr")[4], col="white")
  for (nx in c(0, 28, 56))
    segments(Date1 + nx, par("usr")[3], Date1 + nx, par("usr")[4], col="white", lwd=2)
  grid(nx=NA, ny=NULL, col="white", lty=1)

  lines(turbidity$Date, turbidity$result_num_value, col="grey90", lwd=2)
  points(turbidity$Date, turbidity$result_num_value, pch=16, col="grey20", cex=1.2)
  pointLabel(turbidity$Date, turbidity$result_num_value,
             as.character(signif(turbidity$result_num_value), 3), cex=0.7, pos=1)
  #rect(par("usr")[1], par("usr")[3], par("usr")[2], par("usr")[4], border="grey60")
} else {
  plot(c(Date1, Date2), c(0, 1), xlim=c(as.numeric(Date1), as.numeric(Date2)),
       type="n", xlab="", ylab="", xaxt="n", yaxt="n", col="grey60",
       sub=DateStamp("txt"), cex.sub=0.7)
  text((par("usr")[2] - par("usr")[1]) / 2,
       (par("usr")[4] - par("usr")[3]) / 2,
       "No turbidity data available")
}
rect(par("usr")[1], par("usr")[3], par("usr")[2], par("usr")[4], border="grey60")
dev.off()

# add lines to table of E.coli, pH, temperature, turbidity, risk
#pH = 3, TURB = 66, EC = 56, TEMP-Phys_Water = 54
fil.flash <- paste(wdr0, "Chart_nmmp", featid, ".html", sep="")
fil.png <- paste(wdr0, "Chart_nmmp_", featid, ".png", sep="")
write(paste("<tr><td><b>", n.site, "</b></td><td><b><a href='\"../nmmp\",
            featid, \".kmz\">", featid,
            "</a></b> [<a href='\"", basename(fil.pl),
            "\" target='\"_blank\">2-month plot</a>]",
            sep=""),
      file=fil.htm, append=TRUE)
#if (file.exists(fil.flash) )
write(paste("<br />", toTitle(name), "</td>", sep=""), file=fil.htm, append=TRUE)
write("<td>", file=fil.htm, append=TRUE)

```

```

if (file.exists(fil.fpng) )
  write(paste("<a href='../", basename(fil.fpng), "\" target='_blank'>",
    "<img src='../nmmp_', featid, \"_p.png\" title='Plot ', featid, \">\",
    "</a>", sep=""), file=fil.htm, append=TRUE)
write("</td>", file=fil.htm, append=TRUE)
for(nr in 1:nrow(efcolis)) {
  efdate <- efcolis$sample_begin_date[nr]
  if (is.na(efcolis$ecoli[nr])) {
    ecol.fmt <- "-"
  } else {
    ecol.fmt <- sprintf("%6.0f", efcolis$ecoli[nr])
  }
  if (is.na(efcolis$fcoli[nr])) {
    fcol.fmt <- "-"
  } else {
    fcol.fmt <- sprintf("%6.0f", efcolis$fcoli[nr])
  }
  ccol <- efcolis$ccoli[nr]
  if(nr > 1) write(paste("<tr><td>", n.site, "</td><td>", featid,
    "</td></td><td>"),
    file=fil.htm, append=TRUE)
  write(paste("<td nowrap='nowrap'>", efdate, "</td>"), file=fil.htm, append=TRUE)
  write(paste("<td align='right'>", ecol.fmt, "</td>"), file=fil.htm, append=TRUE)
  write(paste("<td align='right'>", fcol.fmt, "</td>"), file=fil.htm, append=TRUE)

  # get turbidity value for same date as E. coli -
  # TODO : flag return of multiple values, usually a result of incorrect data entry
  qs <- paste("SELECT mon_feature_id, sample_begin_date, sample_begin_time, sample_begin_depth, ",
    "result_num_value FROM released_result WHERE mon_variable_id = ", 66,
    " AND mon_feature_id = ", featid,
    " AND sample_begin_date = \'", efdate, "\'",
    sep="")
  turbidity1 <- sqlQuery(channel, qs, rows_at_time = 1)
  WmsCheck(turbidity1)
  if(is.na(turbidity1$result_num_value[1])) Turbidity <- "-"
  else Turbidity <- round(turbidity1$result_num_value[1])
  write(paste("<td align='right'>", Turbidity, "</td>"), file=fil.htm, append=TRUE)

  # get pH value for same date as E. coli
  qs <- paste("SELECT mon_feature_id, sample_begin_date, sample_begin_time, sample_begin_depth, ",
    "result_num_value FROM released_result WHERE mon_variable_id = ", 3,
    " AND mon_feature_id = ", featid,
    " AND sample_begin_date = \'", efdate, "\'",
    sep="")
  pH1 <- sqlQuery(channel, qs, rows_at_time = 1)
  WmsCheck(pH1)
  if(is.na(pH1$result_num_value[1])) pHvalue <- "-"
  else pHvalue <- sprintf("%4.1f", pH1$result_num_value[1])
  write(paste("<td align='right'>", pHvalue, "</td>"), file=fil.htm, append=TRUE)

  # get temperature value for same date as E. coli
  qs <- paste("SELECT mon_feature_id, sample_begin_date, sample_begin_time, sample_begin_depth, ",
    "result_num_value FROM released_result WHERE mon_variable_id = ", 54,
    " AND mon_feature_id = ", featid,
    " AND sample_begin_date = \'", efdate, "\'",
    sep="")
  degC1 <- sqlQuery(channel, qs, rows_at_time = 1)
  WmsCheck(degC1)

```

```

if(is.na(degC1$result_num_value[1])) temperature <- "-"
else temperature <- sprintf("%4.1f", degC1$result_num_value[1])
write(paste("<td align='right'>", temperature, "</td>", file=fil.htm, append=TRUE)

txt <- "HIGH"; cfill <- glcolpastel[3]
if (ccol < gl.risk.untreated[2]) {txt <- "Med"; cfill <- glcolpastel[2]}
if (ccol < gl.risk.untreated[1]) {txt <- "low"; cfill <- "#FFFFFF"}
write(paste("<td align='center' bgcolor='", cfill, "'>", txt, "</td>", sep=""), file=fil.htm, append=TRUE)
txt <- "HIGH"; cfill <- glcolpastel[3]
if (ccol < gl.risk.lim_treat[2]) {txt <- "Med"; cfill <- glcolpastel[2]}
if (ccol < gl.risk.lim_treat[1]) {txt <- "low"; cfill <- "#FFFFFF"}
write(paste("<td align='center' bgcolor='", cfill, "'>", txt, "</td>", sep=""), file=fil.htm, append=TRUE)
txt <- "HIGH"; cfill <- glcolpastel[3]
if (ccol < gl.risk.contact[2]) {txt <- "Med"; cfill <- glcolpastel[2]}
if (ccol < gl.risk.contact[1]) {txt <- "low"; cfill <- "#FFFFFF"}
write(paste("<td align='center' bgcolor='", cfill, "'>", txt, "</td>", sep=""), file=fil.htm, append=TRUE)
txt <- "HIGH"; cfill <- glcolpastel[3]
if (ccol < gl.risk.irrigation[2]) {txt <- "Med"; cfill <- glcolpastel[2]}
if (ccol < gl.risk.irrigation[1]) {txt <- "low"; cfill <- "#FFFFFF"}
write(paste("<td align='center' bgcolor='", cfill, "'>", txt, "</td>", sep=""), file=fil.htm, append=TRUE)
write(paste("</tr>", file=fil.htm, append=TRUE)
}
}
}
write(paste("</table>", file=fil.htm, append=TRUE)
write(paste("<center><img src='", basename(fil.p), "' alt='", basename(fil.p), "' />", sep=""), file=fil.htm, append=TRUE)
write("<br /></center>", file=fil.htm, append=TRUE)
write("<table border='0' cellpadding='2' cellspacing='2' summary='Map key'>", file=fil.htm, append=TRUE)
write("<tr align='left'>", file=fil.htm, append=TRUE)
write(paste("<td><img src='loc_', version.wma, '_', pf.wman, '.png' alt='", pf.wman, "' /></td>", sep=""),
      file=fil.htm, append=TRUE)
for (ntyp in 1:5) write(paste("<td><font color='", glcols[ntyp], "' size='", ntyp+1,
                              ">&#8226;</font></td><td><small>", glclassn[ntyp], "</small></td>", sep=""),
                        file=fil.htm, append=TRUE)
write("</tr>", file=fil.htm, append=TRUE)
write("</table>", file=fil.htm, append=TRUE)
write("<center>", file=fil.htm, append=TRUE)
write(DateStamp("htm"), file=fil.htm, append=TRUE)
write("</center>", file=fil.htm, append=TRUE)

b <- bbox(wmarg[wmarg$NUMBER==p,])
xr <- c(b[1],b[3])
yr <- c(b[2],b[4])
xwid <- b[3]-b[1]
ywid <- b[4]-b[2]
if (xwid >= ywid ) { xpix <- xpixls; ypix <- round((ywid/xwid)*xpixls) }
if (xwid < ywid ) { ypix <- ypixls; xpix <- round((xwid/ywid)*ypixls) }

print(fil.p)
png(filename=fil.p,width=xpix,height=ypix)
or <- par(mar=c(0,0,0,0))
#plot(pri,col="grey80",xlim=xr,ylim=yr,lwd=0.7)
plot(wmarg[wmarg$NUMBER!=p, ], pbg="transparent", col="grey87", xlim=xr, ylim=yr, lwd=1.7)
for(ri in 2:7) { plot(rv[rv$STRAHLER==ri,], add=TRUE,lwd=ri/10, col="lavender") }
plot(lak,col="lightcyan",border="lightcyan",add=TRUE)
plot(wmarg[wmarg$NUMBER==0,],pbg="transparent",col="grey85",add=TRUE)
plot(pri[pri$PRIMARY=="Y",],col="grey85",border="grey75",add=TRUE)

```

```

plot(pri[pri$PRIMARY=="Z",], col="grey85", border="grey75", add=TRUE)
plot(ter, border="grey80", lwd=0.7, add=TRUE)
plot(pri, border="grey80", lwd=2, add=TRUE)
plot(pri[pri$PRI_CODE=="00",], col="lightcyan", border="cyan", add=TRUE)
plot(town, col="grey80", border="grey70", add=TRUE)
#for(ri in 2:7) { plot(rv[riv$STRAHLER==ri,], add=TRUE, lwd=ri/7, col="lightcyan") }
#plot(lak, col="azure", border="lightcyan", add=TRUE)
#pointLabel(coordinates(twn_big), labels=twn_big$NAMETAG, cex=0.6, col="#C0C0C0AA")
text(coordinates(twn_big), labels=twn_big$NAMETAG, cex=0.8, col="#333333AA")

n.site=0
for (nf in 1:length(ids)) {
  featid <- sites$mon_feature_id[nf]
  name <- sites$mon_feature_name[nf]
  lat <- sites$point_latitude[nf]
  lon <- sites$point_longitude[nf]
  points(lon, lat, pch=1, col="grey50", cex=0.67)
  colis <- efcolis.a[efcolis.a$mon_feature_id == featid, ]
  if(nrow(colis) > 0) {
    n.site <- n.site + 1
    medcoli <- median(colis$ccoli)
    #print(paste(featid, medcoli))
    if(medcoli > glrange[4])
      points(lon, lat, pch=20, col=glcol[5], cex=gsize[5])
    if(medcoli > glrange[3] && medcoli <= glrange[4])
      points(lon, lat, pch=20, col=glcol[4], cex=gsize[4])
    if(medcoli > glrange[2] && medcoli <= glrange[3])
      points(lon, lat, pch=20, col=glcol[3], cex=gsize[3])
    if(medcoli > glrange[1] && medcoli <= glrange[2])
      points(lon, lat, pch=20, col=glcol[2], cex=gsize[2])
    if(medcoli <= glrange[1])
      points(lon, lat, pch=20, col=glcol[1], cex=gsize[1])
    pointLabel(lon, lat, labels=as.character(n.site), cex=1, font=2, method="SANN") #, trace=TRUE)
    print(paste(n.site, featid, nrow(colis), "median colis", medcoli, rgn.wma, lat, lon, toTitle(name)))
  }
}
box(col="grey")
dev.off()
}
write ( "<!-- Google Analytics page tracker -->", file=fil.htm, append=TRUE)
write ( "<script type='text/javascript'>", file=fil.htm, append=TRUE)
write ( "var gaJsHost = ((\"https:\" == document.location.protocol) ? \"https://ssl.\" : \"http://www.\");", file=fil.htm, ap
write ( "document.write(unescape('%3Cscript src='\" + gaJsHost + '\"google-analytics.com/ga.js' type='text/javascr
write ( "</script>", file=fil.htm, append=TRUE)
write ( "<script type='text/javascript'>", file=fil.htm, append=TRUE)
write ( "var pageTracker = _gat._getTracker(\"UA-2572820-1\");", file=fil.htm, append=TRUE)
write ( "pageTracker._initData();", file=fil.htm, append=TRUE)
write ( "pageTracker._trackPageview();", file=fil.htm, append=TRUE)
write ( "</script>", file=fil.htm, append=TRUE)
write ( "</body>", file=fil.htm, append=TRUE)
write ( "</html>", file=fil.htm, append=TRUE)
}
write(paste("<tr>\n</table>"), file=fil.nmmp, append=TRUE)
}
write(DateStamp("htm"), file=fil.nmmp, append=TRUE)
# insert Google Analytics script
write ( "<!-- Google Analytics page tracker -->", file=fil.nmmp, append=TRUE)
write ( "<script type='text/javascript'>", file=fil.nmmp, append=TRUE)

```

```

write ( "var gaJsHost = ((\"https:\\\" == document.location.protocol) ? \"https://ssl.\" : \"http://www.\");", file=fil.nmmp, ap
write ( "document.write(unescape(\"%3Cscript src=\" + gaJsHost + \"google-analytics.com/ga.js\" type='text/javascript
write ( "</script>", file=fil.nmmp, append=TRUE)
write ( "<script type='\"text/javascript\">", file=fil.nmmp, append=TRUE)
write ( "var pageTracker = _gat._getTracker(\"UA-2572820-1\");", file=fil.nmmp, append=TRUE)
write ( "pageTracker._initData()", file=fil.nmmp, append=TRUE)
write ( "pageTracker._trackPageview()", file=fil.nmmp, append=TRUE)
write ( "</script>", file=fil.nmmp, append=TRUE)
write ( "</body>", file=fil.nmmp, append=TRUE)
write ( "</html>", file=fil.nmmp, append=TRUE)

}

print(noquote(paste("Output in", wdir, "and", wdr0)))

odbcCloseAll()
if(auto.xtras) {
  source ("C:/data/program/R/NMMP_TimeLine.R")
  source ("C:/data/program/R/NMMP_miniplots.R")
  source ("C:/data/program/R/NMMP_KML_balloons.R")
  source ("C:/data/program/R/NMMP_R2leaflet.R")
} else {
  print(noquote("Remember to source (\"C:/data/program/R/NMMP_TimeLine.R\")"))
  print(noquote("Remember to source (\"C:/data/program/R/NMMP_miniplots.R\")"))
  print(noquote("Remember to source (\"C:/data/program/R/NMMP_KML_balloons.R\")"))
  print(noquote("Remember to source (\"C:/data/program/R/NMMP_R2leaflet.R\")"))
}
print(noquote("Run this batch file to upload the files to the web site: C:/data/program/bat/robocopy_nmmp.bat"))

# commands for a dark plot
#plot(wmarg[wmarg$NUMBER!=p,],col="grey75",xlim=xr,ylim=yr,lwd=1.7)
#plot(prip[prp$PRI_CODE=="00",],col="lightcyan",border="cyan",add=TRUE)
#plot(wmarg[wmarg$NUMBER==p,],col="grey10",add=TRUE)
#for(ri in 3:7) { plot(rv[riv$STRAHLER==ri,], add=TRUE,lwd=ri/10, col="lightskyblue") }
#plot(lak,col="lightskyblue",border="lightcyan",add=TRUE)
#plot(ter,col="grey80",lwd=0.7,add=TRUE)
#plot(town,col="grey80",border="yellow",add=TRUE) # too yellow
#plot(town,col="wheat",border="grey70",add=TRUE)
#points(20, -34, pch=20, col=glcol[3], cex=gsiz[3])
#points(20, -34, pch=21, col="white", bg="blue", cex=gsiz[3]) # sizes need to be smaller for pch=21, colours brighter
#pointLabel(20,-34.5,labels=as.character(feaid), cex=1, col="white", font=2)

```