## ProcessXLSXfromSEN.R.

## rstudio

Mon Mar 4 22:04:46 2019

```
############ Process xlsx from Stuart
# Routines to import and process xlsx files for ECC and Southrepps as supplied by SEN
# EAP 2019-02-14
# Files are called
   2019-02-12\_SN\_EP\_Classifier\_results\_SRepp.xlsx, and
   2019-02-12\_SN\_EP\_Classifier\_results\_Eccles.xlsx
## Update ## 2019-02-28 a further file recieved for Southrepps for 2016 - 2018,
## Update ## 2019-02-28, this file is called
   2019-02-28_SN_EAP_Classifier_results_Southrepps2.xlsx
# Files are delivered as Microsoft Excel .xlsx format
# Files have the following structure
  filename
                : chr > character string, see below for details.
                  : chr > 6 character string with species code
   confidence_index: num > Confidence index assigned by the classifier range 0.00 to 1.00 (0.99?)
#
   real_error : num > Relative Error calculated by the classifier range 0.00 to 1.00 (0.99?) See
# Structure of values in the filename column:
                   : chr > 3 digit site code SR2 = Southrepps (Dowlands), ECC == Eccls
#
                  : chr > separator
  yyyymmdd
#
                  : num > date of recording (assigned by SM2) ISO format
#
                   : chr > separator
#
                  : num > time of recording (assigned by SM2 no DST correction applied. hours since m
#
                  : chr > separator
                    : num > 3 digit number assigned by classifier, thought to be the call number in th
# Processing will be required to:
# load data xlsx into a data.frame
#
  extract date & time from filename
   create new column fo observation date/time
#
#
# Input file are located in the following locations:
  ~/R-Test/intermed/ECC, and
#
  ~/R-Test/intermed/SR2
# Output files will be writen to the following locations:
  \sim/R-Test/tidy/ECC, and
   ~/R-Test/tidy/SR2
# Output files will have the following structure:
  2019-02-12_SEN_Evaluation_XXX.csv : where XXX is either ECC or SR2 as relevant
# Load required libraries
# Load tidyvers functions
```

```
#if (!require(tidyverse)) install.packages('tidyverse')
#library(tidyverse)
#library(readr)
#library(dplyr)
#library(purrr)
library(lubridate)
library(readxl) #Needed to process xlxs files
library(knitr)
#Evaluation parameters
re threshold <-
 0.5 #Change this value to set required accuracy cut-off.
#In practice 0.5 is applied by Stuart when agreegating records.
save_csv <-
 TRUE #Change to FALSE if you don't want to create a new csv file
site_code <- "SR2" #See below for alternatives</pre>
input_file_name <-</pre>
  "2019-02-28_SN_EAP_Classifier_results_Southrepps2.xlsx"
output_file_name <- "2019-02-28_SEN_Evaluation_SR2.csv"</pre>
#Directories NB these are only vaid for AWS - RStudio - Server
d_home <- "~/R-Test/"</pre>
d_raw <- paste(d_home, "raw/", site_code, "/", sep = "")</pre>
d_intermed <- paste(d_home, "intermed/", site_code, "/", sep = "")</pre>
d_tidy <- paste(d_home, "tidy/", site_code, "/", sep = "")</pre>
d_output <- paste(d_home, "output/", sep = "")</pre>
# Site Specific Information
validsitecodes <- c("SR2", "ECC")</pre>
# Check if we have a valid site code
if (!(site_code %in% validsitecodes)) {
  stop("Invalid Site Code")
# Configure Environment & paths etc.
setwd(d_home)
getwd()
## [1] "/home/rstudio/R-Test"
# NB Following are hard coded paths rather than derived from site_code
tmp_sourcefile <-</pre>
 paste(d_intermed,
        input_file_name,
        sep = "")
tmp_outputfile <-</pre>
  paste(d_tidy,
        output_file_name,
        sep = "")
```

```
# Read the input file
tmp_SNclassifier_results <- read_excel(tmp_sourcefile)</pre>
tmp_SNclassifier_results <-</pre>
  data.frame(obs_datetime = as.POSIXct(gsub(
    "_", "", substr(tmp_SNclassifier_results$filename, 5, 19)
  tmp_SNclassifier_results) # Create the Date-Time column
#write results to csv
if (save_csv == TRUE) {
  write_csv(tmp_SNclassifier_results, tmp_outputfile, col_names = TRUE)
}
# Monthly Summary, results writen to tbl_mnlyStats
tbl_mnlyStats <- tmp_SNclassifier_results %>%
  dplyr::filter(., real_error >= re_threshold) %>%
  group_by(year(as.Date(obs_datetime, "%Y-%m-%d")),
           month(as.Date(obs_datetime, "%Y-%m-%d")),
           species) %>%
  dplyr::summarise(
   count = n(),
   max = max(confidence_index),
   mean = round(mean(confidence_index), 2),
   min = min(confidence_index),
    std_dev = round(sd(confidence_index), 2)
  )
names(tbl_mnlyStats)[1] <- "Year"</pre>
names(tbl_mnlyStats)[2] <- "Month"</pre>
tbl_mnlyStats <- as.data.frame(tbl_mnlyStats)</pre>
#Now generate species summaries
species_found <- unique(tbl_mnlyStats$species)</pre>
print(paste(site_code, "Evaluation by SN"))
## [1] "SR2 Evaluation by SN"
for (row in 1:length(species_found)) {
  tmp_species <-
   filter(tbl_mnlyStats, species == species_found[row])
  print(knitr::kable(tmp_species))
}
##
##
## Year Month species
                                                         std_dev
                             count
                                      max
                                           mean
                                                    min
## 2016
              9 Barbar
                                15
                                     0.99
                                            0.93
                                                             0.15
                                                   0.48
                                           0.99
                                                   0.99
## 2016
             10 Barbar
                               6
                                    0.99
                                                             0.00
```

##	2017	8	Barbar	3	0.99	0.99	0.99	0.00
##	2017	9	Barbar	13	0.99	0.97	0.84	0.04
##	2017	10	Barbar	24	0.99	0.95	0.70	0.07
##	2018	1	Barbar	1	0.99	0.99	0.99	NA
##	2018	3	Barbar	1	0.84	0.84	0.84	NA
##	2018	4	Barbar	1	0.17	0.17	0.17	NA
##	2018	7	Barbar	1	0.99	0.99	0.99	NA
##	2018	8	Barbar	7	0.99	0.88	0.52	0.18
##	2018	9	Barbar	7	0.99	0.99	0.98	0.00
##	2018	10	Barbar	7	0.99	0.99	0.99	0.00
##	2018	11	Barbar	1	0.98	0.98	0.98	NA
##								
##								
##	Year	Month	species	count	max	mean	min	std_dev
##								
##	2016	9	Myodau	26	0.99	0.77	0.42	0.18
##	2016	10	Myodau	10	0.96	0.71	0.39	0.22
##	2016	11	Myodau	5	0.93	0.67	0.50	0.16
##	2017	3	Myodau	3	0.91	0.60	0.44	0.27
##	2017	8	Myodau	12	0.94	0.72	0.43	0.20
##	2017	9	Myodau	27	0.98	0.74	0.40	0.17
##	2017	10	Myodau	15	0.97	0.80	0.52	0.14
##	2017	11	Myodau	4	0.95	0.69	0.41	0.28
##	2018	1	Myodau	4	0.98	0.66	0.39	0.26
##	2018	3	Myodau	2	0.89	0.74	0.59	0.21
##	2018	4	Myodau	4	0.93	0.67	0.49	0.19
##	2018	5	Myodau	2	0.91	0.70	0.50	0.29
##	2018	7	Myodau	1	0.83	0.83	0.83	NA
##	2018	8	Myodau	9	0.98	0.85	0.63	0.14
##	2018	9	Myodau	5	0.95	0.87	0.73	0.10
##	2018	10	Myodau	6	0.93	0.76	0.46	0.17
##			5					
##								
##	Year	Month	species	count	max	mean	min	std_dev
##								
##	2016	9	Myonat	4	0.99	0.85	0.78	0.09
##	2016	10	Myonat	5	0.98	0.88	0.76	0.10
##	2016	11	Myonat	2	0.99	0.94	0.88	0.08
##	2017	8	Myonat	3	0.99	0.97	0.94	0.03
##	2017	9	Myonat	7	0.99	0.95	0.85	0.05
##	2017	10	Myonat	7	0.99	0.90	0.80	0.07
##	2017	11	Myonat	7	0.99	0.92	0.79	0.08
##	2018	1	Myonat	4	0.98	0.81	0.72	0.12
##	2018	5	Myonat	2	0.96	0.84	0.71	0.18
##	2018	7	Myonat	37	0.99	0.99	0.88	0.02
##	2018	8	Myonat	48	0.99	0.97	0.72	0.05
##	2018	9	Myonat	19	0.99	0.97	0.89	0.03
##	2018	10	Myonat	22	0.99	0.96	0.79	0.05
##	2018	11	Myonat	5	0.96	0.86	0.72	0.13
##								
##								
##	Year	Month	species	count	max	mean	min	std_dev
##								
##	2016	9	Nycnoc	7	0.99	0.92	0.72	0.09

##	2016	10	Nycnoc	2	0.76	0.70	0.65	0.08
##	2017	8	Nycnoc	18	0.99	0.85	0.63	0.13
##	2017	9	Nycnoc	20	0.99	0.83	0.64	0.12
##	2017	10	Nycnoc	19	0.99	0.93	0.68	0.09
##	2018	7	Nycnoc	64	0.99	0.92	0.63	0.09
##	2018	8	Nycnoc	44	0.99	0.90	0.65	0.10
##	2018	9	Nycnoc	12	0.99	0.84	0.63	0.13
##	2018	10	Nycnoc	18	0.99	0.91	0.69	0.08
##	2018	11	Nycnoc	3	0.99	0.91	0.77	0.12
##								
##								
##	Year	Month	species	count	max	mean	min	std_dev
##								
##	2016	9	Pipnat	7	0.87	0.73	0.55	0.10
##	2017	9	Pipnat	2	0.82	0.78	0.74	0.06
##	2017	10	Pipnat	3	0.84	0.66	0.50	0.17
##	2018	4	Pipnat	2	0.85	0.70	0.56	0.21
##	2018	5	Pipnat	1	0.70	0.70	0.70	NA
##	2018	7	Pipnat	6	0.93	0.78	0.55	0.18
##	2018	8	Pipnat	4	0.97	0.85	0.74	0.10
##	2018	9	Pipnat	3	0.94	0.92	0.90	0.02
##	2018	10	Pipnat	3	0.87	0.65	0.52	0.19
##								
##								
##	Year	Month	species	count	max	mean	min	std_dev
##								
##	2016	9	Pippip	106	0.99	0.93	0.38	0.12
##	2016	10	Pippip	43	0.99	0.94	0.51	0.10
##	2016	11	Pippip	11	0.98	0.91	0.39	0.17
##	2017	2	Pippip	1	0.97	0.97	0.97	NA
##	2017	3	Pippip	6	0.99	0.98	0.97	0.01
##	2017	4	Pippip	3	0.99	0.98	0.97	0.01
##	2017	5	Pippip	14	0.99	0.91	0.49	0.14
##	2017	6	Pippip	37	0.99	0.93	0.72	0.06
##	2017	7	Pippip	28	0.99	0.96	0.84	0.03
##	2017	8	Pippip	973 1567	0.99	0.96	0.57	0.03
##	2017	9	Pippip	1567	0.99	0.96	0.41	0.04
##	2017	10	Pippip	187	0.99	0.95	0.55	0.08
##	2017	11	Pippip	26	0.99	0.96	0.83	0.04
##	2017	12	Pippip	2	0.98	0.98 0.97	0.98	0.00
##	2018	1	Pippip	22	0.99		0.93	0.02
##	2018	2	Pippip	4	0.98	0.96	0.93	0.02
##	2018		Pippip	11 29	0.99	0.98 0.94	0.96	0.01
##	2018	4 5	Pippip		0.99		0.62 0.61	0.08
##	2018	7	Pippip	103	0.99 0.99	0.95 0.92		0.06
##	2018	8	Pippip	665		0.92	0.38	0.12
##	2018	9	Pippip	262 69	0.99	0.92	0.45	0.10
##	2018		Pippip		0.99		0.57	0.08
##	2018	10	Pippip Pippip	97 27	0.99	0.95 0.95	0.60 0.81	0.07
## ##	2018	11 12	Pippip Pippip	27	0.99			0.05
##	2018	12	Pippip	4	0.99	0.98	0.95	0.02
##								
##	Year	Month	eneciae	count	mav	mean	min	etd dow
##	rear	PIOHUH	species	count	max	mean	штп	std_dev

##								
##	2016	9	Pippyg	52	0.99	0.93	0.44	0.11
##	2016	10	Pippyg	11	0.99	0.93	0.71	0.09
##	2016	11	Pippyg	5	0.98	0.94	0.86	0.05
##	2017	4	Pippyg	1	0.88	0.88	0.88	NA
##	2017	5	Pippyg	3	0.98	0.93	0.84	0.08
##	2017	6	Pippyg	5	0.97	0.91	0.83	0.07
##	2017	7	Pippyg	2	0.97	0.96	0.94	0.02
##	2017	8	Pippyg	60	0.98	0.95	0.54	0.08
##	2017	9	Pippyg	78	0.99	0.95	0.57	0.06
##	2017	10	Pippyg	28	0.98	0.96	0.84	0.03
##	2017	11	Pippyg	6	0.98	0.95	0.91	0.03
##	2018	1	Pippyg	5	0.98	0.97	0.94	0.02
##	2018	3	Pippyg	2	0.98	0.98	0.98	0.00
##	2018	4	Pippyg	9	0.98	0.97	0.93	0.02
##	2018	5	Pippyg	19	0.99	0.91	0.37	0.15
##	2018	6	Pippyg	1	0.97	0.97	0.97	NA
##	2018	7	Pippyg	161	0.99	0.94	0.34	0.09
##	2018	8	Pippyg	77	0.99	0.88	0.33	0.16
##	2018	9	Pippyg	38	0.99	0.91	0.34	0.11
##	2018	10	Pippyg	46	0.98	0.93	0.57	0.09
##	2018	11	Pippyg	9	0.99	0.95	0.83	0.05
##								
##								
##	Year	Month	species	count	max	mean	min	std_dev
##								
##	2016	9	Pleaur	71	0.99	0.95	0.57	0.07
##	2016	10	Pleaur	22	0.99	0.96	0.88	0.03
##	2017	6	Pleaur	1	0.89	0.89	0.89	NA
##	2017	8	Pleaur	41	0.99	0.94	0.56	0.09
##	2017	9	Pleaur	48	0.99	0.94	0.69	0.08
## ##	2017	10 1	Pleaur	39	0.99 0.99	0.93 0.99	0.60 0.99	0.09
##	2018 2018	2	Pleaur Pleaur	1 2	0.99	0.99	0.99	NA 0.02
##	2018	3	Pleaur	15	0.94	0.82	0.91	0.02
##	2018	4	Pleaur	6	0.99	0.88	0.47	0.18
##	2018	5	Pleaur	2	0.99	0.98	0.39	0.24
##	2018	7	Pleaur	50	0.99	0.96	0.38	0.06
##	2018	8	Pleaur	66	0.99	0.92	0.73	0.15
##	2018	9	Pleaur	25	0.99	0.90	0.41	0.15
##	2018	10	Pleaur	19	0.99	0.93	0.68	0.10
##	2018	11	Pleaur	2	0.99	0.97	0.95	0.03
##				_				
##								
##	Year	Month	species	count	max	mean	min	std_dev
##								
##	2017	8	Eptser	2	0.58	0.55	0.53	0.04
##	2017	10	Eptser	2	0.84	0.70	0.56	0.20
##	2018	7	Eptser	26	0.99	0.83	0.54	0.18
##	2018	8	Eptser	14	0.99	0.86	0.43	0.17
##	2018	9	Eptser	1	0.98	0.98	0.98	NA
##								
##								
##	Year	Month	species	count	max	mean	min	std_dev

```
## 2017
               8 Nyclei
                                     0.79
                                           0.79
                                                                NΑ
                                 1
                                                    0.79
#### NOTE NOTE NOTE ####
# To generate a pdf report from this process it is not possible to use
# the RStudio ctr-K short cut as this throws a number of errors.
# Instead use the following code entered at the console
\# rmarkdown::render(paste(d_home,"bin/snips/ProcessXLSXfromSEN.R", sep = ""), "pdf_document")
#### END END END ####
#### Supplementary code to combine the two SR2 files from SEN.
# Parameters
source files <- c(</pre>
 "2019-02-12_SEN_Evaluation_SR2.csv",
 "2019-02-28 SEN Evaluation SR2.csv"
)
output_file_name <- "2019-03-04_Summary_SEN_Evaluation_SR2.csv"
tmp_file1 <- read_csv(paste(d_tidy, source_files[1], sep = ""))</pre>
## Parsed with column specification:
## cols(
     obs_datetime = col_datetime(format = ""),
##
    filename = col_character(),
##
     species = col_character(),
     confidence_index = col_double(),
##
     real_error = col_double()
tmp_file2 <- read_csv(paste(d_tidy, source_files[2], sep = ""))</pre>
## Parsed with column specification:
## cols(
##
     obs_datetime = col_datetime(format = ""),
##
    filename = col_character(),
    species = col_character(),
##
##
    confidence_index = col_double(),
    real error = col double(),
     actual_date = col_datetime(format = ""),
##
     session date = col datetime(format = ""),
##
##
    time = col_datetime(format = "")
## )
tmp_file1 <- tmp_file1 %>% transmute(
 obs_datetime = obs_datetime,
 filename = filename,
 species = species,
  confidence_index = confidence_index,
 real_error = real_error
)
```

```
tmp_file2 <- tmp_file2 %>% transmute(
    .,
    obs_datetime = obs_datetime,
    filename = filename,
    species = species,
    confidence_index = confidence_index,
    real_error = real_error
)

tmp_SNclassifier_results <- bind_rows(
    tmp_file1,
    tmp_file2,
    .id = NULL
)

write_csv(tmp_SNclassifier_results, paste(d_tidy, output_file_name, sep = ""), col_names = TRUE)</pre>
```