BON-in-a Box 2.0 - Block 2 camera trap workflow

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Organize workflow environment

1. Load packages to use in the script.

```
# name libraries
packagesList<-list("rstudioapi", "magrittr", "dplyr", "plyr", "purrr", "raster", "terra", "auk", "sf","
# load libraries
lapply(packagesList, library, character.only = TRUE)</pre>
```

2. Set working directory.

```
# name working directory
dirfolder<- "~/Bloque2/draft_camera_trap"

# set working directory
setwd(dirfolder)</pre>
```

3. Load records data

```
# Load records data
dir_sites_putumayo<- "~/sites_putumayo.csv"
sp_rec = read.csv2(dir_sites_putumayo) %>% dplyr::select(-"X")

# Change date order if needed (correct format yyyy-mm-dd)
sp_rec$eventDate = lubridate::parse_date_time(x = sp_rec$eventDate, order = c("dmy", "Ymd", "dmY"))
```

4. Load covariates data

```
# Load covariates data
covars = read.csv("~/covars_putumayo_2.csv")

# Select detection covariates
covars = dplyr::select(covars, c("Cam.Site", "No_spp", "events", "Lat_Y", "Long_X", "Instal.Date", "Las

# Change date order, if needed
covars$Instal.Date = lubridate::parse_date_time(x = covars$Instal.Date, order = c("dmy", "Ymd", "dmY"))
covars$Last.eventDate = lubridate::parse_date_time(x = covars$Last.eventDate, order = c("dmy", "Ymd", "dm")
```

5. Load study area

```
# Load study area as shapefile
dir_basemap = "D:/Humboldt_provisional/PRUEBAS_CODIGO/ocupacion_B2/Putumayo.shp"
crs_basemap<- CRS("+init=epsg:3395")
res=1000

# Create study area grid
info_layer<- vapour_layer_info(dir_basemap)
extentBase<- vapour::vapour_read_extent(dir_basemap) %>% {c(min(unlist(map(.,1))), max(unlist(map(.,2)))
extent %>% st_bbox(crs= info_layer$projection$Proj4) %>% st_as_sfc() %>% st_transform(crs = crs_basem
rasterbase = raster(extentBase,crs = crs_basemap, res= res )

tname2 = tempfile(fileext = '.tif'); t_file = writeStart(rasterbase, filename = tname2, overwrite = T)
gdalUtilities::gdal_rasterize(dir_basemap, tname2, burn =1, at=T)
raster_area = rast(t_file) %>% {terra::mask(setValues(., seq(ncell(.))), .)}
cell_area = terra::cells(raster_area)
```

6. Add pixels id to data.frame input data

7. Create survey length matrix for each site

8. Create camera operation name of stations

```
# Add a column with date and time
sp_rec1 = sp_rec1 %>% mutate(DateTimeOriginal = paste(eventDate, eventTime))
sp_rec1$DateTimeOriginal = as.POSIXlt(sp_rec1$DateTimeOriginal) # must be format="%Y-%m-%d:%H:%M:%S"
```

9. Create list with all the species in the survey

```
# list the species in the survey
sp_prior = c("Cabassous unicinctus", "Saimiri cassiquiarensis", "Cebus yaracus",
               "Cuniculus paca", "Dasyprocta fuliginosa", "Dasypus novemcinctus",
              "Didelphis marsupialis", "Eira barbara", "Leopardus pardalis", "Leopardus wiedii", "Mazama americana ", "Myrmecophaga tridactyla",
              "Nasua nasua", "Pecari tajacu", "Philander andersoni",
               "Procyon cancrivorus", "Tamandua tetradactyla", "Tupinambis cuzcoensis",
              "Lontra longicaudis ", "Puma concolor ", "Galictis vittata",
              "Cuniculus Paca", "Leopardus pardalis ", "Mazama americana",
              "Tamandua tetradactyla ", "Dasypus novemcinctus ", "Dasyprocta fuliginosa ",
               "Cuniculus paca ", "Eira barbara ", "Philander andersoni ", "Nasua nasua ",
               "Didelphis marsupialis ", "Panthera onca ", "Leopardus tigrinus",
              "Procyon cancrivorus ", "Potos flavus ", "Metachirus nudicaudatus")
# Filter matrix by species list
sp_prior1 = sp_rec1 %>% filter(scientificName %in%sp_prior)
# Show all unique entries of species cam.sites that are not in the covars sites, and delete it
not_in_sprec = unique(sp_rec1$Cam.Site)[!unique(sp_rec1$Cam.Site) %in% covars$Cam.Site]
sp_rec2 = filter(sp_rec1, !Cam.Site %in% not_in_sprec)
# Validate all unique entries of species cam.sites are in the covers sites
not_in_sprec1 = unique(sp_rec2$Cam.Site)[!unique(sp_rec2$Cam.Site) %in% covars$Cam.Site]
```

10. Create detection history for one specie, Cuniculus paca is used as an example

11. Save the result

```
write.csv(DH_paca, "~/DH_paca.csv")
```