EPIDEMIA Malaria Forecasting System: Detailed Walk-through Guide

For epidemia-demo v3.0 using epidemiar v3.1.0

Dawn Nekorchuk, Michael Wimberly, and EPIDEMIA Team Members
Department of Geography and Environmental Sustainability, University of Oklahoma
dawn.nekorchuk@ou.edu; mcwimberly@ou.edu

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Contents

1 Introduction

This detailed walk-through will explain each section of the `run_epidemiar_demo.R` script in the `epidemiar-demo` R project.

All surveillance data in this demo is *simulated* and for *demo use only*. The epidemiological data are artificial and should not be used for research of public health purposes. The environmental data, from Google Earth

Engine, is real. This walk-through is adapted from documentation given to our colleagues in Ethiopia.

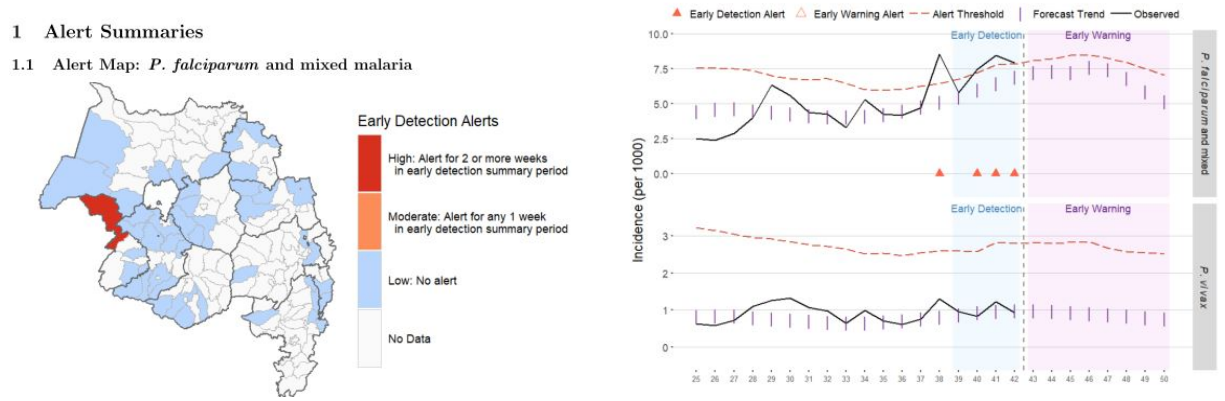
For more details on the `epidemiar` package, see the vignettes (in package, or attached to the latest release in Github as pdfs:

- Overview: `vignette("overview-epidemiar", package = "epidemiar")`
- Input data and modeling parameters: `vignette("data-modeling", package = "epidemiar")`
- Validation guide: `vignette("validation-assessment", package = "epidemiar")`
- Output report data review: `vignette("output-report-data", package = "epidemiar")`

This demo is an example of how data and settings can be organized to feed into `epidemiar::run_epidemia()`.

Goal & end product: The final report presents a malaria forecasting report for 47 woredas in the Amhara region for the past 18 weeks through 8 weeks forecasted into the future (26 total weeks). Malaria is broken out by species: *Plasmodium falciparum* and mixed species, and also *P. vivax*. The report includes environmental and epidemiological surveillance data.

Example sections of the final report:



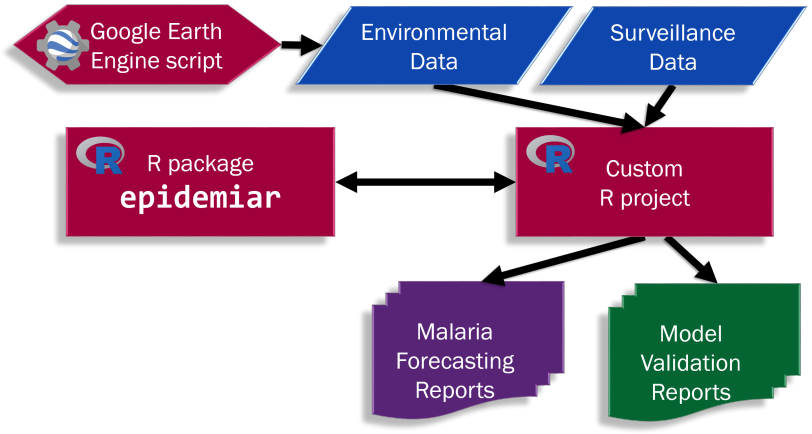
We are going to use R scripts to:

- bring in malaria surveillance and remotely-sensed environmental data
- set some model and event detection parameters
- call the epidemiar functions to run the model, forecast, event detection, produce & save the report data ouput
- send the results to a formatting script (`report/epidemia_report_demo.Rnw`, a Sweave file) to create the final pdf report.
- We can also do the same for validation, see the Validation Guide for epidemiar-demo

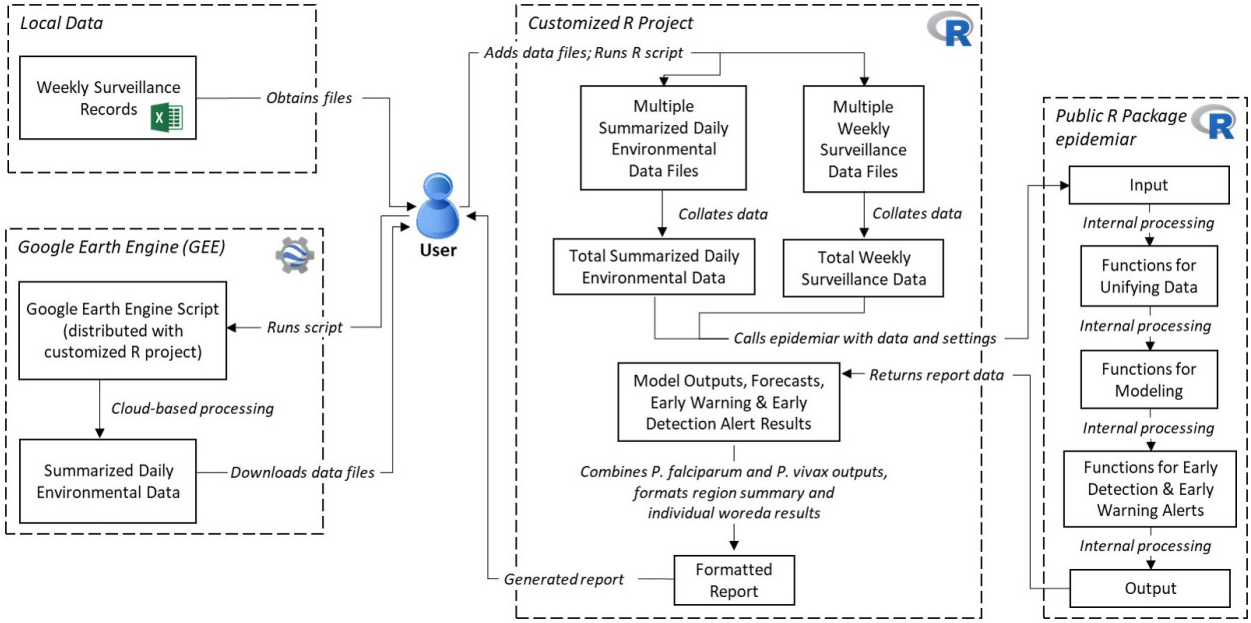
If you have not installed `epidemiar`, or MikTeX ("Install missing packages on-the-fly" = Yes; and restart the computer) yet, please see the Install & Update Guide (`"documentation/install_update.pdf"`) for details on those steps.

Video tutorials were made for our colleagues using a previous version of the software. Some of the details have since changed, but you can view them here: https://www.youtube.com/channel/UC-NKR1cer4wkg8hHHP7K9Vw.

Overview diagram of how `epidemiar-demo` (custom R project) fits into the EPIDEMIA Forecasting System:



A more detailed look at the system:



2 R scripts

Open the `epidemiar_demo.Rproj`. From here, there are three scripts of major importance for forcasting.

1. The script `run_epidemiar_demo.R` will bring in data, run and create the model and forecasts, and generate a pdf report.
2. The script `create_model_demo.R` generates only the forecasting model, which can be used in subsequent runs of `run_epidemiar_demo.R`, saving processing time.
3. The parameter file `data/epidemiar_settings_demo.R` contains the common parameters for both scripts.

2.1 `run_epidemiar_demo.R`: Part I

This script is divided into sections:

1. Loading packages & functions
2. Reading in the data

3. Run EPIDEMIA forecasting & create report data
4. Merge species data, save, and create pdf report

Part I covers the first two sections.

2.1.1 Loading packages & functions

First, we need to load the R packages and functions we will use in this R script.

```
## Load packages necessary for script

#make sure pacman is installed
if (!require("pacman")) install.packages("pacman")
```

```
## Loading required package: pacman
```

```
#load packages
  #note: data corrals use dplyr, tidyr, lubridate, readr, readxl, epidemiar
  #note: pdf creation requires knitr, tinytex
pacman::p_load(dplyr,
               knitr,
               lubridate,
               parallel,
               readr,
               readxl,
               tidyr,
               tinytex,
               tools)
#load specialized package (https://github.com/EcoGRAPH/epidemiar)
library(epidemiar)
```

Using pacman is a convenient way of loading libraries (`library(package-name)`). If a package is missing, it will install it before continuing and prevent the script from stopping with an error.

We use `library()` for the epidemiar package, because this is our project-specific package and does not exist on the R package repository (CRAN), so pacman would fail trying to install epidemiar. See the Install & Update Guide (`"documentation/install_update.pdf"`) for how to install epidemiar, if you have not done so already.

There are also some local R functions, which are local user-defined functions but not part of any package. The data_corrals functions are how the epidemiological and environmental data are each read in and merged together to create data sets to be given to the epidemiar function for modeling. The report_save_create_helpers offer functions that merge the results from *P. falciparum* & mixed species and *P. vivax* model data, sends the result data to the formatting script to produce the pdf report, and saves & creates the formatted validation reports.

```
## Locally-defined Functions
source("R/data_corrals.R")
source("R/report_save_create_helpers.R")
```

2.1.2 Reading in the data

The epidemiar modeling and code requires 3 main sets of data:

1) epidemiological data,
2) daily environmental data, and
3) historical environmental reference/climatology data.

A few look-up tables (metadata or informational reference sets) are needed as well.

2.1.2.1 Woreda metadata

First, we read in some information about the woredas in the Amhara region. We are going to create a subset of woredas that are going to be included in the report. A column named `report` in the metadata file `"data/amhara_woredas.csv"` indicates if the woreda should be in the report. Currently, these are the 47 pilot woredas. To be included in the report, the woreda would need sufficient epidemiological data, environmental data, and model cluster ID. (Note: See documentation inside the `epidemiar` package regarding cluster information. Options are available for clustering, or not, of various geographic areas.)

```
# read in woreda metadata
report_woredas <- read_csv("data/amhara_woredas.csv") %>%
  filter(report == 1)
```

```
## Parsed with column specification:
## cols(
##   WID = col_double(),
##   region = col_character(),
##   zone = col_character(),
##   woreda_name = col_character(),
##   report = col_double(),
##   pilot = col_double()
## )
```

2.1.2.2 Epidemiological data

For the epidemiology data, we will need weekly case counts per woreda of confirmed *P. falciparum* & mixed, and *P. vivax* malaria. To merge data from multiple files, we will use a "data corral" subfolder `data_epidemiological` in the `epidemia-demo` folder.

The data in this demo project have been **simulated**. These data should not be used beyond this demonstration of what a disease report could look like, and should not be taken as indicative of actual epidemiological data.

The `corral_epidemiological()` function will merge all xlsx files in this directory, so you can have multiple files, e.g. one for each year, month, or even by week. No special file names are expected, so you are free to use your standard naming convention. The script is expecting the file to be in your standard format. Specifically, it is looking for the fields: `Woreda/Hospital`, `Budget Year`, `Epi- Week`, `Blood film P. falciparum`, `RDT P. falciparum`, `Blood film P. vivax`, `RDT P. vivax`.

There should be a line for each week and woreda, even for missing data. Any missing (NA) values in the data will be filled in by linear interpolation inside of the epidemiar modeling functions. Gaps in the data, like missing weeks for a woreda, will trigger an warning message. A log file of missing dates will be written, `log_missing_report_epidemiology.csv`, which can be opened with Excel. However, the script will continue and the epidemiar package will add an assumed NA entry for that woreda-week.

No other files should be in this folder. An Excel file that is not epidemiological data will cause the script to fail.

The `corral_epidemiological()` function will loop through all of your xlsx files and combine them. Next, the function will remove any duplicates, choosing data from the file that was most recently modified. The `corral_epidemiological()` function is flexible enough to handle overlapping or partial year files, as long as there are no gaps in dates.

In regards to dates: Conversion from Ethiopian date to Gregorian date was done by adding 7 (ISO week >= 28) or 8 (ISO week < 28) years, e.g. budget year 2011 is in year 2018 for weeks 28 - 52, and 2019 for weeks 1 - 27. Currently, no R function exists for converting full Ethiopian dates to full Gregorian calendar dates. The `obs_date` field is the last day of ISO-8601 week.

The epidemiar package needs total malaria case counts per species. To create this variable, we will add the count of positive blood tests and the count of positive rapid diagnositic tests, for each species. `test_pf_tot` = `'Blood film P. falciparum'` + `'RDT P. falciparum'` and `test_pv_only` = `'Blood film P. vivax'` + `'RDT P. vivax'`.

The `corral_epidemiological()` function also needs three additional metadata files:

- Spelling crosswalk: `data/woreda_spellings.xlsx`: This is a crosswalk between the spellings found in the shapefile and the ones found in the epidemiological xlsx file. Additional alternative spellings can be added into this metafile as needed: `woreda_name` is the shapefile spelling, and `to_replace` is the alternative spelling, and a woreda may have multiple entries. (Note: This is not needed in the demo dataset, but kept for reference how a possible way of handling transliteration differences or common alternative spellings.)
- Split woreda information: `"data/woredas_split.xlsx"`: This is a list of woredas that have split since the model was fitted and produced. Until the woredas have existed for long enough for the model to be refitted, the shapefile updated, historical GEE data gathered, and all metadata/references updated, these will be combined back to the original woredas. Model fitting with cluster identification was done on the pre-split woreda and until the model has been updated, the report can only be generated on the combined woreda. The split woredas will be added back together, to match the original woreda before the split. More splits can be added: `woreda_name` is the original woreda, and `split_1` and `split_2` are the two woredas that it was split into. (Note: This is not needed in the demo dataset, but kept for reference.)
- Population data: `"data/population_weekly_2012_2030.csv"`: This population data is from the EPIDEMIA project: population living in malarious areas, called population at risk, and total population numbers. The population numbers were estimated out into the past and future, using an estimated population growth factor of 1.018.

The script will use the most recent week of data as the malaria report date, i.e. it will produce a report with forecasting starting the following future week.

```
# read & process case data needed for report
epi_data <- corral_epidemiological(report_woreda_names = report_woredas$woreda_name)
```

```
## Reading epidemiological data...

## Processing epidemiological data...

## Epidemiological data date range is 2012-07-15 to 2018-12-30 (YYYY-MM-DD).
```

2.1.2.3 Environmental data

For the environmental data, daily data is expected for each environmental variable for each woreda.

We are using the previous 181 days of environmental data in modeling the effects of the environmental variables to the case numbers, and so we must have environmental data at least that number of days *before* the first epidemiology data date. The included EPIDEMIA project environmental dataset has environmental data starting 2001/2002 for demonstration of how to make a historical/reference data set, but to run the report would only require data from 2012 W1. We will set the lag length to 181 days (`lag_length`) in the Forecasting section below. Updated environmental data will be obtained from Google Earth Engine (GEE), which is a repository for many different types of satellite imagery and will process and summarize this data for us, so that we only have to download a small text-based file.

The script can run with more recent epidemiological data than environmental data (or vice versa). Missing environmental data, either gaps within the known past or in a forecasted future are filled in using a progressive blending technique that combines the last known value (of the previous week) and week by week blends it more with the historical/climatic data set for that week (for that geogroup, if there are different geogroups). The longer the run of missing data, the more it reverts to the climatic average. If possible, we recommend getting the latest environmental data available before running a report.

The `corral_environment()` function works similarly to its epidemiological counterpart. All environmental data files are stored in subfolder `data_environmental/`. The `corral_environment()` function will loop through all csv (GEE) files and combine them. Next, the function will remove any duplicates, choosing data from the file that was most recently modified. Finally, it will check for any gaps in data. Missing days (not NA entries, but missing rows) for any environmental variable will cause an error and stop the script. A log file of the missing days will be written, `log_missing_environmental.csv` which can be opened in Excel. To fix

the error, run the GEE script for the missing dates and copy the files into the `data_environmental` subfolder. The corral function missing checks are slightly different from the checks inside epidemiar. The corral function only checks per environmental variable (not by woreda), but checks over the entire dataset presented. The epidemiar package checks per environmental variable per woreda, but only in the past data back to what is needed for lag length, and no checking is done during the report period (where future/unknown values can be being imputed).

Only GEE downloaded data in csv format should be added to the `data_environmental/` folder. An csv file that is not GEE-formated environmental data will cause the script to fail.

The `corral_environment()` function takes a single argument, a tibble of woredas that will be included in the report. This list of woredas is used to filter the environmental data into a smaller subset of data. The smaller dataset will take less time to process and the script will run faster.

```
# read & process environmental data for woredas in report
env_data <- corral_environment(report_woredas = report_woredas)
```

```
## Reading environmental data...

## Processing environmental data...

## Environmental data date range (YYYY-MM-DD):

## # A tibble: 9 x 3
##   environ_var_code start_dt   end_dt
##   <chr>            <date>     <date>
## 1 evi              2001-01-01 2018-12-30
## 2 lst_day          2002-01-01 2018-12-30
## 3 lst_mean         2002-01-01 2018-12-30
## 4 lst_night        2002-01-01 2018-12-30
## 5 ndvi             2001-01-01 2018-12-30
## 6 ndwi5            2001-01-01 2018-12-30
## 7 ndwi6            2001-01-01 2018-12-30
## 8 savi             2001-01-01 2018-12-30
## 9 totprec          2002-01-01 2018-12-31
```

2.1.2.4 Environmental reference/climatology data

The environmental reference / climate data file `"data/env_ref_data_2002_2018.csv"` contains a average value for each the environmental variable for each woreda for each week of the year. These data are used with the most recently known daily environmental values to estimate future values of the environmental variables for forecasting. These data are also used to calculate anomalies. Anomalies are the difference between the current value and the historical average value. The anomalies are used in the modeling. The current reference file is a 16-year average (2002 - 2018).

```
# read in climatology / environmental reference data
env_ref_data <- read_csv("data/env_ref_data_2002_2018.csv",
                         col_types = cols())
```

The demo project contains the large history of daily environmental data to also demonstrate the `epidemiar::env_daily_to_ref()` function that will create a reference/climatology data set from daily data. Because of processing time (especially for long histories), it is recommended that you run this infrequently to generate a reference dataset that is then saved to be read in later, rather than regenerated each time. The `week_type` of this function defaults to "ISO" for ISO8601/WHO standard week of year and should match the week type for the epidemiological data. This function also requires the `env_info` data, see next section.

```
#provided as an example, not found in the scripts
env_ref_data <- epidemiar::env_daily_to_ref(daily_env_data = env_data,
                                            groupfield = woreda_name,
                                            obsfield = environ_var_code,
```

```
                                        valuefield = obs_value,
                                        week_type = "ISO",
                                        env_info = env_info)
```

2.1.2.5 Environmental variable information

The environmental variable information file `"data/environ_info.xlsx"` lists the environmental variables and important information about the variable.

```
# read in environmental info file
env_info <- read_xlsx("data/environ_info.xlsx", na = "NA")
```

- `environ_var_code`: Short name for the environmental variable, using the GEE variable names
- `reference_method`: 'sum' or 'mean' for how to aggregate daily values into weekly values. For example, rainfall would be the 'sum' of the daily values, while LST would be the 'mean' value during that week
- `report_label`: The axis label to be used in creating the formatted report graphs

```
# read in forecast and event detection parameters
source("data/epidemiar_settings_demo.R")
```

2.1.2.6 Parameter file

This parameter file contains all the report settings for the overall report, forecasting, and early detection. If a pre-built model is used, this should be the same parameters as when the model was generated. See next section for a full description of this file.

2.2 `model_parameters_demo.R`

The parameter file contains all the settings for the overall report, model, forecasting, and early detection.

2.2.1 Set up general report and epidemiological parameters

In this section we set up some parameters for the overall report and for the epidemiological data.

First set the number of weeks in the report and set up for modeling and forecasting. The malaria forecasting report will show a total of 26 weeks. This includes the number of weeks for the future forecast portion (the early warning period). The report will show a number of historical weeks plus the forecast weeks for a total of 26 weeks. (Note: These week lengths were not arbitrary, but a consensus agreement from discussions with our Ethiopian colleagues.)

```
#total number of weeks in report (including forecast period)
report_period <- 26
```

For the Amhara report, we have population data and we wanted the output in incidence (instead of case counts) and in rates of malaria cases per 1000 people at risk.

```
#report out in incidence
report_value_type <-  "incidence"

#report incidence rates per 1000 people
report_inc_per <- 1000
```

The epidemiological data is collected based on WHO (ISO-8601 standard) epidemiological weeks.

We do not use any transformation of the case counts for modeling, but there is an option for a "log_plus_one" transformation (and back-transformation), if relevant for certain model families.

The Amhara dataset had few missing values, which we linearly interpolate. If there are large numbers of missing values, we recommend other methods of interpolation before feeding the data to run_epidemia.

```
#date type in epidemiological data
epi_date_type <- "weekISO"

#interpolate epi data?
epi_interpolate <- TRUE
```

In this demo model, we are using a Gaussian model, with a transformation of log+1 on the case counts (and back-transform after predicting). Here we set the transformation. The default is "none" for no transformation.

```
#use a transformation on the epi data for modeling? ("none" if not)
#Note that this is closely tied with the model family parameter below
#   fc_model_family <- "gaussian()"
epi_transform <- "log_plus_one"
```

Depending on the type of model being run, it may take several minutes for the model to be fit and generated. There is an option to do a model run, which will only create the regression object(s). This can then be passed back in via `model_cached` to skip model generation. See the larger optional Model Caching section below. Our demo project does not by default use model runs or model caching, and thus are set as such in the parameter file here:

```
#model runs and objects
model_run <- FALSE
model_cached <- NULL
```

2.2.2 Set up environment variable parameters

Next, we are going to read in a file that contain which environmental variables to use.

- These envvars files just have a list of which `environ_var_code` variables to use in the modeling.

For the *P. falciparum* and mixed malaria model, the environmental variables are rainfall, daytime Land Surface Temperature (LST), and Normalized Difference Water Index (NDWI6; a satellite-derived index for vegetation water content). For the *P. vivax* model, the environmental variables are rainfall, the mean of daytime and nighttime LST, and NDWI6.

```
#read in model environmental variables to use
pfm_model_env <- read_csv("data/falciparum_model_envvars.csv",
                          col_types = cols())
pv_model_env <- read_csv("data/vivax_model_envvars.csv",
                         col_types = cols())
```

There are also two other parameters directly related to the environmental variables: the total length of the lags we want to consider for the environmental conditions, and whether to use the raw values or rather the amount the values deviate from normal (i.e. the anomalies).

We want to use the previous 181 days, the "lag length", of environmental data in modeling the effects of the environmental variables on malaria case numbers. Each woreda and week is associated with environmental data on the day the week began, up to 180 days in the past, so that each woreda-week has a 181-day history of weather data. When using `fc_splines = "tp"` (set in the next section for forecasting, see below), a smooth term is created for the 181-day history, for example `s(lag, by = totprec, bs = "tp")`, where lag is a simple 181 counter and totprec is a matrix of 181 daily values of precipitation. Importantly, in order to include cluster as a factor for the environmental variables, a separate model is created for each cluster (see description of clusters below). This is done through functions in the new EPIDEMIA system package `clusterapply`. To allow for clusters with only one geogroup, a fall-back equation built around one geogroup is generated and passed to be used if the original model fails. When using `fc_splines = "modbs"` a distributed lag basis is created with the natural cubic splines function, including intercept, with knots at 25%, 50%, and 75% of the lag length. The 5 basis functions that result are multiplied by each woreda's

history, so that there are just 5 summary statistics, instead of 181, for every combination of woreda, week, and environmental co-variate.

There is a switch to use the raw values of environmental variables or to use the anomaly values (residuals from a simple bam model with only geographic area (group) and day of year). The default is FALSE, but for our demo Poisson model we use the anomalies.

```
#set maximum environmental lag length (in days)
env_lag_length <- 181

#use environmental anomalies for modeling?
# TRUE for poisson model
env_anomalies <- TRUE
```

2.2.3 Set up the forecast controls

In our demo version, we use a Gaussian model, which we designate by passing the model family function `gaussian()` to the `fc_model_family` parameters. The EPIDEMIA system uses `mgcv::bam()` for regression, and can accept any quadratically penalized GLM model family and also the extended families in `family.mgcv`.

For the long-term trend per woreda, and the lagged environmental co-variates by woreda and cluster, we offer two different spline methods for the regression terms. 1) With the installation of a companion package (`clusterapply`), thin plate splines are used instead (`report_settings$fc_splines = "tp"` and the default when `clusterapply` is installed). The `clusterapply` package is our specialized wrapper over some of the mgcv functions so that we can use thin plate splines for each lagged environmental variable *by cluster*. 2) Using modified b-splines (`report_settings$fc_splines = "modbs"`), a distributed lag basis is created with the natural cubic splines function (ns, splines library), including intercept, with knots at 25%, 50%, and 75% of the lag length. The 5 basis functions that result are multiplied by each group's history, so that there are just 5 summary statistics, instead of lag length, for every combination of group, week, and environmental anomaly co-variate. We have found that thin plate splines are more effective at capturing complex, non-linear relationships and our preliminary analyses show that using thin plate splines produce better predictions without over-fitting.

The demo model for synthetic malaria data in Amhara is a Gaussian, and note that the `epi_transform` parameter from earlier is closely tied to the model choice parameters here.

The demo model also includes a cyclical term based on day of year (doy) to the regression model: `s(doy, bs = "cc", by = woreda_name)`, a cubic spline smooth term per woreda.

For the forecast report, we extend the forecast out for 8 weeks past known epidemiological data. There is another available parameter, `fc_start_date` to set a specific week to start forecasting. This is discussed in the Optional settings at the beginning of Part II of run_epidemiar_demo.R script walkthrough below.

```
#Model choice and parameters
#Note that this is closely tied with the epi_transform <- "log_plus_one"
# parameter in the report and epidemiological parameter settings
fc_model_family <- "gaussian()"

#Spline choice for long-term trend and lagged environmental variables
#fc_splines <- "modbs" #modified b-splines
fc_splines <- "tp" #requires clusterapply companion package

#Include seasonal cyclical in modeling?
fc_cyclicals <- TRUE

#forecast 8 weeks into the future
fc_future_period <- 8
```

Woredas were clustered by the pattern of how the malaria incidence responds to the environmental variables. Woredas where these *interactions* between malaria incidence and environment variables were similar were placed in the same cluster. This gives us greater power for the forecast modeling because we have more data points in that cluster than in a single woreda alone. These clusters were identified in a genetic algorithm that discovered optimal combinations of clusters and environmental variables. However, clustering can be assigned based on other criteria, such as ecozone, elevation, or region.

- The field `cluster_id` gives the cluster value for each woreda, by `woreda_name`.

(Note: Clustering is not necessary, you may also run with a global or individual model. See the vignette in `epidemiar` on modeling data inputs `vignette("data-modeling", package = "epidemiar")` for more details.)

```
#read in model cluster information
pfm_fc_clusters <- readr::read_csv("data/falciparum_model_clusters.csv",
                                   col_types = readr::cols())
pv_fc_clusters <- readr::read_csv("data/vivax_model_clusters.csv",
                                  col_types = readr::cols())
```

The epidemiar functions will try to take advantage of parallel processing when available on the machine that is running the script. It will test for the number of physical cores on the computer and take advantage of all of them for multi-threading when running regression models or predicting values. The user can override the automatic detection with the `fc_nores` argument (which, here, is the same detection function as what epidemiar will do internally, for explanation). There is also a `fc_nthreads` argument that the user can set instead, if they know exactly how many concurrent processes (threads) they want to run with. If unset, epidemiar will use the number of physical cores either given by the user or detected.

```
#info for parallel processing on the machine the script is running on
fc_ncores <- max(parallel::detectCores(logical=FALSE),
                 1,
                 na.rm = TRUE)
```

2.2.4 Set up early detection controls

In this section, we set up the parameters for the early detection algorithm.

The malaria forecasting report shows a total of 26 weeks (set by `report_period <- 26` earlier). This will be 18 weeks of known data, and 8 weeks of forecasted values (set by `fc_future_period <- 8` earlier). Within the 18 weeks of known data, the most recent four (4) weeks are designated as the 'early detection period' by the parameter `ed_summary_period` here. (Note: These lengths were not arbitrary, but a consensus agreement from discussions with our Ethiopian colleagues.)

```
#number of weeks in early detection period (last n weeks of known epidemiological data to summarize ale
ed_summary_period <- 4
```

Next, we are going to set up the parameters used in the Farrington improved event detection algorithm. We will be using the `farringtonFlexible()` function as implemented in the `surveillance` package. We specify that we are using this algorithm with `ed_method = "farrington"`. Currently, the only other built option is "None" for no event detection.

The central idea of event detection is to identify when the number of cases exceeds a baseline threshold, and this detection happens as close to real-time as possible. Event detection is done in a prospective manner, where the algorithm knows past data up to the present. This is different from retrospective methods, where events are identified from historical data. There are many different prospective event detection algorithms. Each algorithm calculates baseline thresholds differently and have different assumptions about the pattern of disease transmission, speed of outbreak development, seasonality, and trends.

The Farrington Original method was developed in 1996 and an improved version was released in 2013. The original method is used at Statens Serum Institut in Denmark, Centre for Infections of the Health Protection

Agency (HPA) UK, National Institute for Public Health and the Environment (RIVM) the Netherlands (as of 2010). The Farrington methods are based on quasi-Poisson regression, and allows for long-term trend adjustments, seasonality, and re-weighting of past event case numbers.

The parameters below are the Farrington improved versions we tested that had the highest percent of events caught and the lowest rate of false alarms. The Farrington method performed better than the other methods we compared: Center for Disease Control and Prevention (CDC) Early Aberation Reporting System (EARS) and the first EPIDEMIA system using dynamic linear modeling. We tested each species separately, so there are different settings for *P. falciparum* (and mixed) and *P. vivax*. The parameters are all added to a list so that we have one object that has all the controls for Farrington event detection.

```
#event detection algorithm
ed_method <- "Farrington"

#settings for Farrington event detection algorithm
pfm_ed_control <- list(
  w = 3, reweight = TRUE, weightsThreshold = 2.58,
  trend = TRUE, pThresholdTrend = 0,
  populationOffset = TRUE,
  noPeriods = 12, pastWeeksNotIncluded = 4,
  limit54=c(1,4),
  thresholdMethod = "nbPlugin")

pv_ed_control <- list(
  w = 4, reweight = TRUE, weightsThreshold = 2.58,
  trend = TRUE, pThresholdTrend = 0,
  populationOffset = TRUE,
  noPeriods = 10, pastWeeksNotIncluded = 4,
  limit54 = c(1,4),
  thresholdMethod = "nbPlugin")
```

Farrington flexible settings:

- w: the number of timepoints in the window
- reweight: if identified past events are reweighted lower (so past events don't raise the new thresholds too high)
- weightsThreshold: the default value 2.58 in the Farrington revised algorithm that was found to be best performing by the authors who updated the algorithm
- trend: Use trend weighting over the past years
- pThresholdTrend: 0 value means always use trend adjustment
- populationOffset: Use population to adjust case numbers
- noPeriods: break up the year into 10 periods for modeling
- pastWeeksNotIncluded: Discount the first 4 weeks when testing for events to avoid incorrect results when an event is occuring right at the beginning of the period
- limit54: (cases, period) for when no alarm should be triggered if there are fewer than these number of cases in the past period. This was not part of our initial parameter investigation, but added later to satisfy a request that thresholds be should even when few cases were happening.
- thresholdMethod: Use the recommended statistical method for calculating thresholds.

For more details, please run `?surveillance::farringtonFlexible` in the RStudio console to get the help file for this function.

2.2.5 Combine into report settings

Finally, we just put the forecasting controls into a list, so that we have one list object per species with all the controls for the forecasting. Note that `fc_model_family` set in Forecast section is a top-level parameter and separate from the rest of the report_settings.

IMPORTANT: If you have added or removed parameters above, you will need to edit these control lists as well.

```
pfm_report_settings <- epidemiar::create_named_list(report_period,
                                                    report_value_type,
                                                    report_inc_per,
                                                    epi_date_type,
                                                    epi_interpolate,
                                                    epi_transform,
                                                    model_run,
                                                    env_var = pfm_env_var,
                                                    env_lag_length,
                                                    env_anomalies,
                                                    fc_splines,
                                                    fc_cyclicals,
                                                    fc_future_period,
                                                    fc_clusters = pfm_fc_clusters,
                                                    fc_ncores,
                                                    ed_summary_period,
                                                    ed_method,
                                                    ed_control = pfm_ed_control)

pv_report_settings <- epidemiar::create_named_list(report_period,
                                                   report_value_type,
                                                   report_inc_per,
                                                   epi_date_type,
                                                   epi_interpolate,
                                                   epi_transform,
                                                   model_run,
                                                   env_var = pv_env_var,
                                                   env_lag_length,
                                                   env_anomalies,
                                                   fc_splines,
                                                   fc_cyclicals,
                                                   fc_future_period,
                                                   fc_clusters = pv_fc_clusters,
                                                   fc_ncores,
                                                   ed_summary_period,
                                                   ed_method,
                                                   ed_control = pv_ed_control)
```

2.3 `run_epidemiar_demo.R`: Part II

This script is divided into sections:

1. Loading packages & functions
2. Reading in the data
3. Run epidemia & create report data
4. Merge species data, save, and create pdf report

Part II covers the last two sections.

2.3.1 Optional adjustments and settings

After we have read in the parameter file, there are a couple of optional adjustment we could make (if we did not want to edit the parameter file directly). Any parameter could be updated by name. Here are three

optional settings depending on the situation, which are not used as defaults in the demo example.

2.3.1.1 Optional: Date Filtering

By default, the report will be generated for the last week of available epidemiological data in the `data_epidemiological/` corral folder. If you wish to run a report for a particular previous week, with censoring of data up to that week, you can simply quickly filter the data after the corrals. Environmental data does not need to be filtered as it will run with whatever environmental data is or is not available. But if you are simulating a forecast report as if it was run on that week, you should filter back to that date as well. This option is not to be confused with the `report_settings$fc_start_date` parameter under forecasting controls in the settings file, which allows you to set a date, past, present or future, for the start of the forecast period instead, but does *not* filter data.

```
## Optional: Date Filtering for running certain week's report
# week is always end of the week, 7th day
req_date <- epidemiar::make_date_yw(year = 2018, week = 52, weekday = 7)
epi_data <- epi_data %>%
  filter(obs_date <= req_date)
env_data <- env_data %>%
  filter(obs_date <= req_date)
```

2.3.1.2 Optional: Set forecast start date

By default, the forecasting report will begin forecasting 'future' weeks for one week past the last known/observed epidemiological data date. If instead you wish to set the forecast further into the future (or in the past without data censoring), you can set the `fc_start_date` parameter. Note that model accuracy decreases without recent environmental data (as we are imputing 'future' values), and that there may be no known data (and therefore results) for 'early detection' in the event detection section if the `report_settings$fc_start_date` is more than `report_settings$ed_summary_period` weeks after known/observed epidemiological data.

```
## OPTIONAL: If instead the forecast should be beyond known epi data,
# then you can set the forecast start date directly
pfm_report_settings$fc_start_date <- epidemiar::make_date_yw(2019, 4, 7)
pv_report_settings$fc_start_date <- epidemiar::make_date_yw(2019, 4, 7)
```

2.3.1.3 Optional: Model caching

If previous models have been built, they can be read in here. This will skip the model building steps inside of `run_epidemia()` and save on processing time. Models will need to be rebuilt periodically, and how often that needs to be done is heavily dependent on the specific dataset and reporting needs. The script will look for all of the *P. falciparum* and mixed models (RDS files that start with "pfm") and separately for *P. vivax*. It will automatically choose the model with the latest (most recent) file creation time. This is given as an option, but is not used with our Amhara reports (the model run settings are set to FALSE and NULL inside the parameter file, discussed later).

```
# OPTIONAL: If you have created cached models to use instead of generating a new model:
# selects the model per species with latest file created time
# pfm
all_pfm_models <- file.info(list.files("data/models/",
                                       full.names = TRUE,
                                       pattern="^pfm.*\\.RDS$"))
if (nrow(all_pfm_models) > 0){
  latest_pfm_model <- rownames(all_pfm_models)[which.max(all_pfm_models$ctime)]
  pfm_model_cached <- readRDS(latest_pfm_model)
}
pfm_report_settings$model_cached <- readRDS(latest_pfm_model)

#pv
all_pv_models <- file.info(list.files("data/models/",
                                      full.names = TRUE,
```

```
                                        pattern="^pv.*\\.RDS$"))
if (nrow(all_pv_models) > 0){
  latest_pv_model <- rownames(all_pv_models)[which.max(all_pv_models$ctime)]
  pv_model_cached <- readRDS(latest_pv_model)
}
pv_report_settings$model_cached <- readRDS(latest_pv_model)
```

Alternatively, specific models files can be selected instead:

```
##or select specific file
latest_pfm_model <- "data/pfm_model_xxxxxxx.RDS"
pfm_report_settings$model_cached <- readRDS(latest_pfm_model)

latest_pv_model <- "data/pv_model_xxxxxxxx.RDS"
pv_report_settings$model_cached <- readRDS(latest_pv_model)
```

Or, to create a fresh model inside the run, do not set at all (or set as null). This is the default.

The pfm or pv model_cached is what will be given as the `model_cached` argument to `run_epidemia()`. The file path and name in `latest_pfm_model` and `latest_pv_model` will be added to the output report data metadata (`params_meta`) for record keeping.

2.3.2 Run epidemiar & create report data

Now to actually run the model and generate the report data! Basically, we gather up all the data and settings, and feed it to the `run_epidemia()` function in our `epidemiar` package.

Each malaria species is run on its own, with their respective settings. The main epidemiological dataset contains both species in different columns, and therefore the `casefield` changes between "test_pf_tot" for *P. falciparum* and mixed species, and "test_pv_only" for *P. vivax*. Similarly, the controls for event detection (`ed_control`) and forecasting (`pfm_fc_control`) also change.

After the report data objects have been generated, we add to the metadata, `$params_meta`, a field `$model_used`, to give the file location and name of the model used if a cached model was used.

Note: Since this is a long script, and early error messages may have been missed, we've added a simple check to make sure the epidemiological and environmental data sets have been generated, and if not, it'll produce an informative message towards this end of the script.

```
#Run modeling to get report data
# with check on current epidemiology and environmental data sets

if (exists("epi_data") & exists("env_data")){

  # P. falciparum & mixed
  message("Running P. falciparum & mixed")
  pfm_reportdata <- run_epidemia(
    #data
    epi_data = epi_data,
    env_data = env_data,
    env_ref_data = env_ref_data,
    env_info = env_info,
    #fields
    casefield = test_pf_tot,
    groupfield = woreda_name,
    populationfield = pop_at_risk,
    obsfield = environ_var_code,
```

```
    valuefield = obs_value,
    #required settings
    fc_model_family = fc_model_family,
    #other settings
    report_settings = pfm_report_settings)

  # P. vivax
  message("Running P. vivax")
  pv_reportdata <- run_epidemia(
    #data
    epi_data = epi_data,
    env_data = env_data,
    env_ref_data = env_ref_data,
    env_info = env_info,
    #fields
    casefield = test_pv_only,
    groupfield = woreda_name,
    populationfield = pop_at_risk,
    obsfield = environ_var_code,
    valuefield = obs_value,
    #required settings
    fc_model_family = fc_model_family,
    #other settings
    report_settings = pv_report_settings)

  #if using cached models:
  #append model information to report data metadata
  if (exists('pfm_model_cached')){
    pfm_reportdata$params_meta$model_used <- latest_pfm_model
  }
  if (exists('pv_model_cached')){
    pv_reportdata$params_meta$model_used <- latest_pv_model
  }

} else {
  message("Error: Epidemiological and/or environmental datasets are missing.
          Check Section 2 for data error messages.")
}
```

```
## Running P. falciparum & mixed

## Preparing for forecasting...

## Anomalizing the environmental variables...

## Creating equation using thin plate splines...

## Including seasonal cyclicals into model...

## Creating regression model...

## Creating predictions...

## Running early detection: Farrington...

## Finished.

## Running P. vivax
```

```
## Preparing for forecasting...

## Anomalizing the environmental variables...

## Creating equation using thin plate splines...

## Including seasonal cyclicals into model...

## Creating regression model...

## Creating predictions...

## Running early detection: Farrington...

## Finished.
```

The processing time depends on how powerful your computer is and the settings used for modeling. Passing in a model reduces the time, since it does not have to calculate the model first. Expect this to take about 3 to 10 minutes per species on an average computer or laptop.

The `run_epidemia()` function returns one object. For *P. falciparum* we called this object `pfm_reportdata`, and `pv_repordata` for *P. vivax*. The reportdata object is a list of tibbles of the outputs from the modeling, early detection and early warning algorithms, and other results. (Note: In the Amhara implementation, we have two species that we then combine the results before sending it to the formatting script. You could have multiple diseases you are working with, or you could have only one. Your situation will then drive how you code your report formatting script/Rnw file.)

2.3.3 Report data output

The `run_epidemia()` function returns one object. For *P. falciparum* we called this object `pfm_reportdata`. This object is a list of tibbles, or dataframes. These tibbles are the outputs from the modeling, early detection and early warning algorithms, and other results.

1. `summary_data`
2. `epi_summary`
3. `modeling_results_data`
4. `environ_timeseries`
5. `environ_anomalies`
6. `params_meta`
7. `regression_object`

(Note: For a more generic description of the reportdata object, including per column definitions, see the output data vignette in the `epidemiar` package: `vignette("output-report=data", package = "epidemiar")`. The following description is specific to the malaria demo data.)

```
pfm_reportdata$summary_data
```

2.3.3.1 summary_data

```
## # A tibble: 47 x 5
##    woreda_name     ed_alert_count ed_sum_level ew_alert_count ew_level
##    <chr>                    <dbl> <ord>                 <dbl> <ord>
##  1 Abargelie                    0 Low                       0 Low
##  2 Alefa                        0 Low                       0 Low
##  3 Andabiet                     0 Low                       0 Low
##  4 Ankesha                      0 Low                       0 Low
##  5 Antsokiya Gemza              0 Low                       0 Low
##  6 Artuma Fursi                 0 Low                       0 Low
##  7 Awabel                       0 Low                       0 Low
```

```
##  8 Bahir Dar Zuria              0 Low                       0 Low
##  9 Baso Liben                   0 Low                       0 Low
## 10 Borena                       0 Low                       0 Low
## # ... with 37 more rows
```

This tibble contains the early detection and early warning alert levels for each woreda.

Early detection alerts (`ed_alert_count`) are alerts that are triggered during the early detection period, which is defined as the 4 most recent weeks of known epidemiology data. Similarly, early warning alerts (`ew_alert_count`) are alerts in the future forecast estimates. "High" level indicates two or more weeks in this period had incidences greater than the alert threshold, "Medium" means that one week was in alert status, and "Low" means no weeks had alerts (`ed_sum_level` and `ew_level`, respectively).

- `woreda_name`: The field name of the different woredas
- `ed_alert_count`: Number of alerts triggered in the early detection period
- `ed_sum_level`: High/Medium/Low depending on the number of alerts, 2+/1/0 respectively
- `ew_alert_count`: Number of alerts triggered in the early warning period (future forecast period)
- `ew_level`: High/Medium/Low depending on the number of alerts, 2+/1/0 respectively

```
pfm_reportdata$epi_summary
```

2.3.3.2 epi_summary

```
## # A tibble: 47 x 2
##    woreda_name     mean_epi
##    <chr>              <dbl>
##  1 Abargelie         1.77
##  2 Alefa             0.533
##  3 Andabiet          0.115
##  4 Ankesha           0.258
##  5 Antsokiya Gemza   0.0151
##  6 Artuma Fursi      0.0220
##  7 Awabel            0.0463
##  8 Bahir Dar Zuria   0.135
##  9 Baso Liben        0.684
## 10 Borena            0.0606
## # ... with 37 more rows
```

This tibble holds the mean incidence of malaria in the early detection period per woreda, and is used to generate maps in the third section of the pdf report.

- `woreda_name`: The field name of the different woredas
- `mean_epi`: The mean disease incidence (or cases, depending on the setting in `report_settings$report_value_type`) per woreda summarized over the early detection period

```
pfm_reportdata$modeling_results_data
```

2.3.3.3 modeling_results_data

```
## # A tibble: 4,512 x 9
##    woreda_name obs_date   series value lab   upper lower week_epidemiar
##    <chr>       <date>     <chr>  <dbl> <chr> <dbl> <dbl>          <dbl>
##  1 Abargelie   2018-09-02 obs    0.900 Obse~    NA    NA             35
##  2 Abargelie   2018-09-09 obs    0.919 Obse~    NA    NA             36
##  3 Abargelie   2018-09-16 obs    0.937 Obse~    NA    NA             37
##  4 Abargelie   2018-09-23 obs    1.07  Obse~    NA    NA             38
```

```
##  5 Abargelie   2018-09-30 obs    1.14  Obse~    NA    NA             39
##  6 Abargelie   2018-10-07 obs    1.41  Obse~    NA    NA             40
##  7 Abargelie   2018-10-14 obs    1.56  Obse~    NA    NA             41
##  8 Abargelie   2018-10-21 obs    1.80  Obse~    NA    NA             42
##  9 Abargelie   2018-10-28 obs    2.10  Obse~    NA    NA             43
## 10 Abargelie   2018-11-04 obs    2.40  Obse~    NA    NA             44
## # ... with 4,502 more rows, and 1 more variable: year_epidemiar <dbl>
```

This tibble dataset contains multiple timeseries values for observed, forecast, and alert thresholds of malaria incidence, for each woreda over the report period. These data are used in creating the individual woreda control charts in the pdf report.

- `woreda_name`: The field name of the different woredas
- `obs_date`: The last day of the epidemiological week, Date object
- `series`: "obs" = observed disease incidence, "fc" = modeled/forecast incidence values, "thresh" = event detection threshold values, "ed" = early detection alert (binary), "ew" = early warning alert (binary)
- `value`: Value of the `series` for that geographic group for that week
- `lab`: Labels for the series ("Observed", "Forecast Trend", "Alert Threshold", "Early Detection Alert", "Early Warning Alert")
- `upper`: Unused
- `lower`: Unused
- `week_epidemiar`: ISO week number
- `year_epidemiar`: ISO year

```
pfm_reportdata$environ_timeseries
```

2.3.3.4 environ_timeseries

```
## # A tibble: 3,666 x 16
##    woreda_name environ_var_code year_epidemiar week_epidemiar obs_date
##    <chr>       <chr>                    <dbl>          <dbl> <date>
##  1 Abargelie   lst_day                   2018             35 2018-09-02
##  2 Abargelie   ndwi6                     2018             35 2018-09-02
##  3 Abargelie   totprec                   2018             35 2018-09-02
##  4 Abargelie   lst_day                   2018             36 2018-09-09
##  5 Abargelie   ndwi6                     2018             36 2018-09-09
##  6 Abargelie   totprec                   2018             36 2018-09-09
##  7 Abargelie   lst_day                   2018             37 2018-09-16
##  8 Abargelie   ndwi6                     2018             37 2018-09-16
##  9 Abargelie   totprec                   2018             37 2018-09-16
## 10 Abargelie   lst_day                   2018             38 2018-09-23
## # ... with 3,656 more rows, and 11 more variables: val_epidemiar <dbl>,
## #   reference_method <chr>, data_source <chr>, ref_value <dbl>, ref_sd <dbl>,
## #   ref_yrcount <dbl>, ref_max <dbl>, ref_uq <dbl>, ref_median <dbl>,
## #   ref_lq <dbl>, ref_min <dbl>
```

This tibble dataset contains multiple timeseries for the environmental variables for each woreda, and are used to generate the environmental timeseries graphs on the individual woreda report pages. * `woreda_name`: The field name of the different woredas * `environ_var_code`: The field for the different environmental variables * `week_epidemiar`: ISO week number * `year_epidemiar`: ISO year * `obs_date`: The last day of the epidemiological week (ISO), Date object * `val_epidemiar`: Value of the environmental variable for that geographic group for that week. Values are a combination of observed, or interpolated (for missing) or extended (future estimated) values.
* `reference_method`: Method for creating a weekly summary from daily data (e.g. "sum" for rainfall, or "mean" for NDWI) * `data_source`: "Observed" or "Imputed". Environment data was either observed, or

if it was NA/missing, it was filled in (imputed). For gaps less than 2 weeks, the values are filled in with a persistence method (carry-forward). The recent values are calculated as the average of the past 7 days for 'mean' type variables (as defined in the user's `environ_info` metadata, e.g. for NDWI, LST), or the past 14 known days for 'sum' type variables (as defined in the user's `environ_info` metadata, e.g. for precipitation-like measures). For periods longer than 2 weeks, daily values were imputed using a progressive blend of the recent values (as above) with the climatology/historical averages for that week of the year (from `environ_ref_data`). * `ref_value`: From `env_ref_data`.
* `ref_*`: Fields from `env_ref_data` that begin with `ref_` have been propagating through to here. (Potentially useful for plotting later, for example.)

```
pfm_reportdata$environ_anomalies
```

2.3.3.5 environ_anomalies

```
## # A tibble: 141 x 3
##    woreda_name environ_var_code anom_ed_mean
##    <chr>       <chr>                   <dbl>
##  1 Abargelie   lst_day               -0.228
##  2 Abargelie   ndwi6                  0.000362
##  3 Abargelie   totprec               -1.37
##  4 Alefa       lst_day               -0.338
##  5 Alefa       ndwi6                  0.0147
##  6 Alefa       totprec                0.463
##  7 Andabiet    lst_day               -1.01
##  8 Andabiet    ndwi6                  0.00647
##  9 Andabiet    totprec               -0.662
## 10 Ankesha     lst_day               -0.442
## # ... with 131 more rows
```

This tibble dataset contains the differences of the environmental variable values from the climatology/reference average during the early detection period. These data are used to make anomaly maps in the third section of the pdf report.

- `woreda_name`: The field name of the different woredas
- `environ_var_code`: The field for the different environmental variables
- `anom_ed_mean`: The mean of the anomalies per environmental variable per geographic group summarized during the early detection period. These anomalies are calculated as the difference from the observed value to the historical mean for that week of the year. (Not to be confused with the daily anomalies calculated for modeling and forecasting.)

2.3.3.6 params_meta This lists all the dates, settings, and parameters that were used in the `run_epidemiar()` function. This keeps a record of all the settings so you can view them later.

2.3.3.7 regression_object This is the regression object from the general additive model (GAM, parallelized with BAM) regression. This is only for statistical investigation of the model, and is usually not saved because it very large object. To save it, set the `save_reg` argument of `merge_save_report()` to "TRUE" (default is FALSE).

2.3.4 Aside: Model Only Run Output

Model runs and model caching is not by default used in the demo model, however all the code necessary to do so is present.

The results of `run_epidemiar(..., report_settings$model_run = TRUE)` is a cached model: the regression object plus some metadata information about what was used to generate the model. Once a model has

been generated, it can be fed back into `run_epidemiar(..., report_settings$model_cached = {cached model object})` for faster predictions rather than regenerating the model on each run. Determining the balance on how old of a model is still useful is heavily dependent on the specific dataset.

1. `model_obj`
2. `model_info`

2.4 model_obj

The output regression object from the `mgcv::bam()` general additive model regression call, or a list of models per cluster from `clusterapply` depending on the model settings.

2.5 model_info

A list of dates, settings, and relevant parameters that `run_epidemiar()` was called with. Very similar to `params_meta` of a full run.

2.5.1 Merge species data, save, and create pdf report

The Amhara malaria demo data has two different reportdata objects (*P. falciparum* and mixed species, and *P. vivax*), which need to be merged together into one object to save and to create the single pdf report.

(Note: Since this is a long script, and early error messages may have been missed, we've added a simple check to make sure the report data for each species have been generated, and if not, it'll produce an informative message towards this end of the script.)

```
if (exists("pfm_reportdata") & exists("pv_reportdata")){

  #merging pfm & pv data, save out, and create pdf
  merge_save_report(rpt_data_main = pfm_reportdata,
                    rpt_data_secd = pv_reportdata,
                    #mark sections as P. falciparum and mixed (pfm) or P. vivax (pv)
                    # used in the epidemia_report_demo.Rnw file for the formatted report
                    var_labs = c("pfm","pv"),
                    #save out the report data in the file that the formatting file reads
                    save_file = "report/report_data.RData",
                    #save out 2nd copy of report data w/ year & week in the name
                    second_save = TRUE,
                    #create the pdf
                    create_report = TRUE,
                    #which Rnw file to use to create pdf
                    formatting_file = "epidemia_report_demo.Rnw",
                    #append tag to file name (optional)
                    file_name_postfix = "synthetic_data",
                    #show the pdf immediately after creating
                    show_report = TRUE)

} else {
  message("Error: Report data for P. falciparum and/or P. vivax
          have not been generated and are missing.")
}
```

This function will save out the merged report_data object in two places:

- `save_file = "report/report_data.RData"`: this file is the *input* file of the Rnw/formatting script (`epidemia_report_demo.Rnw`). The input file of the rnw cannot be particularly changed except by

editing the rnw file directly. Therefore this is a 'generic' named file, which is overwritten each time to be used as input to the rnw file.
- `second_save = TRUE`: this saves out a more permanent version of the merged report_data object with an autogenerated year and week numbers in the file name (e.g. "report_data_2018W52_AHRB.RData" for the report generated with last known epidemiological data of week 2018 Week 52: 2019-12-24 through 2018-12-30.)

(Note: This function also takes in the location/name of the rnw formatting script as well, so there is the possibility of having multiple different report formatting that uses the same input data. The save_file and input file of the formatting_file will need to match up correctly.)

This function calls a subfunction named `create_pdf()` which calls the Sweave formatting script, `report/epidemia_report_demo.Rnw`, to read in the report data (`report/report_data.RData`, as specified in the rnw file) we just created, and to create the formatted pdf report. This `Rnw` Sweave file has been written specifically for the malaria forecasting report in Amhara. The `Rnw` file also uses some additional data: shapefiles (processed into R data files as `data/am.rda` and `data/am_simpl.rda`), and the woreda reference list (`data/amhara_woredas.csv`).

This subfunction will save two copies of the pdf formatted report:

- `epidemia_report_demo.pdf`: default output of an rnw file - name of the rnw file as a pdf
- `epidemia_report_demo{_YYYY"W"WW}_{file_name_postfix}.pdf`: a renamed version of the file with autogenerated year and week numbers in the file, same scheme as the second_save of the report_data object, above.

(Note: The save function was written to also handle single output dataset, i.e. ones that are not split by species. Give the output to the `rpt_data_main` argument, and leave `rpt_data_secd` NULL.)

2.5.2 Alternative: Create pdf report

You can also call the `create_pdf()` function directly is you want to generate a formatted pdf report from a previously save report_data object. The `new_data` file will overwrite `report_data_file`, which needs to be the input file that is coded inside the `formatting_file` (rnw script).

```
# If you want to later recreate a pdf from a saved report_data file:
# Change the input report_data_file to the previously saved version
# And add a file/name for the saved output.

create_pdf(new_data = "report/report_data_2018W52.RData",
           #file that is loaded in the formatting file
           report_data_file = "report/report_data.RData",
           formatting_file = "epidemia_report_demo.Rnw",
           #specific output file name
           report_save_file = "report/report_data_2018W52.pdf",
           show = TRUE)
```

2.5.3 Alternative: Rnw compile pdf

If you have not set MiKTeX to install missing packages on the fly without asking, the pdf creation will fail. You can compile the pdf once from the Rnw itself, and answer yes to the missing packages installation prompts. Then you can return to using the functions above. In RStudio, open `epidemia_report_demo.Rnw`, and click on `Compile PDF`.

2.6 `create_model_demo.R`

The `create_model_demo.R` is set up like `run_epidemiar_demo.R`, but uses the argument `run_epidemia(..., report_settings$model_run = TRUE)`. This only creates, and returns, a model regression object (or a list of models depending on model settings with `fc_clusters` and `fc_splines`) and metadata on the model.

The last section saves the model in the `data/models` folder with two dates in the file: the first is the year and week of the epidemiological data available when the model was generated, and the second is the date the model was created.

```
# Save models for later use ------------------------------------------

# add last epidemiological known data date, and today's date to file name
save_filetail <- paste0("_", isoyear(max(epi_data$obs_date)),
                        "W", isoweek(max(epi_data$obs_date)),
                        "_", format(Sys.Date(), "%Y%m%d"))
pfm_name <- paste0("pfm_model", save_filetail, ".RDS")
pv_name <- paste0("pv_model", save_filetail, ".RDS")

#save to /data
saveRDS(pfm_model, file.path("data/models", pfm_name))
saveRDS(pv_model, file.path("data/models", pv_name))
```

When the `run_epidemiar_demo.R` script runs, it will automatically pull the model with the latest file creation time to use (if the user does not set a specific model file), and feeds it into `run_epidemiar(..., report_settings$cached_model = {regression + metadata output from model run})`. See the model caching explanation above in `run_epidemiar_demo.R`: Part I.

3 Looping Version

As a prospective report, this script would be run about every week or so as new data comes in. There are times, however, when you want to run a number of historical reports. We've added a version of the script, `run_epidemiar_demo_loopingversion.R` that can be modified (near the top) to run for any number of past weeks.

This is different from just adjusting the `fc_start_date`, because this censors epidemiological and environmental data as well, mimicking what data would be available at the time, rather than changing when forecasting started but using all available data.

The example below would be for isoweeks 23 and 24 in isoyear 2016, plus isoweeks 37, 38, 39, and 40 in 2017. The `weekday` variable is "7" here, indicating the date at the end of the isoweek, which is what is used in the simulated malaria dataset.

```
# This version of the script can be used to loop through multiple weeks
#   to generate reports for each.
#
# Set the loop variable to TRUE, and change the isoyear and isoweeks wanted.
#

loop <- TRUE
wk_list <- c(epidemiar::make_date_yw(year = 2016, week = c(23:24), weekday = 7),
             epidemiar::make_date_yw(year = 2017, week = c(37:40), weekday = 7))
wk_list
```

```
## [1] "2016-06-12" "2016-06-19" "2017-09-17" "2017-09-24" "2017-10-01"
## [6] "2017-10-08"
```

Messages will be printed to the console on which week is currently running. It will save the RData and pdf files with year-week tags in the name, and not immediately pop up pdfs when they are created (`show = FALSE` in `merge_save_report()`).

4 Woreda names

For reference, here is a list of report woreda names:

```
read_csv("data/amhara_woredas.csv") %>%
  filter(report == 1) %>% pull(woreda_name)
```

```
## Parsed with column specification:
## cols(
##   WID = col_double(),
##   region = col_character(),
##   zone = col_character(),
##   woreda_name = col_character(),
##   report = col_double(),
##   pilot = col_double()
## )
```

```
##  [1] "Ankesha"          "Fagita Lekoma"    "Guagusa Shekudad" "Jawi"
##  [5] "Awabel"           "Baso Liben"       "Debre Elias"      "Gozamin"
##  [9] "Alefa"            "Denbia"           "Gondar Zuria"     "Metema"
## [13] "Misrak Belesa"    "Quara"            "Antsokiya Gemza"  "Efratana Gidim"
## [17] "Kewet"            "Merehabete"       "Shewa Robit"      "Bugna"
## [21] "Kobo Town"        "Lasta"            "Mekit"            "Raya Kobo"
## [25] "Artuma Fursi"     "Jilie Timuga"     "Andabiet"         "Dera"
## [29] "Estea"            "Fogera"           "Libokemkem"       "Borena"
## [33] "Kalu"             "Tehulederie"      "Abargelie"        "Dehena"
## [37] "Sehela"           "Bahir Dar Zuria"  "Burie Zuria"      "Dembecha"
## [41] "Gonji Kolela"     "Jabi Tehnan"      "Mecha"            "North Achefer"
## [45] "South Achefer"    "Womberma"         "Yilmana Densa"
```