



**Barcelona
Supercomputing
Center**
Centro Nacional de Supercomputación



HARMONIZE



Tutorial: clim4health



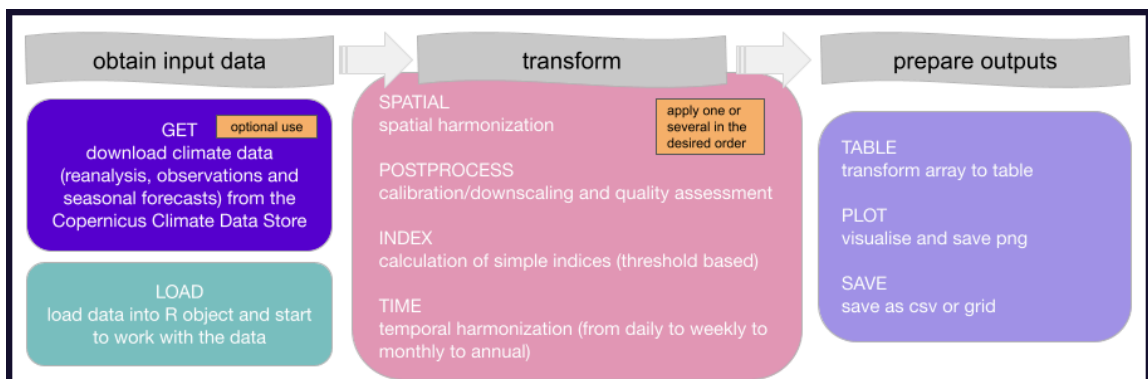
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1. Introduction

clim4health is a tool developed within the HARMONIZE project with the aim of post-processing climate data harmonized to the spatiotemporal aggregation of health data. The tool consists in an R-package and its documentation including examples on how to use the tool and recommendations of parameter selection in some case studies.



2. Setup and Data Loading

```
In [ ]: options(warn = -1)
```

```
In [1]: setwd("dependencies/ghr_libraries/clim4health/")
path <- getwd()

install.packages("exactextractr")
install.packages("ecmwfr")

library(exactextractr)
library(ecmwfr)
library(sf)

source(paste0(path, '/functions/clim4health_load.R'))
source(paste0(path, '/functions/clim4health_index.R'))
source(paste0(path, '/functions/clim4health_time.R'))
source(paste0(path, '/functions/clim4health_spatial.R'))
source(paste0(path, '/functions/clim4health_get.R'))
```

Installing package into 'C:/Users/rcapella/AppData/Local/R/win-library/4.4'
(as 'lib' is unspecified)

package 'exactextractr' successfully unpacked and MD5 sums checked

The downloaded binary packages are in
C:\Users\rcapella\AppData\Local\Temp\Rtmpg1y11V\downloaded_packages

Installing package into 'C:/Users/rcapella/AppData/Local/R/win-library/4.4'
(as 'lib' is unspecified)

package 'ecmwfr' successfully unpacked and MD5 sums checked

The downloaded binary packages are in
C:\Users\rcapella\AppData\Local\Temp\Rtmpg1y11V\downloaded_packages

```
Warning message:
"package 'exactextractr' was built under R version 4.4.3"
Warning message:
"package 'ecmwfr' was built under R version 4.4.3"
Warning message:
"package 'sf' was built under R version 4.4.3"
Linking to GEOS 3.13.0, GDAL 3.10.1, PROJ 9.5.1; sf_use_s2() is TRUE
```

```
Attaching package: 's2dv'
```

```
The following object is masked from 'package:base':
```

```
Filter
```

```
Attaching package: 'lubridate'
```

```
The following objects are masked from 'package:base':
```

```
date, intersect, setdiff, union
```

```
Loading required package: maps
```

```
Loading required package: qmap
```

```
Loading required package: fitdistrplus
```

```
Loading required package: MASS
```

```
Loading required package: survival
```

```
Loading required package: easyVerification
```

```
Loading required package: SpecsVerification
```

```
Attaching package: 'SpecsVerification'
```

```
The following object is masked from 'package:s2dv':
```

```
Corr
```

```
Attaching package: 'easyVerification'
```

```
The following object is masked from 'package:SpecsVerification':
```

```
EnsCorr
```

Warning message:
"package 'ncdf4' was built under R version 4.4.3"

3. Download data

```
In [2]: clim4health_get(pat = "1d6e6015-97b6-438f-848f-d8ac628d2014",  
                        dataset = "reanalysis-era5-land-monthly-means",  
                        product_type = "monthly_averaged_reanalysis",  
                        variable = "2m_temperature",  
                        year = c(2010, 2011, 2012),  
                        month = c(4, 5),  
                        area = c(33, -93, -23, -17),  
                        outname = "era5land")
```

4. Load data

```
In [3]: data <- clim4health_load('./sample_data/ecmwf51/forecast/', var = "t2m",  
                                data_type = "fcst", sdates = "20240401", ext = 'nc')
```

```
Warning message:
"! Warning: Parameter 'merge_across_dims' is changed to FALSE because there is no
! *_across argument."
Warning message:
"! Warning: Parameter 'pattern_dims' not specified. Taking the first dimension,
! 'dataset' as 'pattern_dims'."
Warning message:
"! Warning: Could not find any pattern dim with explicit data set descriptions (in
! the form of list of lists). Taking the first pattern dim, 'dataset',
! as dimension with pattern specifications."
Warning message:
"! Warning: Found dimension 'latitude' is required to reorder but no 'latitude_var'
! provided. "latitude_var = 'latitude'" has been automatically added
! to the Start call."
Warning message:
"! Warning: Found dimension 'longitude' is required to reorder but no
! 'longitude_var' provided. "longitude_var = 'longitude'" has been
! automatically added to the Start call."
Warning message:
"! Warning: Not found any dimensions able to be split. The parameter
! 'split_multiselected_dims' is changed to FALSE."
Warning message:
"! Warning: Parameter 'pattern_dims' not specified. Taking the first dimension,
! 'dataset' as 'pattern_dims'."
Warning message:
"! Warning: Could not find any pattern dim with explicit data set descriptions (in
! the form of list of lists). Taking the first pattern dim, 'dataset',
! as dimension with pattern specifications."
* Exploring files... This will take a variable amount of time depending
* on the issued request and the performance of the file server...

Warning message:
"! Warning: Found dimension 'latitude' is required to reorder but no 'latitude_var'
! provided. "latitude_var = 'latitude'" has been automatically added
! to the Start call."
Warning message:
"! Warning: Found dimension 'longitude' is required to reorder but no
! 'longitude_var' provided. "longitude_var = 'longitude'" has been
! automatically added to the Start call."
Warning message:
"! Warning: Not found any dimensions able to be split. The parameter
! 'split_multiselected_dims' is changed to FALSE."
* Detected dimension sizes:

*      dataset:  1
*
*      var:  1
*
*      time:  3
*
*      ensemble: 51
*
*      latitude: 57
*
*      longitude: 77
```

```

* Total size of requested data:

*   1 x 1 x 3 x 51 x 57 x 77 x 8 bytes = 5.1 Mb

* If the size of the requested data is close to or above the free shared
*   RAM memory, R may crash.

* If the size of the requested data is close to or above the half of the
*   free RAM memory, R may crash.

* Will now proceed to read and process 1 data files:

*   ./sample_data/ecmwf51/forecast/t2m_20240401.nc

* Loading... This may take several minutes...

* Successfully retrieved data.

```

5. Mask data

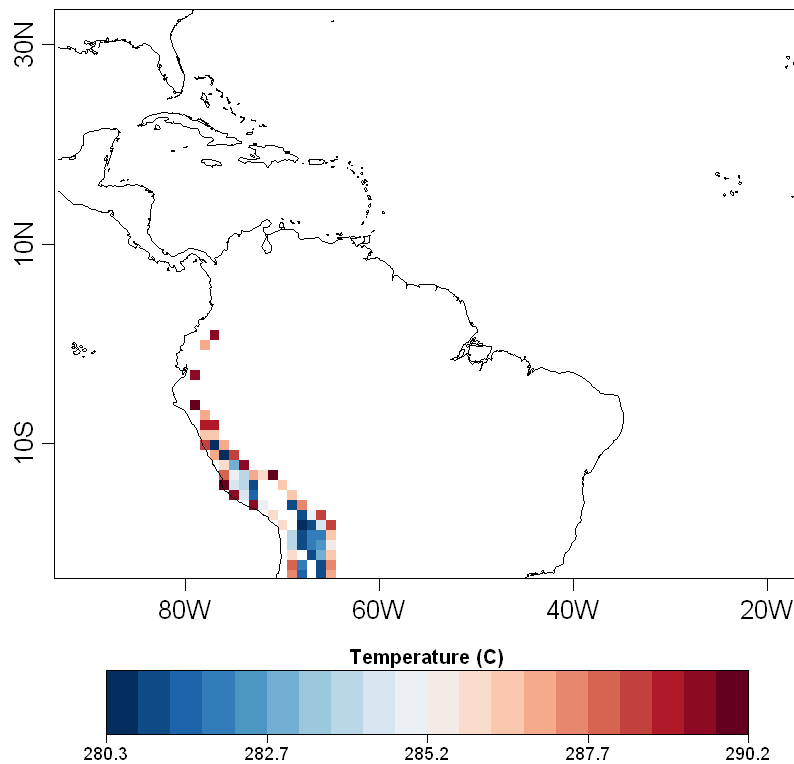
```

In [4]: mask <- clim4health_index(data, mod_vals = TRUE, lower_threshold = 280, upper_thre

PlotEquiMap(var = mask$data[1, 1, 1, 1, , ],
            lat = mask$coords$latitude,
            lon = mask$coords$longitude,
            filled.continents = FALSE,
            units = 'Temperature (C)', # text to appear in the legend
            toptitle = 'Mask temperature between 280 and 290 K', # text to appear a
            colNA = '#ffffff'
            )

```

Mask temperature between 280 and 290 K

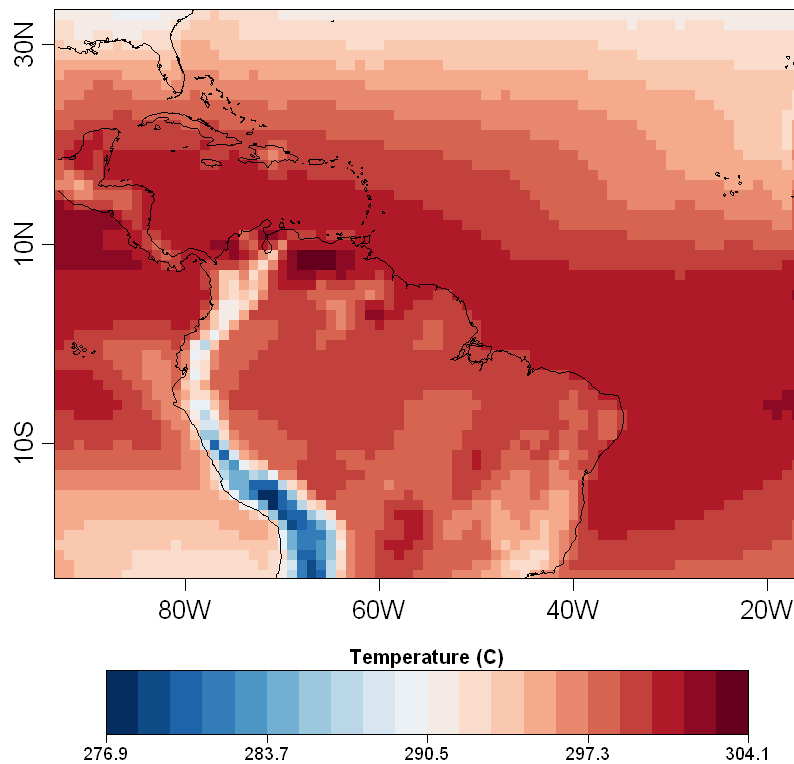


6. Time aggregations

```
In [5]: daily_data <- clim4health_time(data, aggregation = "daily")

PlotEquiMap(var = daily_data$data[1, 1, 1, 1, , ],
            lat = data$coords$latitude,
            lon = data$coords$longitude,
            filled.continents = FALSE,
            units = 'Temperature (C)', # text to appear in the legend
            toptitle = 'Mean daily t2m', # text to appear as overall title
            colNA = '#ffffff'
            )
```

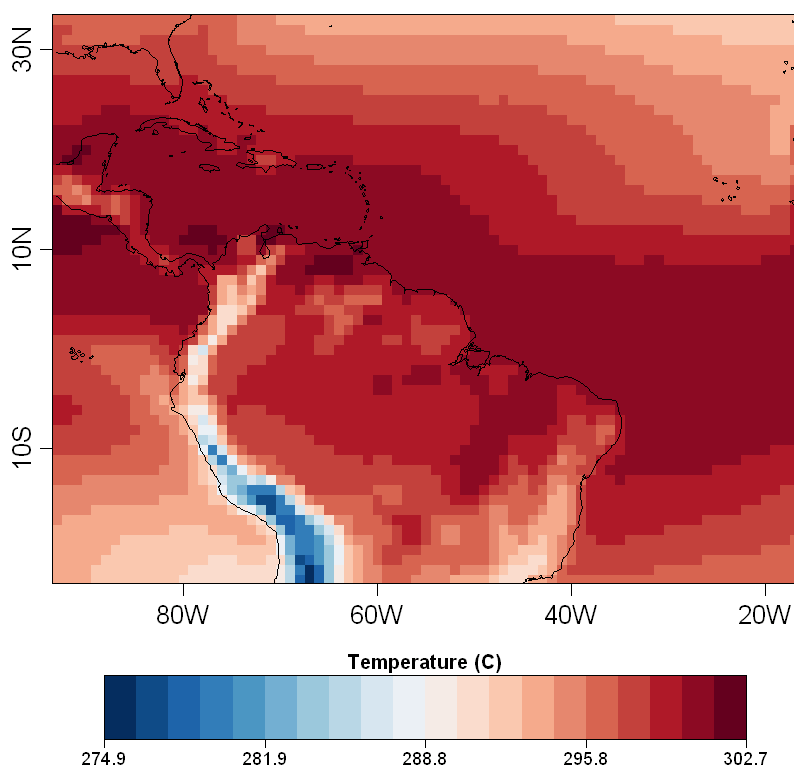
Mean daily t2m



```
In [6]: yearly_data <- clim4health_time(data, aggregation = "yearly")

PlotEquiMap(var = yearly_data$data[1, 1, 1, 1, , ],
  lat = data$coords$latitude,
  lon = data$coords$longitude,
  filled.continents = FALSE,
  units = 'Temperature (C)', # text to appear in the legend
  toptitle = 'Mean yearly t2m', # text to appear as overall title
  colNA = '#ffffff'
)
```


Mean yearly t2m



7. Spatial aggregations

```
In [7]: shp_file <- paste0(path, "/sample_data/shapefiles/MGN_ANM_MPIOS.shp")
result  <- clim4health_spatial(data, shp_file)

dim(result)
```

```
Reading layer `MGN_ANM_MPIOS' from data source
  `C:\Users\rcapella\Documents\GitHub\personal_project\Training_CARPHA\dependencies
\ghr_libraries\clim4health\sample_data\shapefiles\MGN_ANM_MPIOS.shp'
  using driver `ESRI Shapefile'
Simple feature collection with 1122 features and 90 fields
Geometry type: MULTIPOLYGON
Dimension:     XY
Bounding box:  xmin: -81.73562 ymin: -4.229406 xmax: -66.84722 ymax: 13.39473
Geodetic CRS:  MAGNA-SIRGAS
```

```
Warning message in CPL_crs_from_input(x):
"GDAL Message 1: +init=epsg:XXXX syntax is deprecated. It might return a CRS with a
non-EPSG compliant axis order."
```

```
|=====| 100%
```

dataset: 1 var: 1 time: 3 ensemble: 51 region: 1122