



## Compiling a global database of sapflow measurements with R

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**SAPFLUXNET Progress Report** SAPFLUXNET Project Wiki

Start **Sites** Biomes Methods Species Contributors

**204** Sites **34** Countries

See the sites in a map. Feel free to zoom in (in some places you can see the plots) and zoom out. Clicking in the points gives you info about the sites and clicking in the table isolates the selected site in the map for easy inspection

	Country code	Site code
1	ARG	ARG_MAZ
2	ARG	ARG_TRE
3	AUS	AUS_BRI_BRI
4	AUS	AUS_CAN_ST1_EUC
5	AUS	AUS_CAN_ST2_MIX
6	AUS	AUS_CAN_ST3_ACA
7	AUS	AUS_CAR_THI_00F
8	AUS	AUS_CAR_THI_0P0
9	AUS	AUS_CAR_THI_0PF
10	AUS	AUS_CAR_THI_CON
11	AUS	AUS_CAR_THI_T00

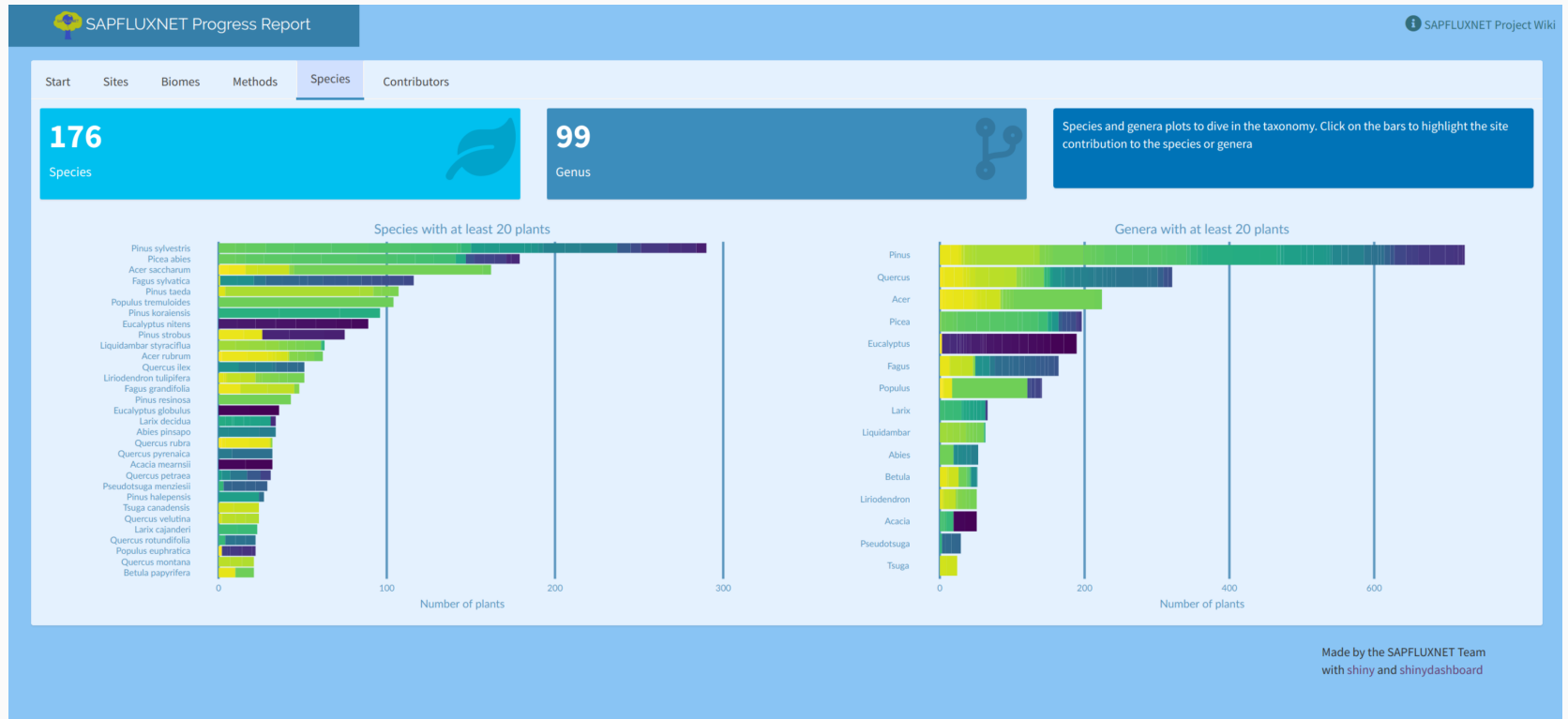
Showing 1 to 11 of 204 entries

Made by the SAPFLUXNET Team with shiny and shinydashboard

# Workflow and tools for the SAPFLUXNET database



Data and tools for scientists and modellers to help them unravel the **global** patterns and drivers of plant transpiration.



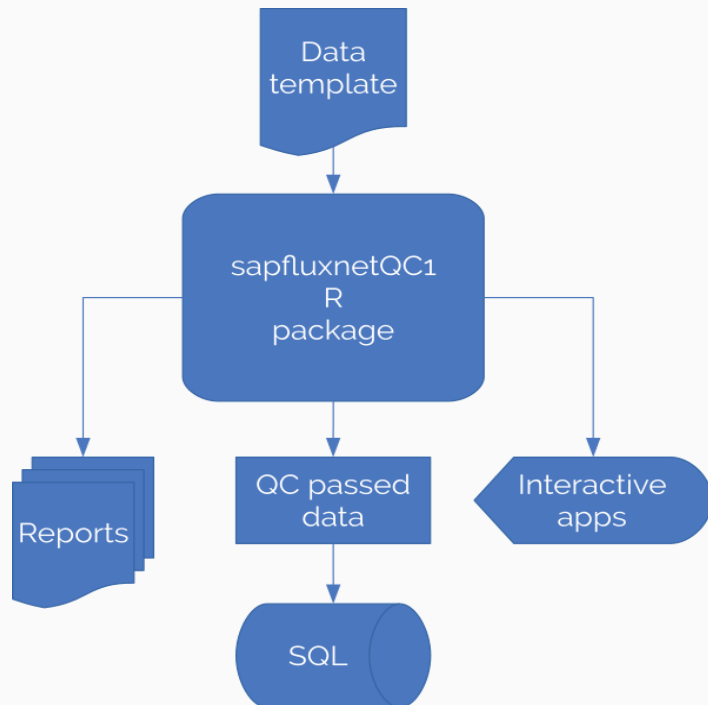


## Openness

- Open science
  - a collaborative effort
- Open source
  - mostly R, but other open source tools are also used
- Open data
  - all the data is available on Zenodo (<https://zenodo.org/record/2530798>)



## Sapfluxnet infraestructure



All data flow and data quality checks are performed by the internal-use intended R package *sapfluxnetQC1*

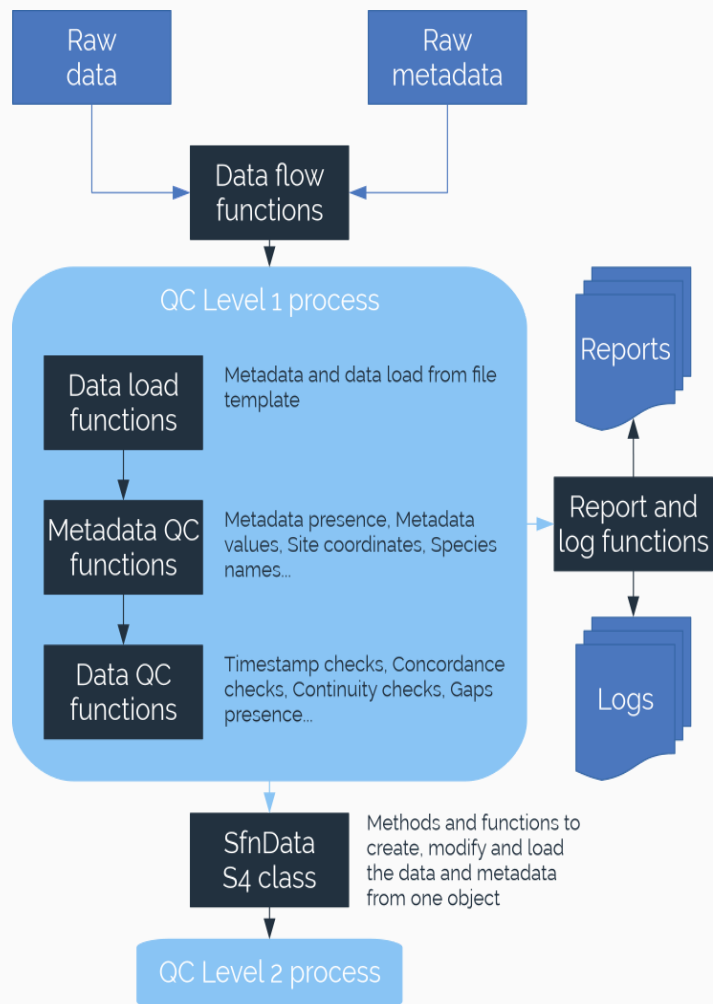
(<https://github.com/sapfluxnet/sapfluxnetQC1>):

- All steps implemented as functions
- Complete reproducibility
- Logs implemented

Manual data quality steps are performed in shiny apps that logs and store all action, again allowing for complete reproducibility.



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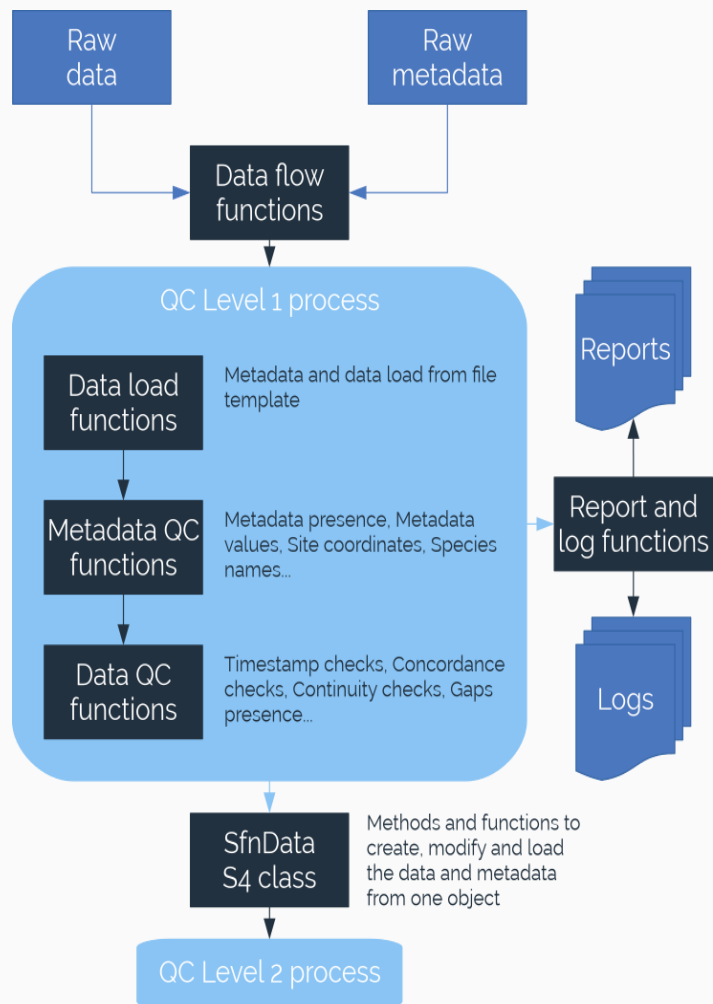
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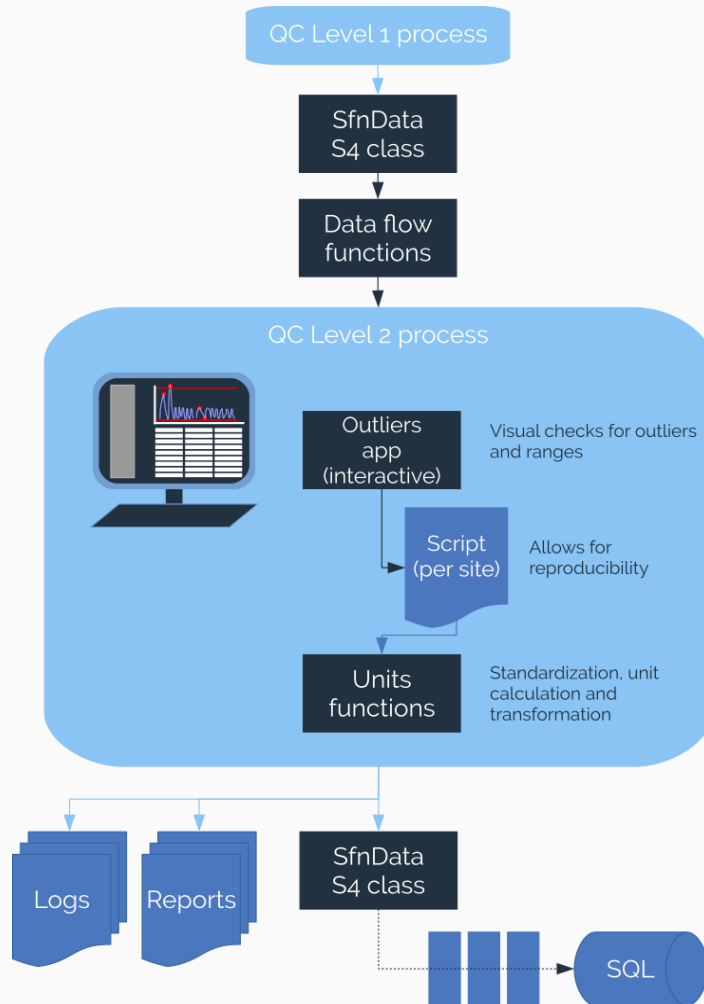
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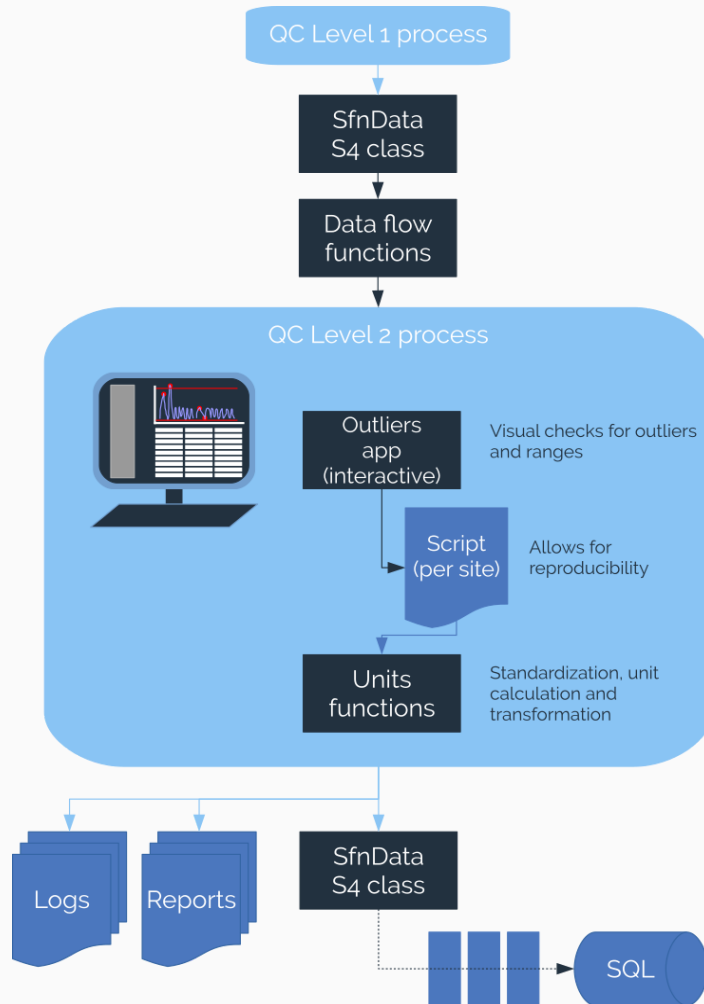
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## Inspection, analysis and visualization of the data

```
install.packages('sapfluxnetr')
library(sapfluxnetr)

folder ← 'sapfluxnet_db/0.1.3/plant'
sfm_metadata ← read_sfm_metadata(folder)

raw_data ← sfm_sites_in_folder(folder) %>%
  filter_sites_by_md(
    si_biome %in% c('Mediterranean', 'Temperate forest'),
    pl_sens_meth = 'HR',
    metadata = sfm_metadata
  ) %>%
  read_sfm_data()

raw_data %>%
  daily_metrics(tidy = TRUE)
```

### **sapfluxnetr** package:

- Data objects -> *snf\_data* S4 class
- Metadata inspection (sites information, individual plant characteristics...)
- Subdaily measures aggregation (to daily, monthly, midday, predawn, custom aggregates)
- Data modification tidyverse-style (filtering, mutating...)
- Data visualization (ggplot2)

<https://github.com/sapfluxnet/sapfluxnetr>



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  ) %>%
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raw_data %>%
  predawn_metrics(tidy = TRUE)
```

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## Inspection, analysis and visualization of the data

```
custom_funs ← list(mean = ~ mean(., na.rm = TRUE), std_dev  
  
# metrics  
raw_data %>%  
  sfn_metrics(  
    period = '7 days',  
    .funs = custom_funs,  
    solar = TRUE,  
    interval = 'daylight'  
  )
```

**sapfluxnetr** package:

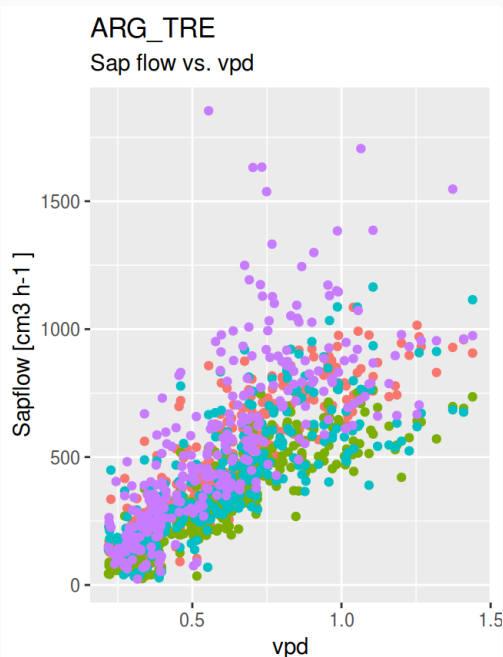
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## Inspection, analysis and visualization of the data

```
all_plots ← raw_data %>%  
  sfn_filter(month(TIMESTAMP) %in% 4:9) %>%  
  sfn_mutate(ws = ws * 3600/1000) %>%  
  sfn_plot(formula = ~ vpd)  
  
all_plots[[1]]
```



### **sapfluxnetr** package:

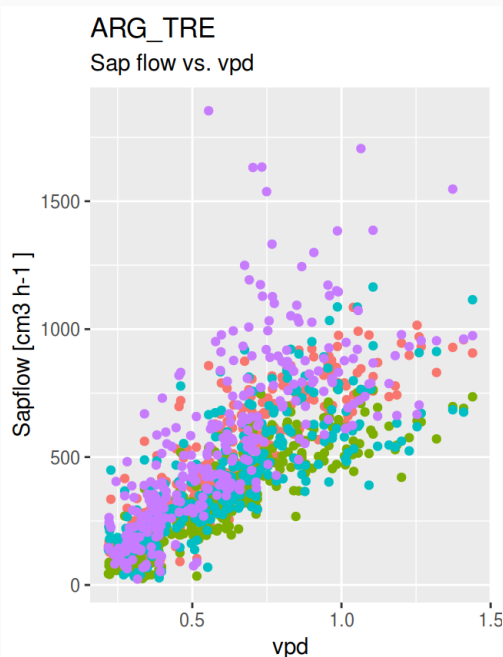
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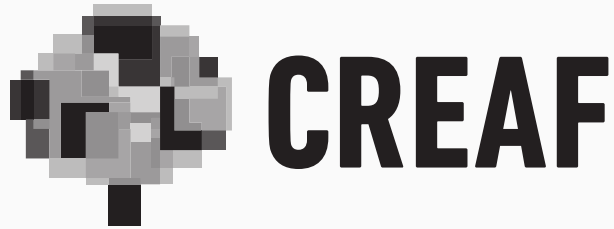


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## Aknowledgements

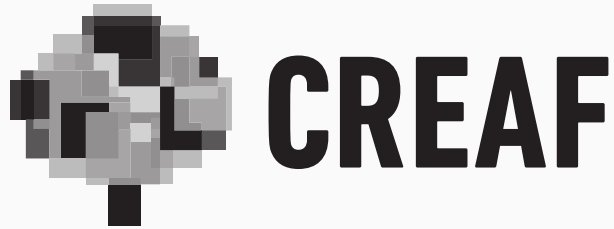


## Contact

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