

# Package ‘hydrographr’

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**Type** Package

**Title** Scalable Hydrographic Data Processing in R

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**Description**

Scalable hydrographic geospatial data processing tools using open-source command-line utilities.

**License** GPL-3

**URL** <https://glowabio.github.io/hydrographr/>

**BugReports** <https://github.com/glowabio/hydrographr/issues>

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.2.3

**Imports** processx (>= 3.7.0),  
data.table (>= 1.14.2),  
tidyr (>= 1.2.1),  
dplyr (>= 1.0.10),  
stringi (>= 1.7.8),  
stringr (>= 1.4.1),  
rlang (>= 1.0.6),  
DBI (>= 1.1.3),  
RSQLite (>= 2.2.19),  
terra (>= 1.6-41),  
sf (>= 1.0-9),  
parallel (>= 4.2.2),  
doParallel (>= 1.0.17),  
foreach (>= 1.5.2),  
future (>= 1.29.0),  
doFuture (>= 0.12.2),  
future.apply (>= 1.10.0),  
memuse (>= 4.2-2),  
igraph (>= 1.3.5),

magrittr (>= 2.0.3),  
methods (>= 4.3.0)

**Collate** 'check\_tiles\_filesize.R'  
'crop\_to\_extent.R'  
'download\_test\_data.R'  
'download\_tiles.R'  
'download\_tiles\_base.R'  
'extract\_from\_gpkg.R'  
'extract\_ids.R'  
'extract\_zonal\_stat.R'  
'get\_catchment\_graph.R'  
'get\_distance.R'  
'get\_pfafstetter\_basins.R'  
'get\_regional\_unit\_id.R'  
'get\_segment\_neighbours.R'  
'get\_tile\_id.R'  
'get\_upstream\_catchment.R'  
'utils.R'  
'merge\_tile.R'  
'read\_geopackage.R'  
'reclass\_raster.R'  
'report\_no\_data.R'  
'set\_no\_data.R'  
'snap\_to\_network.R'  
'snap\_to\_subc\_segment.R'

## R topics documented:

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|                |                              |
|----------------|------------------------------|
| crop_to_extent | <i>Crop raster to extent</i> |
|----------------|------------------------------|

---

## Description

This function crops an input raster layer (.tif) given a bounding box (xmin, ymin, xmax, ymax coordinates, or a spatial object from which to extract a bounding box) or to the boundary of a polygon vector layer (cutline source). The cropping is performed directly on disk, i.e. the input layer does not need to be loaded into R. The output is always written to disk, and can be optionally loaded into R as a SpatRaster (terra package) object (using read = TRUE).

## Usage

```
crop_to_extent(
  raster_layer,
  vector_layer = NULL,
  bounding_box = NULL,
  out_dir,
  file_name,
  compression = "low",
  bigtiff = TRUE,
  read = TRUE,
  quiet = TRUE
)
```

## Arguments

|              |   |
|--------------|---|
| raster_layer | character. Full path to the input raster .tif layer.  |
| vector_layer | character. Full path to a vector layer that is used as a cutline data source (similar to a mask operation).   |
| bounding_box | numeric vector of the coordinates of the corners of a bounding box (xmin, ymin, xmax, ymax), SpatRaster, SpatVector, or other spatial object.                       |
| out_dir      | character. The directory where the output will be stored.   |
| file_name    | character. Name of the cropped output raster .tif file.   |
| compression  | character. Compression of the written output file. Compression levels can be defined as "none", "low", or "high". Default is "low".                                 |
| bigtiff      | logical. Define whether the output file is expected to be a BIGTIFF (file size larger than 4 GB). If FALSE and size > 4GB no file will be written. Default is TRUE. |
| read         | logical. If TRUE, the cropped raster .tif layer gets read into R. If FALSE, the layer is only stored on disk. Default is TRUE.                                      |
| quiet        | logical. If FALSE, the standard output will be printed. Default is TRUE.  |

**Value**

The function returns always a .tif raster file written to disk. Optionally, a SpatRaster (terra object) can be loaded into R with read = TRUE.

**Author(s)**

Yusdiel Torres-Cambas

**Examples**

```
# Download test data into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Define full path to the input raster .tif layer and vector layer
spi_raster <- paste0(my_directory, "/hydrography90m_test_data",
                     "/spi_1264942.tif")
basin_vector <- paste0(my_directory, "/hydrography90m_test_data",
                      "/basin_59.gpkg")

# Crop the Stream Power Index to the basin
spi_basin <- crop_to_extent(raster_layer = spi_raster,
                           vector_layer = basin_vector,
                           out_dir = my_directory,
                           file_name = "spi_basin_cropped.tif",
                           read = TRUE)
```

---

|                    |                           |
|--------------------|---------------------------|
| download_test_data | <i>Download test data</i> |
|--------------------|---------------------------|

---

**Description**

Download the test data of the package, which includes all Hydrography90m and species point observation data for a small geographic extent, to test the functions.

The test data will be automatically downloaded and unzipped with this function to a desired path, or can be alternatively downloaded at

[https://drive.google.com/file/d/1kYNWXmtVm6X7MZLISOePGpvxB1pk1scD/view?usp=share\\_link](https://drive.google.com/file/d/1kYNWXmtVm6X7MZLISOePGpvxB1pk1scD/view?usp=share_link).

**Usage**

```
download_test_data(download_dir = ".")
```

**Arguments**

download\_dir      character. The directory where the files will be downloaded. Default location is the working directory.

## Details

Downloads the test data for the Hydrography90m dataset

## Author(s)

Afroditi Grigoropoulou

## References

Amatulli, G., Garcia Marquez, J., Sethi, T., Kiesel, J., Grigoropoulou, A., Üblacker, M. M., Shen, L. Q., and Domisch, S.: Hydrography90m: a new high-resolution global hydrographic dataset, Earth Syst. Sci. Data, 14, 4525–4550, <https://doi.org/10.5194/essd-14-4525-2022>, 2022.")

Amatulli G., Garcia Marquez J., Sethi T., Kiesel J., Grigoropoulou A., Üblacker M., Shen L. & Domisch S. (2022-08-09 ). Hydrography90m: A new high-resolution global hydrographic dataset. IGB Leibniz-Institute of Freshwater Ecology and Inland Fisheries. dataset. <https://doi.org/10.18728/igb-fred-762.1>

## Examples

```
# Download the test data to the current working directory
download_test_data()

# Download the data to a specific (existing) directory
download_test_data("path/to/your/directory")
```

---

download\_tiles

*Download files of the Hydrography90m dataset*

---

## Description

The function downloads data of the Hydrography90m dataset, which is split into 20°x20° tiles. If a tile ID is specified, then the selected layers (variable) will be downloaded. In addition, the Hydrography90m is organized in non-interrupted drainage basins called regional units. If a regional unit ID (reg\_unit\_id) is specified, then only the raster mask of the drainage basin is downloaded (useful for later processing). Multiple regular tiles, e.g. belonging to regional units, can be downloaded in a single request. The tile or regional unit IDs can be obtained using the functions "get\_tile\_id" and "get\_regional\_unit\_id", respectively. The files will be stored locally in a folder architecture, similar as in the data repository, available at <https://public.igb-berlin.de/index.php/s/agciopgzXjWswF4?path=%2F>.

## Usage

```
download_tiles(
  variable,
  file_format = "tif",
  tile_id = NULL,
  reg_unit_id = NULL,
```

```

    global = FALSE,
    download_dir = "."
  )

```

### Arguments

|              |  |
|--------------|--|
| variable     | character vector of variable names. See Details for all the variable names.                    |
| file_format  | character. Format of the requested file ("tif" or "gpkg"). See Details.                        |
| tile_id      | character vector. The IDs of the requested tiles.  |
| reg_unit_id  | character vector. The IDs of the requested regional units.                                     |
| global       | logical. If TRUE, the global extent file is downloaded. Default is FALSE.                      |
| download_dir | character. The directory where the files will be downloaded. Default is the working directory. |

### Details

In the following table you can find all the variables included in the Hydrography90m dataset. The column "Variable" includes the variable names that should be used as an input in the parameter "variable" of the function. Likewise, the column "File format" contains the input that should be given to the "file\_format" parameter. For more details and visualisations of the spatial layers, please refer to [https://hydrography.org/hydrography90m/hydrography90m\\_layers/](https://hydrography.org/hydrography90m/hydrography90m_layers/).

| Variable type        | Variable name                        | Variable              | Unit            | File format |
|----------------------|--------------------------------------|-----------------------|-----------------|-------------|
| Network              | Drainage basin                       | basin                 |                 | tif         |
| Network              | Drainage basin                       | basin                 |                 | gpkg        |
| Network              | Sub-catchment                        | sub_catchment         |                 | tif         |
| Network              | Sub-catchment                        | sub_catchment         |                 | gpkg        |
| Network              | Stream segment                       | segment               |                 | tif         |
| Network              | Outlet                               | outlet                |                 | tif         |
| Network              | Outlet                               | outlet                |                 | gpkg        |
| Network              | Regional unit                        | regional_unit         |                 | tif         |
| Flow                 | Flow accumulation                    | flow                  | km <sup>2</sup> | tif         |
| Stream slope         | Cell maximum curvature               | slope_curv_max_dw_cel | 1/m             | tif         |
| Stream slope         | Cell minimum curvature               | slope_curv_min_dw_cel | 1/m             | tif         |
| Stream slope         | Cell elevation difference            | slope_elv_dw_cel      | m               | tif         |
| Stream slope         | Cell gradient                        | slope_grad_dw_cel     |                 | tif         |
| Stream distance      | Shortest distance to drainage divide | stream_dist_up_near   | m               | tif         |
| Stream distance      | Longest distance to drainage divide  | stream_dist_up_farth  | m               | tif         |
| Stream distance      | Nearest down stream stream grid cell | stream_dist_dw_near   | m               | tif         |
| Stream distance      | Outlet grid cell in the network      | outlet_dist_dw_basin  | m               | tif         |
| Stream distance      | Down stream stream node grid cell    | outlet_dist_dw_scatch | m               | tif         |
| Stream distance      | Euclidean distance                   | stream_dist_proximity | m               | tif         |
| Elevation difference | Shortest path                        | stream_diff_up_near   | m               | tif         |
| Elevation difference | Longest path                         | stream_diff_up_farth  | m               | tif         |
| Elevation difference | Nearest downstream stream pixel      | stream_diff_dw_near   | m               | tif         |
| Elevation difference | Outlet grid cell in the network      | outlet_diff_dw_basin  | m               | tif         |
| Elevation difference | Downstream stream node grid cell     | outlet_diff_dw_scatch | m               | tif         |
| Segment properties   | Segment downstream mean gradient     | channel_grad_dw_seg   |                 | tif         |

|                    |   |                     |                 |      |
|--------------------|---|---------------------|-----------------|------|
| Segment properties | Segment upstream mean gradient          | channel_grad_up_seg |                 | tif  |
| Segment properties | Cell upstream gradient                  | channel_grad_up_cel |                 | tif  |
| Segment properties | Cell stream course curvature            | channel_curv_cel    |                 | tif  |
| Segment properties | Segment downstream elevation difference | channel_elv_dw_seg  |                 | tif  |
| Segment properties | Segment upstream elevation difference   | channel_elv_up_seg  |                 | tif  |
| Segment properties | Cell upstream elevation difference      | channel_elv_up_cel  |                 | tif  |
| Segment properties | Cell downstream elevation difference    | channel_elv_dw_cel  |                 | tif  |
| Segment properties | Segment downstream distance             | channel_dist_dw_seg |                 | tif  |
| Segment properties | Segment upstream distance               | channel_dist_up_seg |                 | tif  |
| Segment properties | Cell upstream distance                  | channel_dist_up_cel |                 | tif  |
| Stream order       | Strahler's stream order                 | order_strahler      |                 | tif  |
| Stream order       | Shreve's stream magnitude               | order_shreve        |                 | tif  |
| Stream order       | Horton's stream order                   | order_horton        |                 | tif  |
| Stream order       | Hack's stream order                     | order_hack          |                 | tif  |
| Stream order       | Topological dimension of streams        | order_topo          |                 | tif  |
| Stream order       | Strahler's stream order                 | order_vect_segment  |                 | gpkg |
| Stream order       | Shreve's stream magnitude               | order_vect_segment  |                 | gpkg |
| Stream order       | Horton's stream order                   | order_vect_segment  |                 | gpkg |
| Stream order       | Hack's stream order                     | order_vect_segment  |                 | gpkg |
| Stream order       | Topological dimension of streams        | order_vect_segment  |                 | gpkg |
| Stream reach       | Length of the stream reach              | order_vect_segment  | m               | gpkg |
| Stream reach       | Straight length                         | order_vect_segment  | m               | gpkg |
| Stream reach       | Sinusoid of the stream reach            | order_vect_segment  |                 | gpkg |
| Stream reach       | Accumulated length                      | order_vect_segment  | m               | gpkg |
| Stream reach       | Flow accumulation                       | order_vect_segment  | km <sup>2</sup> | gpkg |
| Stream reach       | Distance to outlet                      | order_vect_segment  | m               | gpkg |
| Stream reach       | Source elevation                        | order_vect_segment  | m               | gpkg |
| Stream reach       | Outlet elevation                        | order_vect_segment  | m               | gpkg |
| Stream reach       | Elevation drop                          | order_vect_segment  |                 | gpkg |
| Stream reach       | Outlet drop                             | order_vect_segment  |                 | gpkg |
| Stream reach       | Gradient                                | order_vect_segment  |                 | gpkg |
| Flow index         | Stream power index                      | spi                 |                 | tif  |
| Flow index         | Sediment transportation index           | sti                 |                 | tif  |
| Flow index         | Compound topographic index              | cti                 |                 | tif  |

### Note

If there is an error during the download of a file (more likely in case of files bigger than 3-4GB), you can try to manually download this file by pasting the link that is returned by the error message in your browser.

### Author(s)

Afroditi Grigoropoulou

## References

Amatulli G., Garcia Marquez J., Sethi T., Kiesel J., Grigoropoulou A., Üblacker M., Shen L. & Domisch S. (2022-08-09 ) Hydrography90m: A new high-resolution global hydrographic dataset. IGB Leibniz-Institute of Freshwater Ecology and Inland Fisheries. dataset. <https://doi.org/10.18728/igb-fred-762.1>

## Examples

```
# Download data for two variables in three regular tiles
# to the current working directory
download_tiles(variable = c("sti", "stream_dist_up_farth"),
              file_format = "tif",
              tile_id = c("h00v02", "h16v02", "h16v04"))

# Download the global .tif layer for the variable "direction"
# into the temporary R folder or define a different directory
# Define directory
my_directory <- tempdir()
# Download layer
download_tiles(variable = "direction",
              file_format = "tif",
              global = TRUE,
              download_dir = my_directory)
```

---

|                   |  |
|-------------------|--|
| extract_from_gpkg | <i>Extract values from the stream order .gpkg files.</i> |
|-------------------|--|

---

## Description

The function reads the attribute table of the stream network GeoPackage file (.gpkg) stored on disk and extracts the data for one or more (or all) input sub-catchment (i.e. stream segment) IDs. The output is a data.table, and only the output is loaded into R.

## Usage

```
extract_from_gpkg(
  data_dir,
  subc_id,
  subc_layer,
  var_layer,
  out_dir = NULL,
  file_name = NULL,
  n_cores = NULL,
  quiet = TRUE
)
```



## Arguments

|            |  |
|------------|--|
| data_dir   | character. Path to the directory containing all input data.  |
| subc_id    | a numeric vector of sub-catchment IDs or "all". If "all", the attribute table is extracted for all the stream segments of the input .gpkg layer. The stream segment IDs are the same as the sub-catchment IDs. A vector of the sub-catchment IDs can be acquired from the extract_ids() function, by sub-setting the resulting data.frame. |
| subc_layer | character. Full path to the sub-catchment ID .tif layer  |
| var_layer  | character vector of .gpkg files on disk, e.g. "order_vect_point_h18v04.gpkg".  |
| out_dir    | character. The directory where the output will be stored. If the out_dir is specified, the attribute tables will be stored as .csv files in this location, named after their input variable vector files (e.g. "/path/to/stats_order_vect_point_h18v04.csv"). If NULL, the output is only loaded in R and not stored on disk.              |
| file_name  | character. Name of the .csv file where the output table will be stored. out_dir should also be specified for this purpose.   |
| n_cores    | numeric. Number of cores used for parallelization, in case multiple .gpkg files are provided to var_layer. If NULL, available cores - 1 will be used.  |
| quiet      | logical. If FALSE, the standard output will be printed. Default is TRUE.   |

## Details

The following attributes are stored in the stream network .gpkg files:

\* cat - category \* stream - sub-catchment / stream segment ID (equal to cat) \* next\_stream - downstream sub-catchment / stream segment ID \* prev\_streams; two or more upstream sub-catchment / stream segment IDs \* strahler - Strahler's stream order \* horton - Hortons's stream order \* shreve - Shreve's stream magnitude \* hack - Hack's main streams or Gravelius order \* topo\_dim - Topological dimension streams order \* scheidegger - Scheidegger's Consisted Associated Integers \* drwal - Drwal's stream hierarchy \* length - length of the stream segment \* stright - length of the stream segment as a stright line \* sinusoid - fractal dimension: stream segment length / stright stream \* segment length; \* cum\_length - length of the stream from the source \* flow\_accum - flow accumulation within the sub-catchment of a stream segment \* out\_dist - distance of current stream initialisation from outlet \* source\_elev - elevation at stream segment initialisation \* outlet\_elev - elevation at stream segment outlet \* elev\_drop difference between source\_elev and outlet\_elev + drop outlet \* out\_drop - drop at the outlet of the stream segment \* gradient - drop/length;

## Author(s)

Afroditi Grigoropoulou, Jaime Garcia Marquez, Maria M. Üblacker

## References

<https://grass.osgeo.org/grass82/manuals/v.in.ogr.html> <https://grass.osgeo.org/grass82/manuals/addons/r.stream.order.html>

## Examples

```
# Download test data into temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Define path to the directory containing all input data
test_data <- paste0(my_directory, "/hydrography90m_test_data")

# Define sub-catchment ID layer
subc_raster <- paste0(my_directory, "/hydrography90m_test_data",
                      "/subcatchment_1264942.tif")

# Extract the attribute table of the file order_vect_59.gpkg for all the
# sub-catchment IDs of the subcatchment_1264942.tif raster layer
attribute_table <- extract_from_gpkg(data_dir = test_data,
                                     subc_id = "all",
                                     subc_layer = subc_raster,
                                     var_layer = "order_vect_59.gpkg",
                                     n_cores = 1)

# Show the output table
attribute_table
```

---

extract\_ids

*Extract sub-catchment and/or basin IDs*

---

## Description

Extracts the ID value of the basin and/or sub-catchment raster layer at given point locations. Can also be used for point-based extraction of any .tif layer by specifying the layer in the "basin" parameter.

## Usage

```
extract_ids(
  data,
  lon,
  lat,
  id = NULL,
  basin_layer = NULL,
  subc_layer = NULL,
  quiet = TRUE
)
```

## Arguments

|      |   |
|------|---|
| data | a data.frame or data.table that contains the columns regarding the longitude / latitude coordinates in WGS84. |
|------|---|

|             |  |
|-------------|--|
| lon         | character. The name of the column with the longitude coordinates.  |
| lat         | character. The name of the column with the latitude coordinates.   |
| id          | character. The name of a column containing unique IDs for each row of "data" (e.g., occurrence or site IDs). |
| basin_layer | character. Full path to the .tif layer with the basin ID.  |
| subc_layer  | character. Full path to the .tif layer with the sub-catchment ID.  |
| quiet       | logical. If FALSE, the standard output will be printed. Default is TRUE.                                     |

### Details

For the extraction of a value at a given point location from the basin and/or sub-catchment raster layer of the Hydrography90m dataset, the GDAL function 'gdallocationinfo' is used. The point locations have to be defined by coordinates in the WGS84 reference system. The function can also be used to extract any value from a given raster layer in a WGS84 projection, such as environmental information that is stored in the input raster file.

### Note

Duplicated rows will be removed.

### Author(s)

Afroditi Grigoropoulou, Maria Üblacker

### References

<https://gdal.org/programs/gdallocationinfo.html>

### Examples

```
# Download test data into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Load occurrence data
species_occurrence <- read.table(paste0(my_directory,
                                         "/hydrography90m_test_data",
                                         "/spdata_1264942.txt"),
                                header = TRUE)

# Define full path to the basin and sub-catchments raster layer
basin_raster <- paste0(my_directory,
                      "/hydrography90m_test_data/basin_1264942.tif")
subc_raster <- paste0(my_directory,
                     "/hydrography90m_test_data/basin_1264942.tif")

# Extract basin and sub-catchment IDs from the Hydrography90m layers
hydrography90m_ids <- extract_ids(data = species_occurrence,
                                lon = "longitude",
```

```

lat = "latitude",
id = "occurrence_id",
subc_layer = subc_raster,
basin_layer = basin_raster)

# Show the output table
hydrography90m_ids

```

---

|                    |                                   |
|--------------------|-----------------------------------|
| extract_zonal_stat | <i>Calculate zonal statistics</i> |
|--------------------|-----------------------------------|

---

## Description

Calculate zonal statistics based on one or more environmental variable raster .tif layers. This function aggregates data to 12 summary statistics (mean, min, max, range, ...) for selected or all sub-catchments of the input file. The sub-catchment raster (.tif) input file is read directly from disk. The output is a data.table which is loaded into R. This function can also be used for any zonal statistic calculation by specifying the raster layer zones in the subc\_layer parameter and optionally, also the target zone IDs in the subc\_id parameter.

## Usage

```

extract_zonal_stat(
  data_dir,
  subc_id,
  subc_layer,
  var_layer,
  out_dir = NULL,
  file_name = NULL,
  n_cores = NULL,
  quiet = TRUE
)

```

## Arguments

|            |   |
|------------|---|
| data_dir   | character. Path to the directory containing all input data.   |
| subc_id    | Vector of sub-catchment IDs or "all". If "all", zonal statistics are calculated for all sub-catchments of the given sub-catchment raster layer. A vector of the sub-catchment IDs can be acquired from the extract_ids() function, and by sub-setting the resulting data.frame.   |
| subc_layer | character. Full path to the sub-catchment ID .tif layer.  |
| var_layer  | character vector of variable raster layers on disk, e.g. "slope_grad_dw_cel_h00v00.tif". Note that the variable name appears in the output table columns (e.g. slope_grad_dw_cel_mean). To speed up the processing, the selected variable raster layers can be cropped to the extent of the sub-catchment layer, e.g. with <a href="#">crop_to_extent()</a> . |



```

                    513850467, 513868394,
                    513870312),
    subc_layer = subc_raster,
    var_layer = c("spi_1264942.tif",
                  "sti_1264942.tif"),
    out_dir = output_folder,
    file_name = "zonal_statistics.csv",
    n_cores = 2)

# Show output table
stat

```

---

|                     |  |
|---------------------|--|
| get_catchment_graph | <i>Get catchment from stream network graph</i> |
|---------------------|--|

---

## Description

Subset the stream network graph by extracting the upstream, downstream or entire catchment, for one or multiple stream segments. The function will return either one or more data.tables or graph objects for each input stream segment. Note that the stream segment and sub-catchment IDs are identical, and for consistency, we use the term "subc\_id".

By switching the mode to either "in", "out" or "all", only the upstream, downstream or all connected segments will be returned, respectively. The function [read\\_geopackage\(\)](#) can be used to create the input network graph.

## Usage

```

get_catchment_graph(
  g,
  subc_id = NULL,
  outlet = FALSE,
  mode = NULL,
  as_graph = FALSE,
  n_cores = 1,
  max_size = 1500
)

```

## Arguments

|                      |   |
|----------------------|---|
| <code>g</code>       | igraph object. A directed graph.  |
| <code>subc_id</code> | numeric vector of a single or multiple IDs, e.g (c(ID1, ID2, ID3, ...)). The sub-catchment (equivalent to stream segment) IDs for which to delineate the upstream drainage area. If empty, then outlets will be used as sub-catchment IDs (with <code>outlet = TRUE</code> ). Note that you can browse the entire network online at <a href="https://geo.igb-berlin.de/maps/351/view">https://geo.igb-berlin.de/maps/351/view</a> and to left hand side, select the "Stream segment ID" layer and click on the map to get the ID. Optional. |

|          |   |
|----------|---|
| outlet   | logical. If TRUE, the outlets of the given network graph will be used as additional input subc_ids. Outlets will be identified internally as those stream segments that do not have any downstream connected segment. Default is FALSE.   |
| mode     | character. One of "in", "out" or "all". "in" returns the upstream catchment, "out" returns the downstream catchment (all catchments that are reachable from the given input segment), and "all" returns both.   |
| as_graph | logical. If TRUE, the output will be a new graph or a list of new graphs with the original attributes. If FALSE, the output will be a new data.table or a list of data.tables. List objects are named after the subc_ids. Default is FALSE.   |
| n_cores  | numeric. Number of cores used for parallelization in the case of multiple stream segments / outlets. Default is 1. Currently, the parallelization process requires copying the data to each core. In case the graph is very large, and many segments are used as an input, setting n_cores to a higher value can speed up the computation. This comes however at the cost of possible RAM limitations and even slower processing since the large data will be copied to each core. Hence consider testing with n_cores = 1 first. Optional. |
| max_size | numeric. Specifies the maximum size of the data passed to the parallel back-end in MB. Default is 1500 (1.5 GB). Consider a higher value for large study areas (more than one 20°x20° tile). Optional.  |

### Value

A graph or data.table that reports all subc\_ids. In case of multiple input segments, the results are stored in a list.

### Author(s)

Sami Domisch

### References

Csardi G, Nepusz T: The igraph software package for complex network research, InterJournal, Complex Systems 1695. 2006. <https://igraph.org>

#' @seealso [read\\_geopackage](#) to create a network graph.

### Examples

```
# Download test data into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Load stream network as a graph
my_graph <- read_geopackage(gpkg = paste0(my_directory,
                                           "/hydrography90m_test_data",
                                           "/order_vect_59.gpkg"),
                           import_as = "graph")

# Pick a random subc_id
```

```

subc_id = "513855877"
# Get the upstream catchment as a graph
g_up <- get_catchment_graph(g = my_graph, subc_id = subc_id, mode = "in",
                           outlet = FALSE, as_graph = TRUE, n_cores = 1)

# Get the downstream segments as a data.table,
g_down <- get_catchment_graph(g = my_graph, subc_id = subc_id, mode = "out",
                             outlet = FALSE, as_graph = FALSE, n_cores = 1)

# Get the catchments of all outlets in the study area as a graph
g_all <- get_catchment_graph(g = my_graph, mode = "in", outlet = TRUE,
                             as_graph = TRUE, n_cores = 1)

```

---

get\_distance

---

*Calculate euclidean or along the network distance between points*


---

## Description

Calculate euclidean or along-the-network distance (in meters) between points. To calculate the distance along the network, point coordinates need to be snapped to the stream network using the function [snap\\_to\\_network](#) or [snap\\_to\\_subc\\_segment](#).

## Usage

```

get_distance(
  data,
  lon,
  lat,
  id,
  basin_id = NULL,
  basin_layer = NULL,
  stream_layer = NULL,
  distance = "both",
  n_cores = 1,
  quiet = TRUE
)

```

## Arguments

|      |   |
|------|---|
| data | a data.frame or data.table that contains the columns regarding the longitude / latitude coordinates in WGS84. |
| lon  | character. The name of the column with the longitude coordinates.   |
| lat  | character. The name of the column with the latitude coordinates.  |
| id   | character. The name of a column containing unique IDs for each row of "data" (e.g., occurrence or site IDs).  |



|              |  |
|--------------|--|
| basin_id     | character. The name of the column with the basin IDs. If NULL and distance is set to 'network' or 'both', the basin IDs will be extracted automatically. Default is NULL.  |
| basin_layer  | character. Full path to the basin ID .tif layer. Needs to be defined to calculate the distance along the network.  |
| stream_layer | character. Full path of the stream network .gpkg file. Needs to be defined to calculate the distance along the network.  |
| distance     | character. One of "euclidean", "network", or "both". If "euclidean", the euclidean distances between all pairs of points are calculated. If "network", the shortest path along the network between all pairs of points is calculated. (see "Details" for more information). If method is set to "both", both distance measures are calculated. Distances are given in meters. Default is "both". |
| n_cores      | numeric. Number of cores used for parallelization. Default is 1.   |
| quiet        | logical. If FALSE, the standard output will be printed. Default is TRUE.   |

### Details

To calculate the euclidian distance between all pairs of points the function uses the `v.distance` command of GRASS GIS, which has been set up to produce a square matrix of distances. The calculation of distances along the stream network has been implemented with the command `v.net.allpairs` of GRASS GIS. The along-the-network distance calculation is done for all pairs of points located within the same basin. If the points are located in different basins, the function can be run in parallel (i.e., each core for the distance calculations of all points within one basin). The distance between points located in different basins is zero because they are not connected through the network.

### Value

If `distance='euclidean'`, a distance matrix, in meters, of the euclidean distances between all the pairs of points (object of class `data.frame`) is returned. If `distance='network'`, a `data.frame` with three columns: `from_id`, `to_id`, `dist` is returned. The 'dist' column includes the distance, in meters, of the shortest path along the network from the point "from\_id" to the point "to\_id". If `distance='both'`, a list containing both objects is returned.

### Author(s)

Afroditi Grigoropoulou, Maria M. Üblacker, Jaime Garcia Marquez

### References

<https://grass.osgeo.org/grass82/manuals/v.net.allpairs.html> <https://grass.osgeo.org/grass82/manuals/v.distance.html>

### See Also

[snap\\_to\\_network](#) to snap the data points to the next stream segment within a given radius and/or a given flow accumulation threshold value. [snap\\_to\\_subc\\_segment](#) to snap the data points to the next stream segment of the sub-catchment the data point is located. [extract\\_ids](#) to extract basin and sub-catchment IDs.

**Examples**

```

# Download test data into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Load occurrence data
species_occurrence <- read.table(paste0(my_directory,
                                          "/hydrography90m_test_data/spdata_1264942.txt"),
                                header = TRUE)

basin_rast <- paste0(my_directory,
                    "/hydrography90m_test_data/basin_1264942.tif")

# Define full path to the sub-catchment raster layer
subc_rast <- paste0(my_directory,
                    "/hydrography90m_test_data/subcatchment_1264942.tif")

# Define full path to the vector file of the stream network
stream_vect <- paste0(my_directory,
                      "/hydrography90m_test_data/order_vect_59.gpkg")

# Automatically extract the basin and sub-catchment IDs and
# snap the data points to the stream segment
snapped_coordinates <- snap_to_subc_segment(data = species_occurrence,
                                           lon = "longitude",
                                           lat = "latitude",
                                           id = "occurrence_id",
                                           basin_layer = basin_rast,
                                           subc_layer = subc_rast,
                                           stream_layer = stream_vect,
                                           n_cores = 2)

# Show head of output table
head(snapped_coordinates)

# Get the euclidean distance and the distance along the network between all
# pairs of points
distance_table <- get_distance(data = snapped_coordinates,
                              lon = "lon_snap",
                              lat = "lat_snap",
                              id = "occurrence_id",
                              basin_id = "basin_id",
                              basin_layer = basin_rast,
                              stream_layer = stream_vect,
                              distance = "network")

# Show table
distance_table

```

---

get\_pfafstetter\_basins

*Get Pfafstetter sub-basins*


---

## Description

Subset a basin or catchment into up to nine smaller sub-basins following the Pfafstetter basin delineation scheme. The function takes a network graph as the input and splits it into smaller sub-basins following a hierarchical topological coding scheme (see Verdin & Verdin (1999) for details), using the flow accumulation as the basis. The user has to define the sub-catchment (stream segment) ID that serves as the outlet of the basin. Note that this can be any stream segment that has an upstream catchment. The input graph can be created with [read\\_geopackage\(\)](#) and [get\\_catchment\\_graph.\(\)](#)

## Usage

```
get_pfafstetter_basins(
  g,
  subc_raster,
  out_dir,
  file_name,
  data_table = FALSE,
  n_cores = NULL
)
```

## Arguments

|                          |   |
|--------------------------|---|
| <code>g</code>           | igraph object. A directed graph of a basin with one outlet. The outlet can be any stream / sub-catchment for which the upstream basin should be split into smaller sub-basins. The input graph can be created with <a href="#">read_geopackage()</a> and <a href="#">get_catchment_graph.()</a> |
| <code>subc_raster</code> | character. Full path to the sub-catchment raster file of the basin. Does not need to be cropped / masked to the basin, but the IDs of the sub-catchments need to match with those in the input graph.   |
| <code>out_dir</code>     | character. The path of the output directory where the Pfafstetter raster layer will be written. Only needed when <code>data.table=FALSE</code> .  |
| <code>file_name</code>   | character. The filename and extension of the Pfafstetter raster layer (e.g. 'pfafstetter_raster.tif'). Only needed when <code>data.table=FALSE</code> .   |
| <code>data_table</code>  | Logical. If TRUE, then the result will be loaded into R as a 2-column data.table (sub-catchment ID and Pfafstetter code). If FALSE, the result is loaded as a raster (terra object) in R and written to disk. Default is FALSE.   |
| <code>n_cores</code>     | numeric. Number of cores used for parallelization. Default is NULL (= <code>detectCores(logical=FALSE)-1</code> ). Optional.  |

## Value

Either a data.table, or a raster (terra object) loaded into R. In case the result is a raster, then a .tif file is written to disk.

## Note

You can use the online map at <https://geo.igb-berlin.de/maps/351/view> to identify an ID of a stream segment (use the "Stream segment ID" layer to the left)

**Author(s)**

Sami Domisch

**References**

Verdin, K.L. & Verdin, J.P. (1999). A topological system for delineation and codification of the Earth's river basins. *Journal of Hydrology*, 218(1-2), 1-12. doi:10.1016/s0022-1694(99)00011-6

**See Also**

[read\\_geopackage\(\)](#) and [get\\_catchment\\_graph.\(\)](#) to create the input graph.

**Examples**

```
# Download test data into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Import the stream network as a graph
# Load stream network as a graph
my_graph <- read_geopackage(gpkg = paste0(my_directory,
                                           "/hydrography90m_test_data",
                                           "/order_vect_59.gpkg"),
                           import_as = "graph")

# Subset the graph such that it contains only one basin. You can use
# a random ID, i.e. it does not need to be the real outlet of the basin.
g_subset <- get_catchment_graph(g = my_graph,
                               subc_id = "513867227",
                               outlet = FALSE,
                               mode = "in",
                               as_graph = TRUE)

# Specify the sub-catchment raster file
subc_raster <- paste0(my_directory, "/hydrography90m_test_data",
                      "/subcatchment_1264942.tif")

# Specify the output directory
out_dir <- my_directory

# Calculate the Pfafstetter sub-basins and write the raster layer to disk (
# and import into R)
pfafstetter <- get_pfafstetter_basins(g = g_subset ,
                                     subc_raster = subc_raster,
                                     out_dir = out_dir,
                                     file_name = "pfafstetter_raster.tif",
                                     data_table = FALSE,
                                     n_cores = 4)
```

---

`get_regional_unit_id` *Get Hydrography90m regional unit IDs*

---

### Description

Given the coordinates of input points (in WGS84), the function identifies the IDs of the regional units of the Hydrography90m in which the points are located. Input is a point data frame. The regional units refer to non-interrupted basins (as opposed to the 20°x20° tiles). These IDs can then be used to download the Hydrography90m regional unit raster mask(s) using [download\\_tiles\(\)](#).

### Usage

```
get_regional_unit_id(data, lon, lat, quiet = TRUE)
```

### Arguments

|                    |   |
|--------------------|---|
| <code>data</code>  | a data.frame or data.table that contains the columns regarding the longitude / latitude coordinates in WGS84. |
| <code>lon</code>   | character. The name of the column with the longitude coordinates.   |
| <code>lat</code>   | character. The name of the column with the latitude coordinates.  |
| <code>quiet</code> | logical. If FALSE, the standard output will be printed. Default is TRUE.                                      |

### Author(s)

Afroditi Grigoropoulou

### References

<https://gdal.org/programs/gdallocationinfo.html>

### Examples

```
# Download test data into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Read the species data
species_occurence <- read.table(paste0(my_directory,
                                         "/hydrography90m_test_data",
                                         "/spdata_1264942.txt"),
                                header = TRUE)

# Get the regional unit ID
get_regional_unit_id(species_occurence, lon = "longitude",
                     lat = "latitude")
```

---

get\_segment\_neighbours

*Get stream segment neighbours*


---

## Description

For each input stream segment, reports those upstream, downstream, or up-and downstream segments that are connected to the input segment(s) within a specified neighbour order, with the option to summarize attributes across these segments. Note that the stream segment and sub-catchment IDs are identical, and for consistency, we use the term "subc\_id". The input graph can be created with [read\\_geopackage\(\)](#) and [get\\_catchment\\_graph.\(\)](#)

This function can be used to obtain the neighbour stream segments / sub-catchments for spatially explicit models or for spatial prioritization analyses (e.g. Marxan/Gurobi).

## Usage

```
get_segment_neighbours(
  g,
  subc_id = NULL,
  var_layer = NULL,
  stat = NULL,
  attach_only = FALSE,
  order = 5,
  mode = "in",
  n_cores = 1,
  max_size = 1500
)
```

## Arguments

|                          |  |
|--------------------------|--|
| <code>g</code>           | igraph object. A directed graph.   |
| <code>subc_id</code>     | numeric vector of the input sub-catchment IDs (=stream segment IDs) for which to search the connected segments.  |
| <code>var_layer</code>   | character vector. One or more attributes (variable layers) of the input graph that should be reported for each output segment_id ("to_stream"). Optional. Default is NULL.   |
| <code>stat</code>        | one of the functions mean, median, min, max, sd (without quotes). Aggregates (or summarizes) the variables for the neighbourhood of each input segment (e.g., the average land cover in the next five upstream segments or sub-catchments). Default is NULL. |
| <code>attach_only</code> | logical. If TRUE, the selected variables will be only attached to each segment without any further aggregation. Default is FALSE.  |
| <code>order</code>       | numeric. The neighbouring order as in <code>igraph::ego</code> . Order = 1 would be immediate neighbours of the input sub-catchment IDs, order = 2 would be the order 1 plus the immediate neighbours of those sub-catchment IDs in order 1, and so on.      |

|          |  |
|----------|--|
| mode     | character. One of "in", "out", or "all". "in" returns only upstream neighbouring segments, "out" returns only the downstream segments, and "all" returns both.   |
| n_cores  | numeric. Number of cores used for parallelisation in the case of multiple stream segments / outlets. Default is 1. Note that the parallelisation process requires copying the data to each core. In case the graph is very large, and many segments are used as an input, setting n_cores to a higher value can speed up the computation. This comes however at the cost of possible RAM limitations and even slower processing since the large data will be copied to each core. Hence consider testing first with n_cores = 1. Optional. |
| max_size | numeric. Specifies the maximum size of the data passed to the parallel back-end in MB. Default is 1500 (1.5 GB). Consider a higher value for large study areas (more than one 20°x20° tile). Optional.   |

**Author(s)**

Sami Domisch

**References**

Csardi G, Nepusz T: The igraph software package for complex network research, InterJournal, Complex Systems 1695. 2006. <https://igraph.org>

**See Also**

[read\\_geopackage\(\)](#) and [get\\_catchment\\_graph.\(\)](#) to create the input graph.

**Examples**

```
# Download test data into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Load the stream network as graph
my_graph <- read_geopackage(gpkg= paste0(my_directory,
                                          "/hydrography90m_test_data",
                                          "/order_vect_59.gpkg"),
                           import_as = "graph")

# Get the upstream segment neighbours in the 5th order
# and report the length and source elevation
# for the neighbours of each input segment
get_segment_neighbours(g = my_graph, subc_id = subc_id,
                       order = 5, mode = "in", n_cores = 1,
                       var_layer = c("length", "source_elev"),
                       attach_only = TRUE)

# Get the downstream segment neighbours in the 5th order
# and calculate the median length and source elevation
# across the neighbours of each input segment
get_segment_neighbours(g = my_graph, subc_id = subc_id,
```

```

order = 2, mode = "out", n_cores = 1,
var_layer = c("length", "source_elev"),
stat = median)

# Get the up-and downstream segment neighbours in the 5th order
# and report the median length and source elevation
# for the neighbours of each input segment
get_segment_neighbours(g = my_graph, subc_id = subc_id, order = 2,
mode = "all", n_cores = 1,
var_layer = c("length", "source_elev"),
stat = mean, attach_only = TRUE)

```

---

get\_tile\_id

*Get the Hydrography90m 20°x20° tile ID*


---

### Description

Identifies the 20°x20° tile IDs of the Hydrography90m data in which the input points are located. The IDs can then be used to download the data using [download\\_tiles\(\)](#). The input is a data frame with point coordinates.

### Usage

```
get_tile_id(data, lon, lat)
```

### Arguments

|      |   |
|------|---|
| data | a data.frame or data.table that contains the columns regarding the longitude / latitude coordinates in WGS84. |
| lon  | character. The name of the column with the longitude coordinates.   |
| lat  | character. The name of the column with the latitude coordinates.  |

### Author(s)

Afroditi Grigoropoulou

### Examples

```

# Download test data into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Load species occurrence data
species_occurrence <- read.table(paste0(my_directory,
"/hydrography90m_test_data",
"/spdata_1264942.txt"),
header = TRUE)

```



```
# Get the tile ID
get_tile_id(data = species_occurrence,
            lon = "longitude", lat = "latitude")
```

---

get\_upstream\_catchment

*Delineate the upstream catchment*


---

## Description

Delineates the upstream catchment of a given point, where the point is considered as the outlet.

## Usage

```
get_upstream_catchment(
  data,
  id,
  lon,
  lat,
  direction_layer = NULL,
  out_dir = NULL,
  n_cores = NULL,
  compression = "low",
  bigtiff = TRUE,
  quiet = TRUE
)
```

## Arguments

|                 |  |
|-----------------|--|
| data            | a data.frame or data.table that contains the columns regarding the longitude / latitude coordinates in WGS84. Note that the points need to be snapped to the stream network with <a href="#">snap_to_network()</a> or <a href="#">snap_to_subc_segment()</a> . |
| id              | character. The name of a column containing unique IDs for each row of "data" (e.g., occurrence or site IDs).   |
| lon             | character. The name of the column with the longitude coordinates.  |
| lat             | character. The name of the column with the latitude coordinates.   |
| direction_layer | character. Full path to the flow direction raster file.  |
| out_dir         | Full path to the directory where the output(s) will be stored. The output file name includes the "id" which helps identifying the upstream corresponding catchment.  |
| n_cores         | numeric. Number of cores used for parallelisation. If NULL, available cores - 1 will be used. Default is NULL.   |
| compression     | character. Compression of the written output file. Compression levels can be defined as "none", "low", or "high". Default is "low", referring to compression type "DEFLATE" and compression level 2. "high" refers to compression level 9.                     |

|                      |   |
|----------------------|---|
| <code>bigtiff</code> | logical. Define whether the output file is expected to be a BIGTIFF (file size larger than 4 GB). If FALSE and size > 4GB no file will be written. Default is TRUE. |
| <code>quiet</code>   | logical. If FALSE, the standard output will be printed. Default is TRUE.  |

**Author(s)**

Jaime Garcia Marquez, Afroditi Grigoropoulou, Maria M. Üblacker

**References**

<https://grass.osgeo.org/grass82/manuals/r.water.outlet.html> <https://grass.osgeo.org/grass82/manuals/r.region.html>

**See Also**

[snap\\_to\\_network](#) to snap the data points to the next stream segment within a given radius and/or a given flow accumulation threshold value. [snap\\_to\\_subc\\_segment](#) to snap the data points to the next stream segment within the sub-catchment the point is located. [extract\\_ids](#) to extract basin and sub-catchment IDs.

**Examples**

```
# Download test data into temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Before running the function get_upstream_catchment(), snap the points to
# to the stream segment. There are multiple ways to snap the points. Here is
# one example:

# Load occurrence data
species_occurence <- read.table(paste0(my_directory,
                                       "/hydrography90m_test_data",
                                       "/spdata_1264942.txt"),
                               header = TRUE)

# Define full path to the basin and sub-catchments raster layer
basin_raster <- paste0(my_directory,
                      "/hydrography90m_test_data/basin_1264942.tif")
subc_raster <- paste0(my_directory,
                     "/hydrography90m_test_data/subcatchment_1264942.tif")

# Define full path to the vector file of the stream network
stream_vector <- paste0(my_directory,
                       "/hydrography90m_test_data/order_vect_59.gpkg")

# Automatically extract the basin and sub-catchment IDs and
# snap the data points to the stream segment
snapped_coordinates <- snap_to_subc_segment(data = species_occurence,
```

```

lon = "longitude",
lat = "latitude",
id = "occurrence_id",
basin_layer = basin_raster,
subc_layer = subc_raster,
stream_layer = stream_vector,
n_cores = 2)

# Define full path to the direction .tif
direction_raster <- paste0(my_directory,
                           "/hydrography90m_test_data/direction_1264942.tif")
# Define the path for the output file(s)
output_folder <- paste0(my_directory, "/upstream_catchments")
if(!dir.exists(output_folder)) dir.create(output_folder)
# Get the upstream catchment for each point location
get_upstream_catchment(snapped_coordinates,
                       lon = "lon_snap",
                       lat = "lat_snap",
                       id = "occurrence_id",
                       direction_layer = direction_raster,
                       out_dir = output_folder,
                       n_cores = 2)

```

---

merge\_tiles

---

*Merge raster or vector objects*


---

## Description

Merge multiple raster or spatial vector objects from disk to form a new raster or spatial vector object with a larger spatial extent. A directory with at least two raster .tif or spatial vector geopackage files should be provided. Depending on the input, the output is a .tif or a .gpkg file (saved under out\_dir). If read = TRUE, the output is read into R as a SpatRaster (terra package) object in case of .tif files, or as a SpatVector (terra package) object in case of .gpkg files.

## Usage

```

merge_tiles(
  tile_dir,
  tile_names,
  out_dir,
  file_name,
  name = "stream",
  compression = "low",
  bigtiff = TRUE,
  read = FALSE,
  quiet = TRUE
)

```

**Arguments**

|             |  |
|-------------|--|
| tile_dir    | character. The directory containing the raster or spatial vectors tiles, which should be merged.   |
| tile_names  | character. The names of the files to be merged, including the file extension (.tif or .gpkg).  |
| out_dir     | character. The directory where the output will be stored.  |
| file_name   | character. Name of the merged output file, including the file extension (.tif or .gpkg).   |
| name        | character. The attribute table column name of the stream segment ("stream"), sub-catchment ("ID"), basin ("ID") or outlet ("ID") column which is used for merging GeoPackages. Default is "stream".  |
| compression | character. Compression of the written output file. Compression levels can be defined as "none", "low", or "high". Default is "low", referring to compression type "DEFLATE" and compression level 2. "high" refers to compression level 9. |
| bigtiff     | logical. Define whether the output file is expected to be a BIGTIFF (file size larger than 4 GB). If FALSE and size > 4GB no file will be written. Default is TRUE.  |
| read        | logical. If TRUE, the merged layer gets read into R. If FALSE, the layer is only stored on disk. Default is FALSE.   |
| quiet       | logical. If FALSE, the standard output will be printed. Default is TRUE.   |

**Value**

A .tif raster file or .gpkg spatial vector object that is always written to disk, and optionally loaded into R.

**Author(s)**

Thomas Tomiczek, Jaime Garcia Marquez, Afroditi Grigoropoulou

**References**

<https://gdal.org/programs/gdalbuildvrt.html>  
[https://gdal.org/programs/gdal\\_translate.html](https://gdal.org/programs/gdal_translate.html)  
<https://gdal.org/programs/ogrmerge.html#ogrmerge>  
<https://gdal.org/programs/ogr2ogr.html>

**Examples**

```
# Download tiles into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_tiles(variable = "basin",
               file_format = "tif",
               tile_id = c("h22v08", "h22v10"),
```

```

download_dir = my_directory)

# Define folder containing only the tiles, which should be merged
tiles_folder <- paste0(my_directory, "/r.watershed/basin_tiles20d")
# Define output folder
output_folder <- paste0(my_directory, "/merged_tiles")
# Create output folder if it doesn't exist
if(!dir.exists(output_folder)) dir.create(output_folder)

# Merge tiles
merged_tiles <- merge_tiles(tile_dir = tiles_folder,
                           tile_names = c("basin_h22v08.tif", "basin_h22v10.tif"),
                           out_dir = output_folder,
                           file_name = "basin_merged.tif",
                           read = TRUE)

```

---

|                 |                               |
|-----------------|-------------------------------|
| read_geopackage | <i>Read a GeoPackage file</i> |
|-----------------|-------------------------------|

---

## Description

Reads an entire, or a subset of a GeoPackage vector file from disk either as a table (data.table), as a directed graph object (igraph), a spatial dataframe (sf) or a SpatVect object (terra).

## Usage

```

read_geopackage(
  gpkg,
  import_as = "data.table",
  layer_name = NULL,
  subc_id = NULL,
  name = "stream"
)

```

## Arguments

|            |  |
|------------|--|
| gpkg       | character. Full path of the GeoPackage file.   |
| import_as  | character. "data.table", "graph", "sf", or "SpatVect". "data.table" imports data as a data.table. "graph" imports the layer as a directed graph (igraph object). This option is only possible for a network layer (e.g. the stream network) and it needs to contain the attributes "stream" and "next_stream". "sf" imports the layer as a spatial data frame (sf object). "SpatVect" imports the layer as a SpatVector (terra object). Default is "data.table". |
| layer_name | character. Name of the specific data layer to import from the GeoPackage. A specific data layer only needs to be defined if the GeoPackage contains multiple layers. To see the available layers the function st_layers() from the R package 'sf' can be used. Optional. Default is NULL.  |

|         |   |
|---------|---|
| subc_id | numeric. Vector of the sub-catchment (or stream segment) IDs in the form of (c(ID1, ID2, ...)) for which the spatial objects or attributes of the GeoPackage should be imported. Optional. Default is NULL.                         |
| name    | character. The attribute table column name of the stream segment ("stream"), sub-catchment ("ID"), basin ("ID") or outlet ("ID") column which is used for subsetting the GeoPackage prior importing. Optional. Default is "stream". |

### Author(s)

Sami Domisch, Maria M.Üblacker

### Examples

```
# Download test data into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Read the stream network as a graph
my_graph <- read_geopackage(gpkg = paste0(my_directory,
                                           "/hydrography90m_test_data",
                                           "/order_vect_59.gpkg"),
                           import_as = "graph")

# Read the stream network as a data.table
my_dt <- read_geopackage(gpkg = paste0(my_directory,
                                       "/hydrography90m_test_data",
                                       "/order_vect_59.gpkg"))

# Read the stream network as a data.table for specific IDs
my_dt <- read_geopackage(gpkg = paste0(my_directory,
                                       "/hydrography90m_test_data",
                                       "/order_vect_59.gpkg"),
                           subc_id = c(513833203, 513833594))

# Read the sub-catchments as a SF-object
my_sf <- read_geopackage(gpkg = paste0(my_directory,
                                       "/hydrography90m_test_data",
                                       "/sub_catchment_59.gpkg"),
                           import_as = "sf",
                           layer_name = "sub_catchment")

# Read a subset of sub-catchments as a SF-object
my_sf <- read_geopackage(gpkg = paste0(my_directory,
                                       "/hydrography90m_test_data",
                                       "/sub_catchment_59.gpkg"),
                           import_as = "sf",
                           subc_id = c(513833203, 513833594),
                           name = "ID")

# Read the basin as SpatVect object
```

```
my_sv <- read_geopackage(gpkg = paste0(my_directory,
                                         "/hydrography90m_test_data",
                                         "/basin_59.gpkg"),
                        import_as = "SpatVect")
```

---

|                |                                  |
|----------------|----------------------------------|
| reclass_raster | <i>Reclassify a raster layer</i> |
|----------------|----------------------------------|

---

## Description

Reclassifies a raster .tif layer based on a look-up table, such that the output raster contains the new values. The function uses the `r.reclass` function of GRASS GIS.

Note that the input raster needs to be of type integer. If the input raster layer has floating point values, you can multiply it by some factor (e.g. 1000) to achieve integer values, otherwise the GRASS GIS `r.reclass` will round the raster values down to the next integer which is not always desired.

## Usage

```
reclass_raster(
  data,
  rast_val,
  new_val,
  raster_layer,
  recl_layer,
  no_data = -9999,
  type = "Int32",
  compression = "low",
  bigtiff = TRUE,
  read = FALSE,
  quiet = TRUE
)
```

## Arguments

|                           |   |
|---------------------------|---|
| <code>data</code>         | a data.frame or data.table with the original and new values to be written to the raster.  |
| <code>rast_val</code>     | character. The name of the column with the original raster values.  |
| <code>new_val</code>      | character. The name of the column with the new raster values, which need to be integer values. In case of floating point values, consider multiplying the values e.g. by 1000 to keep three decimals. |
| <code>raster_layer</code> | Full path to the input raster .tif layer.   |
| <code>recl_layer</code>   | character. Full path of the output .tif layer, i.e., the reclassified raster file.  |
| <code>no_data</code>      | numeric. The <code>no_data</code> value of the new .tif layer. Default is -9999.  |

|             |  |
|-------------|--|
| type        | character. Data type; Options are Byte, Int16, UInt16, Int32, UInt32, CInt16, CInt32. Default is Int32. Note that only integer values are allowed.   |
| compression | character. Compression of the written output file. Compression levels can be defined as "none", "low", or "high". Default is "low", referring to compression type "DEFLATE" and compression level 2. "high" refers to compression level 9. |
| bigtiff     | logical. Define whether the output file is expected to be a BIGTIFF (file size larger than 4 GB). If FALSE and size > 4GB no file will be written. Default is TRUE.  |
| read        | logical. If TRUE, then the reclassified raster .tif layer gets read into R as a SpatRaster (terra object). If FALSE, the layer is only stored on disk. Default is FALSE.   |
| quiet       | logical. If FALSE, the standard output will be printed. Default is TRUE.   |

### Author(s)

Maria M. Üblacker

### References

<https://grass.osgeo.org/grass82/manuals/r.reclass.html>

### Examples

```
# Download test data into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Read the stream order for each sub-catchment as a data.table
my_dt <- read_geopackage(gpkg= paste0(my_directory,
                                     "/hydrography90m_test_data",
                                     "/order_vect_59.gpkg"),
                        import_as = "data.table")

# Select the stream segment ID and the Strahler stream order
str_ord <- my_dt[,c("stream", "strahler")]

# Define input and output raster layer
stream_raster <- paste0(my_directory,
                        "/hydrography90m_test_data/stream_1264942.tif")

recl_raster <- paste0(my_directory,
                    "/hydrography90m_test_data/reclassified_raster.tif")

# Reclassify the stream network to obtain the Strahler stream order raster
str_ord_rast <- reclass_raster(data = str_ord,
                             rast_val = "stream",
                             new_val = "strahler",
```



```
raster_layer = stream_raster,
recl_layer = recl_raster)
```

---

|                |                            |
|----------------|----------------------------|
| report_no_data | <i>Report NoData value</i> |
|----------------|----------------------------|

---

## Description

This function reports the defined NoData value of a raster layer. The NoData value of a raster layer represents the absence of data. In computations the NoData value can be treated in different ways. Either the NoData value will be reported or the Nodata value will be ignored and a value is computed from the available values of a specified location.

## Usage

```
report_no_data(data_dir, var_layer, n_cores = NULL)
```

## Arguments

|           |   |
|-----------|---|
| data_dir  | character. Path to the directory containing all input data.   |
| var_layer | character vector of variable raster layers on disk, e.g. "slope_grad_dw_cel_h00v00.tif".                  |
| n_cores   | numeric. Number of cores used for parallelization, in case multiple .tif files are provided to var_layer. |

## Author(s)

Afroditi Grigoropoulou, Maria M. Üblacker

## References

<https://gdal.org/programs/gdalinfo.html>

## Examples

```
# Download test data into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Report the NoData value
report_no_data(data_dir = paste0(my_directory, "/hydrography90m_test_data"),
               var_layer = c("subcatchment_1264942.tif", "flow_1264942.tif",
                             "spi_1264942.tif"),
               n_core = 2)
```

---

|             |                          |
|-------------|--------------------------|
| set_no_data | <i>Set no data value</i> |
|-------------|--------------------------|

---

### Description

Change or set the NoData value for a raster layer. The change happens in-place, meaning that the original file is overwritten on disk.

### Usage

```
set_no_data(data_dir, var_layer, no_data, quiet = TRUE)
```

### Arguments

|           |  |
|-----------|--|
| data_dir  | character. Path to the directory containing all input data.  |
| var_layer | character vector of variable layers on disk, e.g. c("sti_h16v02.tif", "slope_grad_dw_cel_h00v00.tif"). The original files will be overwritten. |
| no_data   | numeric. The desired NoData value.   |
| quiet     | logical. If FALSE, the standard output will be printed. Default is TRUE.   |

### Author(s)

Afroditi Grigoropoulou, Maria M. Üblacker

### References

[https://gdal.org/programs/gdal\\_edit.html](https://gdal.org/programs/gdal_edit.html)

### Examples

```
# Download test data into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Define no data value
set_no_data(data_dir = paste0(my_directory, "/hydrography90m_test_data"),
            var_layer = "cti_1264942.tif",
            no_data = -9999)
```

---

|                 |   |
|-----------------|---|
| snap_to_network | <i>Snap points to stream segment based on distance or flow accumulation</i> |
|-----------------|---|

---

### Description

Snap points to the next stream segment within a defined radius (in map pixels) or a minimum flow accumulation.

### Usage

```
snap_to_network(
  data,
  lon,
  lat,
  id,
  stream_layer,
  accu_layer = NULL,
  method = "distance",
  distance = 500,
  accumulation = 0.5,
  quiet = TRUE
)
```

### Arguments

|              |   |
|--------------|---|
| data         | a data.frame or data.table that contains the columns regarding the longitude / latitude coordinates in WGS84.   |
| lon          | character. The name of the column with the longitude coordinates.   |
| lat          | character. The name of the column with the latitude coordinates.  |
| id           | character. The name of a column containing unique IDs for each row of "data" (e.g., occurrence or site IDs). The unique IDs need to be numeric.   |
| stream_layer | character. Full path of the stream network .tif file  |
| accu_layer   | character. Full path of the flow accumulation .tif file. Needed if the point should be snapped to the next stream segment having an accumulation value higher than the flow accumulation threshold (set by 'accumulation'). This prevents points from being snapped to small stream tributaries. Optional. Default is NULL. |
| method       | character. One of "distance", "accumulation", or "both". Defines if the points are snapped using the distance or flow accumulation (see "Details" for more information). If method is set to "both" the output will contain the new coordinates for both calculations. Default is "distance" (in map pixels).               |
| distance     | numeric. Maximum radius in map pixels. The points will be snapped to the next stream within this radius. Default is 500.  |
| accumulation | numeric. Minimum flow accumulation. Points will be snapped to the next stream with a flow accumulation equal or higher than the given value. Default is 0.5.  |
| quiet        | logical. If FALSE, the standard output will be printed. Default is TRUE.  |



```

stream_layer = stream_raster,
accu_layer = flow_raster,
method = "both",
distance = 300,
accumulation = 0.8)

# Show head of output table
head(snapped_coordinates)

```

---

snap\_to\_subc\_segment    *Snap points to stream segment within the sub-catchment*

---

## Description

Move points to the stream segment within the sub-catchment where the point is located.

## Usage

```

snap_to_subc_segment(
  data,
  lon,
  lat,
  id,
  basin_id = NULL,
  subc_id = NULL,
  basin_layer,
  subc_layer,
  stream_layer,
  n_cores = 1,
  quiet = TRUE
)

```

## Arguments

|             |  |
|-------------|--|
| data        | a data.frame or data.table that contains the columns regarding the longitude / latitude coordinates in WGS84.  |
| lon         | character. The name of the column with the longitude coordinates.  |
| lat         | character. The name of the column with the latitude coordinates.   |
| id          | character. The name of a column containing unique IDs for each row of "data" (e.g., occurrence or site IDs). The unique IDs need to be numeric.          |
| basin_id    | character. The name of the column with the basin IDs. If NULL, the basin IDs will be extracted automatically. Optional. Default is NULL                  |
| subc_id     | character. The name of the column with the sub-catchment IDs. If NULL, the sub-catchment IDs will be extracted automatically. Optional. Default is NULL. |
| basin_layer | character. Full path to the basin ID .tif layer.   |

|              |  |
|--------------|--|
| subc_layer   | character. Full path to the sub-catchment ID .tif layer.                 |
| stream_layer | character. Full path of the stream network .gpkg file.                   |
| n_cores      | numeric. Number of cores used for parallelisation. Default is 1.         |
| quiet        | logical. If FALSE, the standard output will be printed. Default is TRUE. |

## Details

The function uses the network module of GRASS GIS (v.net), to connect a vector line map (stream network) with a point map (occurrence/sampling points). After masking the stream segment and the sub-catchment where the target point is located, the connect operation snaps the point to the stream segment using a distance threshold. This threshold is automatically calculated as the longest distance between two points within the sub-catchment. In this way the snapping will always take place. From the new location, the function extracts the new snapped coordinates.

## Author(s)

Jaime Garcia Marquez, Maria M. Üblacker

## References

<https://grass.osgeo.org/grass82/manuals/v.net.html>

## See Also

[snap\\_to\\_network](#) to snap the data points to the next stream segment within a given radius and/or a given flow accumulation threshold value. [extract\\_ids](#) to extract basin and sub-catchment IDs.

## Examples

```
# Download test data into the temporary R folder
# or define a different directory
my_directory <- tempdir()
download_test_data(my_directory)

# Load occurrence data
species_occurrence <- read.table(paste0(my_directory,
                                          "/hydrography90m_test_data/spdata_1264942.txt"),
                                 header = TRUE)

basin_rast <- paste0(my_directory,
                     "/hydrography90m_test_data/basin_1264942.tif")
subc_rast <- paste0(my_directory,
                    "/hydrography90m_test_data/subcatchment_1264942.tif")

# Define full path to the vector file of the stream network
stream_vect <- paste0(my_directory,
                      "/hydrography90m_test_data/order_vect_59.gpkg")

hydrography90m_ids <- extract_ids(data = species_occurrence,
                                 lon = "longitude",
                                 lat = "latitude",
```

```
      id = "occurrence_id",
      subc_layer = subc_rast,
      basin_layer = basin_rast)

# Snap data points to the stream segment of the provided sub-catchment ID
snapped_coordinates <- snap_to_subc_segment(data = hydrography90m_ids,
      lon = "longitude",
      lat = "latitude",
      id = "occurrence_id",
      basin_id = "basin_id",
      subc_id = "subcatchment_id",
      basin_layer = basin_rast,
      subc_layer = subc_rast,
      stream_layer = stream_vect,
      n_cores = 2)

# Show head of output table
head(snapped_coordinates)

# OR
# Automatically extract the basin and sub-catchment IDs and
# snap the data points to the stream segment
snapped_coordinates <- snap_to_subc_segment(data = species_occurence,
      lon = "longitude",
      lat = "latitude",
      id = "occurrence_id",
      basin_layer = basin_rast,
      subc_layer = subc_rast,
      stream_layer = stream_vect,
      n_cores = 2)

# Show head of output table
head(snapped_coordinates)
```

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