

# Package: mrorganic (via r-universe)

August 25, 2024

**Type** Package

**Title** Provide soil organic carbon and biomass data

**Version** 0.5.6

**Date** 2023-06-02

**Description** mrorganic supports downloading and preparing soil organic carbon and biomass data for further scientific work.

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**URL** <https://github.com/tscheypidi/mrorganic>

**Depends** madrat(>= 3.1.1), magclass(>= 3.17), R(>= 2.10.0)

**Imports** geodata, terra, utils, withr

**Suggests** covr, knitr, rmarkdown

**VignetteBuilder** knitr

**Encoding** UTF-8

**LazyData** no

**RoxygenNote** 7.2.3

**Repository** <https://pik-piam.r-universe.dev>

**RemoteUrl** <https://github.com/tscheypidi/mrorganic>

**RemoteRef** HEAD

**RemoteSha** 4f2c8daa7c44051763f2787fbbf23751524be15f

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mrorganic-package	<i>mrorganic: Provide soil organic carbon and biomass data</i>
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## Description

mrorganic supports downloading and preparing soil organic carbon and biomass data for further scientific work.

## Author(s)

**Maintainer:** Jan Philipp Dietrich <dietrich@pik-potsdam.de>

Authors:

- Pascal Führlich <pascal.fuehrlich@pik-potsdam.de>

Other contributors:

- Hugo Valin [contributor]

## See Also

Useful links:

- <https://github.com/tscheypidi/mrorganic>

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calcBiomassByLandType	<i>Calculate Biomass by land type</i>
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## Description

Estimate soil organic carbon content split by land type.

## Usage

```
calcBiomassByLandType(subtype)
```

**Arguments**

subtype            "aboveground" or "belowground"

**Value**

data

**Author(s)**

Jan Philipp Dietrich

**See Also**

[calcOutput](#)

**Examples**

```
## Not run:  
a <- calcOutput("BiomassbyLandType", subtype = "aboveground")  
  
## End(Not run)
```

---

*calcEcoregions2017Raster*  
*calcEcoregions2017Raster*

---

**Description**

Produces a raster with ecoregion information.

**Usage**

```
calcEcoregions2017Raster(nrows = 720, ncols = 1440)
```

**Arguments**

nrows            Number of rows in the raster produced.  
ncols            Number of columns in the raster produced.

**Value**

A raster with ecoregion information as a data.frame

**Author(s)**

Pascal Führlich

calcLandTypeAreas      *Calculate land type areas*

---

**Description**

Convert ESACCI landcover information into area information for selected land types cropland, grassland and other.

**Usage**

```
calcLandTypeAreas(categories = "CropGrassOther")
```

**Arguments**

categories      Categories land should be segregated into. Only available options are currently "CropGrassOther" and "CropGrassForestOthernatvegResidual".

**Value**

data

**Author(s)**

Jan Philipp Dietrich

**See Also**

[calcOutput](#)

**Examples**

```
## Not run:  
a <- calcOutput("LandTypeAreas")  
  
## End(Not run)
```

---

calcLandTypeAreasAggregated  
    *Aggregate land type areas*

---

**Description**

Aggregate land type area information to a desired resolution

**Usage**

```
calcLandTypeAreasAggregated(res, zeroValue = 0)
```

**Arguments**

res                    target resolution  
zeroValue            value for cells with no area. Useful to change to a very small number if the area information should be used as weight.

**Value**

data

**Author(s)**

Jan Philipp Dietrich

**See Also**

[calcOutput](#)

**Examples**

```
## Not run:  
a <- calcOutput("LandTypeAreas")  
  
## End(Not run)
```

---

calcSOCbyLandType            *Calculate SOC by land type*

---

**Description**

Estimate soil organic carbon content split by land type

**Usage**

```
calcSOCbyLandType()
```

**Value**

data

**Author(s)**

Jan Philipp Dietrich

**See Also**

[calcOutput](#)

**Examples**

```
## Not run:  
a <- calcOutput("SOCbyLandType")  
  
## End(Not run)
```

---

calcWorldCountries      *Calculate world countries*

---

**Description**

Partition the world into countries with their respective ISO codes

**Usage**

```
calcWorldCountries()
```

**Value**

data

**Author(s)**

Patrick v. Jeetze, Jan Philipp Dietrich

**See Also**

[calcOutput](#)

**Examples**

```
## Not run:  
a <- calcOutput("WorldCountries", aggregate = FALSE)  
  
## End(Not run)
```

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fullORGANIC	<i>fullORGANIC</i>
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**Description**

Bundle function for mrorganic which bundles all relevant outputs and write them to a tgz file.

**Usage**

```
fullORGANIC(rev)
```

**Arguments**

rev	data revision
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**Details**

Use `regionmapping = "regionmappingGTAP11.csv"`) to produce outputs for GTAP11 world regions.

**Author(s)**

Jan Philipp Dietrich

**See Also**

[retrieveData](#), [calcOutput](#), [readSource](#), [setConfig](#)

**Examples**

```
## Not run:  
retrieveData("Organic", rev = 2.1, regionmapping = "regionmappingGTAP11.csv")  
  
## End(Not run)
```

---

plotMap	<i>plotMap</i>
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**Description**

Create a plot showing a map.

**Usage**

```
plotMap(x, name, createPng = FALSE, range = NULL, ...)
```

**Arguments**

x	The data to plot as magclass object
name	The name/title of the plot/png
createPng	If TRUE save plot as png
range	range of values for the color bar. If NULL range will be detected automatically
...	Further arguments passed to terra::plot

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`readESACCI`*Read ESACCI*

---

**Description**

Read ESACCI data

**Usage**

```
readESACCI(subtype = "landcover2010")
```

**Arguments**

subtype	Subtype to be read in
---------	-----------------------

**Value**

data

**Author(s)**

Jan Philipp Dietrich

**See Also**

[readSource](#)

**Examples**

```
## Not run:  
a <- readSource("ESACCI")  
  
## End(Not run)
```



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readGSOCseq	<i>Read GSOCseq</i>
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**Description**

Read GSOCseq data

**Usage**

```
readGSOCseq(subtype = "ini")
```

**Arguments**

subtype            data set to use (currently available "ini" and "finalSSM1")

**Value**

data

**Author(s)**

Jan Philipp Dietrich

**See Also**

[readSource](#)

**Examples**

```
## Not run:  
a <- readSource("GSOCseq")  
  
## End(Not run)
```

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readSpawn	<i>Read Spawn</i>
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**Description**

Read Spawn data

**Usage**

```
readSpawn(subtype)
```

**Arguments**

subtype            Subtype to be read in. Available types are "abovegroundBiomass", "abovegroundBiomassUncertainty", "belowgroundBiomass" and "belowgroundBiomassUncertainty".

**Value**

data

**Author(s)**

Jan Philipp Dietrich

**See Also**

[readSource](#)

**Examples**

```
## Not run:  
a <- readSource("Spawn", "abovegroundBiomass")  
  
## End(Not run)
```

---

readWorldBankMaps      *readWorldBankMaps*

---

**Description**

Read World Bank Maps

**Usage**

```
readWorldBankMaps(subtype = "CountryPolygons")
```

**Arguments**

subtype            data set to use (currently available "CountryPolygons", "CountryBoundaries", "DisputedAreas" and "DisputedAreasBoundaries")

**Value**

data

**Author(s)**

Jan Philipp Dietrich

### See Also

[readSource](#)

### Examples

```
## Not run:  
a <- readSource("WorldBankMaps")  
  
## End(Not run)
```

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*toolAddEcoregions*      *toolAddEcoregions*

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### Description

Enriches a magclass object with ecoregion and region information.

### Usage

```
toolAddEcoregions(x, ecoregions, regionmapping)
```

### Arguments

<code>x</code>	A magclass object
<code>ecoregions</code>	Ecoregions dataframe, as returned by <code>calcEcoregions2017Raster</code>
<code>regionmapping</code>	A regionmapping

### Value

`x` with additional ecoregion and region information. Spatial subdimensions: `c("x", "y", "country", "region", "biome", "country_biome", "region_biome")`

### Author(s)

Pascal Fährlich

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toolAggregateByLandType

*toolAggregateByLandType*

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**Description**

Aggregate raster object by land type and return as 0.25degx0.25deg magclass object

**Usage**

```
toolAggregateByLandType(x, weight)
```

**Arguments**

x	data to be aggregated
weight	weight to be used for aggregation (land type)

**Value**

data

**Author(s)**

Jan Philipp Dietrich

**See Also**

[calcOutput](#)

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