

Package: map (via r-universe)

October 6, 2024

Type Package

Title Defines a meta class of geographical objects, the 'map' class, and associated tools

Description The map class is a collection of map objects ('sp', 'raster', 'sf'), with a number of metadata additions to enable powerful methods, e.g., for leaflet, reproducible GIS etc.

URL <http://map.predictiveecology.org>,
<https://github.com/PredictiveEcology/map>

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'map-class.R' 'map-package.R' 'map.R' 'rbindlistAG.R' 'zzz.R'

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<code>.rasterToMemory</code>	<code>.rasterToMemory</code>
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Description

`.rasterToMemory`

Usage

`.rasterToMemory(x, ...)`

Arguments

- | | |
|-----|---------------------------------------|
| x | A Raster* object |
| ... | Additional arguments passed to raster |

area, map-method	<i>Calculate area of (named) objects the map obj</i>
------------------	--

Description

Calculate area of (named) objects the map obj

Usage

```
## S4 method for signature 'map'  
area(x)
```

Arguments

- | | |
|---|-----------------------------------|
| x | Raster* or SpatialPolygons object |
|---|-----------------------------------|

See Also

Other mapMethods: [crs](#), [map-method](#), [mapRm\(\)](#), [rasterToMatch](#), [map-method](#), [rasters\(\)](#), [studyAreaName\(\)](#), [studyArea\(\)](#)

areaAndPolyValue	areaAndPolyValue
------------------	------------------

Description

Determine the area of each zone in a raster. TODO: improve description

Usage

```
areaAndPolyValue(ras)
```

Arguments

- | | |
|-----|------------------|
| ras | A Raster* object |
|-----|------------------|

Value

list containing: sizeInHa, the area; and polyID, the polygon ID.

<code>buildMetadata</code>	<i>Build map obj metadata table</i>
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Description

Build map obj metadata table

Usage

```
buildMetadata(
  metadata,
  isStudyArea,
  isRasterToMatch,
  layerName,
  obj,
  columnNameForLabels,
  objHash,
  leaflet,
  envir,
  ...
)
```

Arguments

<code>metadata</code>	TODO: description needed
<code>isStudyArea</code>	TODO: description needed
<code>isRasterToMatch</code>	Logical. Is this(these) layer(s) the <code>rasterToMatch</code> layers. If TRUE, then this layer can be accessed by <code>rasterToMatch(map)</code>
<code>layerName</code>	TODO: description needed
<code>obj</code>	TODO: description needed
<code>columnNameForLabels</code>	TODO: description needed
<code>objHash</code>	TODO: description needed
<code>leaflet</code>	Logical or Character vector of path(s) to write tiles. If TRUE or a character vector, then this layer will be added to a leaflet map. For RasterLayer object, this will trigger a call to <code>gdal2tiles</code> , making tiles. If path is not specified, it will be the current path. The tile base file path will be <code>paste0(layerName, "_", rndstr(1, 6))</code> .
<code>envir</code>	TODO: description needed
<code>...</code>	Additional arguments.

crs, map-method	<i>Extract the crs of a map</i>
-----------------	---------------------------------

Description

Extract the crs of a map

Usage

```
## S4 method for signature 'map'  
crs(x, ...)
```

Arguments

x	Raster* or Spatial object
...	additional arguments. None implemented

See Also

Other mapMethods: [area, map-method, mapRm\(\)](#), [rasterToMatch, map-method](#), [rasters\(\)](#), [studyAreaName\(\)](#), [studyArea\(\)](#)

fasterize2	<i>Fasterize with crop & spTransform first</i>
------------	--

Description

Fasterize with crop & spTransform first

Usage

```
fasterize2(emptyRaster, polygonToFasterize, field)
```

Arguments

emptyRaster	An empty raster with res, crs, extent all correct for to pass to fasterize
polygonToFasterize	passed to fasterize, but it will be cropped first if extent(emptyRaster) < extent(polygonToFasterize)
field	passed to fasterize

gdal_polygonizeR *Polygonize with GDAL*

Description

Based on <https://johnbaumgartner.wordpress.com/2012/07/26/getting-rasters-into-shape-from-r/>.

Usage

```
gdal_polygonizeR(
  x,
  outshape = NULL,
  gdalformat = "ESRI Shapefile",
  pypath = NULL,
  readpoly = TRUE,
  quiet = TRUE
)
```

Arguments

x	TODO: description needed
outshape	TODO: description needed
gdalformat	TODO: description needed
pypath	TODO: description needed
readpoly	TODO: description needed
quiet	TODO: description needed

leafletTiles *Extract leaflet tile paths from a map obj*

Description

Extract leaflet tile paths from a map obj

Usage

```
leafletTiles(map)
```

Arguments

map	A map class obj
-----	-----------------

Value

A vector of paths indicating the relative paths. Any layers that don't have leaflet tiles will return NA.

makeTiles	<i>Make tiles (pyramids) using gdal2tiles</i>
-----------	---

Description

Make tiles (pyramids) using gdal2tiles

Usage

```
makeTiles(tilePath, obj, overwrite = FALSE, ...)
```

Arguments

tilePath	A director to write tiles
obj	A raster objects with or without file-backing
overwrite	Logical. If FALSE, and the director exists, then it will not overwrite any files.
...	Passed to <code>reproducible::projectInputs</code> e.g., <code>useGDAL</code>

map-class	<i>The map class</i>
-----------	----------------------

Description

Contains a common system for organizing vector and raster layers, principally for use with **leaflet** and **shiny**.

Slots

metadata	<code>data.table</code> with columns describing metadata of map objects in <code>maps</code> slot.
.xData	Named environment of map-type objects (e.g., <code>sf</code> , <code>Raster*</code> , <code>Spatial*</code>). Each entry may also be simply an environment, which indicates where to find the object, i.e., via <code>get(layerName, envir = environment)</code> .
CRS	The common crs of all layers
paths	File paths. A named list of paths. The default is a list of length 2, <code>dataPath</code> and <code>tilePath</code>
analyses	A <code>data.table</code> or <code>data.frame</code> of the types of analyses to perform.
analysesData	A <code>data.table</code> or <code>data.frame</code> of the results of the analyses.

<code>mapAdd</code>	<i>Append a spatial object to map</i>
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Description

If `isStudyArea` = TRUE, then several things will be triggered:

1. This layer will be added to metadata with `studyArea` set to `max(studyArea(map)) + 1`.
2. update CRS slot to be the CRS of the study area.

Usage

```
mapAdd(obj, map, layerName, overwrite =getOption("map.overwrite", FALSE), ...)

## Default S3 method:
mapAdd(
  obj = NULL,
  map = new("map"),
  layerName = NULL,
  overwrite =getOption("map.overwrite"),
  columnNameForLabels = 1,
  leaflet = FALSE,
  isStudyArea = FALSE,
  isRasterToMatch = FALSE,
  envir = NULL,
  useCache = TRUE,
  useParallel =getOption("map.useParallel", FALSE),
  ...
)
```

Arguments

<code>obj</code>	Optional spatial object, currently <code>RasterLayer</code> , <code>SpatialPolygons</code> .
<code>map</code>	Optional map object. If not provided, then one will be created. If provided, then the present object or options passed to <code>prepInputs</code> e.g., <code>url</code> , will be appended to this <code>map</code> .
<code>layerName</code>	Required. A label for this map layer. This can be the same as the object name.
<code>overwrite</code>	Logical. If TRUE and this <code>layerName</code> exists in the <code>map</code> , then it will replace the existing object. Default is <code>getOption("map.overwrite")</code>
<code>...</code>	Additonal arguments passed to <code>reproducible::postProcess()</code> , <code>reproducible::projectInputs()</code> , <code>reproducible::fixErrors()</code> , and <code>reproducible::prepInputs()</code> .
<code>columnNameForLabels</code>	A character string indicating which column to use for labels. This is currently only used if the object is a <code>SpatialPolygonsDataFrame</code> .

leaflet	Logical or Character vector of path(s) to write tiles. If TRUE or a character vector, then this layer will be added to a leaflet map. For RasterLayer object, this will trigger a call to gdal2tiles, making tiles. If path is not specified, it will be the current path. The tile base file path will be paste0(layerName, "_", rndstr(1, 6)).
isStudyArea	Logical. If TRUE, this will be assigned the label, "StudyArea", and will be passed into prepInputs for any future layers added.
isRasterToMatch	Logical indicating ... TODO: need description
envir	An optional environment. If supplied, then the obj will not be placed "into" the maps slot, rather the environment label will be placed into the maps slot. Upon re
useCache	Logical. If TRUE, then internal calls to Cache will be used. Default is TRUE
useParallel	Logical. If TRUE, then if there is more than one calculation to do at any stage, it will create and use a parallel cluster via makeOptimalCluster. If running analyses in parallel, it may be useful to pass a function (via .clInit) to be run on each of the nodes immediately upon cluster creation (e.g., to set options).

Examples

```
## Not run:
library(sp)
library(raster)
library(reproducible)
cwd <- getwd()
setwd(tempdir())
coords <- structure(c(-122.98, -116.1, -99.2, -106, -122.98,
                      59.9, 65.73, 63.58, 54.79, 59.9),
                      .Dim = c(5L, 2L))
Sr1 <- Polygon(coords)
Srs1 <- Polygons(list(Sr1), "s1")
StudyArea <- SpatialPolygons(list(Srs1), 1L)
crs(StudyArea) <- paste("+init=epsg:4326 +proj=longlat +datum=WGS84",
                        "+no_defs +ellps=WGS84 +towgs84=0,0,0")
StudyArea <- SpatialPolygonsDataFrame(StudyArea,
                                       data = data.frame(ID = 1, shinyLabel = "zone2"),
                                       match.ID = FALSE)

m1 <- mapAdd(StudyArea, isStudyArea = TRUE, layerName = "Small Study Area",
             poly = TRUE, analysisGroup2 = "Small Study Area")

if (require("SpaDES.tools", quietly = TRUE)) {
  options(map.useParallel = FALSE)
  smallStudyArea <- randomPolygon(studyArea(m1), 1e5)
  smallStudyArea <- SpatialPolygonsDataFrame(smallStudyArea,
                                              data = data.frame(ID = 1, shinyLabel = "zone1"),
                                              match.ID = FALSE)
  m1 <- mapAdd(smallStudyArea, m1, isStudyArea = TRUE, filename2 = NULL,
               analysisGroup2 = "Smaller Study Area",
               poly = TRUE,
```

```

layerName = "Smaller Study Area") # adds a second studyArea within 1st

rasTemplate <- raster(extent(studyArea(ml)), res = 0.001)
tsf <- randomPolygons(rasTemplate, numTypes = 8)*30
crs(tsf) <- crs(ml)
vtm <- randomPolygons(tsf, numTypes = 4)
levels(vtm) <- data.frame(ID = sort(unique(vtm[])),
                           Factor = c("black spruce", "white spruce", "aspen", "fir"))
crs(vtm) <- crs(ml)
ml <- mapAdd(tsf, ml, layerName = "tsf1",
             filename2 = "tsf1.tif", # to postProcess
             # to map object
             tsf = "tsf1.tif", # to column in map@metadata
             analysisGroup1 = "tsf1_vtm1", # this is the label for analysisGroup1
             leaflet = TRUE, # to column in map@metadata; used for visualizing in leaflet
             overwrite = TRUE)
ml <- mapAdd(vtm, ml, filename2 = "vtm1.grd",
             layerName = "vtm1",
             vtm = "vtm1.grd",
             analysisGroup1 = "tsf1_vtm1", leaflet = TRUE, overwrite = TRUE)

ageClasses <- c("Young", "Immature", "Mature", "Old")
ageClassCutOffs <- c(0, 40, 80, 120)

# add an analysis -- this will trigger analyses because there are already objects in the map
#   This will trigger 2 analyses:
#   LeadingVegTypeByAgeClass on each raster x polygon combo (only 1 currently)
#   so there is 1 raster group, 2 polygon groups, 1 analyses - Total 2, 2 run now
ml <- mapAddAnalysis(ml, functionName = "LeadingVegTypeByAgeClass",
                     ageClasses = ageClasses, ageClassCutOffs = ageClassCutOffs)
# add an analysis -- this will trigger analyses because there are already objects in the map
#   This will trigger 2 more analyses:
#   largePatches on each raster x polygon combo (only 1 currently)
#   so there is 1 raster group, 2 polygon groups, 2 analyses - Total 4, only 2 run now
ml <- mapAddAnalysis(ml, functionName = "LargePatches", ageClasses = ageClasses,
                     id = "1", labelColumn = "shinyLabel",
                     ageClassCutOffs = ageClassCutOffs)

# Add a second polygon, trigger
smallStudyArea2 <- randomPolygon(studyArea(ml), 1e5)
smallStudyArea2 <- SpatialPolygonsDataFrame(smallStudyArea2,
                                            data = data.frame(ID = 1, shinyLabel = "zone1"),
                                            match.ID = FALSE)
# add a new layer -- this will trigger analyses because there are already analyses in the map
#   This will trigger 2 more analyses ... largePatches on each *new* raster x polygon combo
#   (now there are 2) -- so there is 1 raster group, 3 polygon groups, 2 analyses - Total 6
ml <- mapAdd(smallStudyArea2, ml, isStudyArea = FALSE, filename2 = NULL, overwrite = TRUE,
             analysisGroup2 = "Smaller Study Area 2",
             poly = TRUE,
             layerName = "Smaller Study Area 2") # adds a second studyArea within 1st

# Add a *different* second polygon, via overwrite. This should trigger new analyses
smallStudyArea2 <- randomPolygon(studyArea(ml), 1e5)

```

```

smallStudyArea2 <- SpatialPolygonsDataFrame(smallStudyArea2,
                                             data = data.frame(ID = 1, shinyLabel = "zone1"),
                                             match.ID = FALSE)
# add a new layer -- this will trigger analyses because there are already analyses in the map
#   This will trigger 2 more analyses ... largePatches on each *new* raster x polygon combo
#   (now there are 2) -- so there is 1 raster group, 3 polygon groups, 2 analyses - Total 6
ml <- mapAdd(smallStudyArea2, ml, isStudyArea = FALSE, filename2 = NULL, overwrite = TRUE,
             analysisGroup2 = "Smaller Study Area 2",
             poly = TRUE,
             layerName = "Smaller Study Area 2") # adds a second studyArea within 1st

# Add a 2nd pair of rasters
rasTemplate <- raster(extent(studyArea(ml)), res = 0.001)
tsf2 <- randomPolygons(rasTemplate, numTypes = 8)*30
crs(tsf2) <- crs(ml)
vtm2 <- randomPolygons(tsf2, numTypes = 4)
levels(vtm2) <- data.frame(ID = sort(unique(vtm2[])),
                           Factor = c("black spruce", "white spruce", "aspen", "fir"))
crs(vtm2) <- crs(ml)
ml <- mapAdd(tsf2, ml, filename2 = "tsf2.tif", layerName = "tsf2",
             tsf = "tsf2.tif",
             analysisGroup1 = "tsf2_vtm2", leaflet = TRUE, overwrite = TRUE)
ml <- mapAdd(vtm2, ml, filename2 = "vtm2.grd", layerName = "vtm2",
             vtm = "vtm2.grd",
             analysisGroup1 = "tsf2_vtm2", leaflet = TRUE, overwrite = TRUE)

# post hoc analysis of data
#   use or create a specialized function that can handle the analysesData slot
ml <- mapAddPostHocAnalysis(map = ml, functionName = "rbindlistAG",
                            postHocAnalysisGroups = "analysisGroup2",
                            postHocAnalyses = "all")
}

## cleanup
setwd(cwd)
unlink(tempdir(), recursive = TRUE)

## End(Not run)

```

mapAddAnalysis*Add an analysis to a map object***Description**

TODO: description needed

Usage

mapAddAnalysis(

```

map,
functionName,
useParallel = getOption("map.useParallel", FALSE),
...
)

```

Arguments

<code>map</code>	A <code>map</code> object
<code>functionName</code>	The name of the analysis function to add
<code>useParallel</code>	Logical indicating whether to use multiple threads. Defaults to <code>getOption("map.useParallel", FALSE)</code> .
...	Additional arguments passed to <code>functionName</code> .

`mapAddPostHocAnalysis` *Add a post hoc analysis function to a map object*

Description

Add a post hoc analysis function to a `map` object

Usage

```

mapAddPostHocAnalysis(
  map,
  functionName,
  postHocAnalysisGroups = NULL,
  postHocAnalyses = "all",
  useParallel = getOption("map.useParallel", FALSE),
  ...
)

```

Arguments

<code>map</code>	Optional <code>map</code> object. If not provided, then one will be created. If provided, then the present object or options passed to <code>prepInputs</code> e.g., <code>url</code> , will be appended to this <code>map</code> .
<code>functionName</code>	A function that is designed for post hoc analysis of <code>map</code> class objects, e.g., <code>rbindlistAG</code> .
<code>postHocAnalysisGroups</code>	Character string with one <code>analysisGroups</code> , i.e., <code>"analysisGroup1"</code> or <code>"analysisGroup2"</code> .
<code>postHocAnalyses</code>	Character vector with <code>"all"</code> , (which will do all <code>analysisGroups</code> ; default), or 1 or more of the the <code>functionNames</code> that are in the <code>analyses</code> slot.

useParallel	Logical. If TRUE, then if there is more than one calculation to do at any stage, it will create and use a parallel cluster via <code>makeOptimalCluster</code> . If running analyses in parallel, it may be useful to pass a function (via <code>.clInit</code>) to be run on each of the nodes immediately upon cluster creation (e.g., to set options).
...	Optional arguments to pass into <code>functionName</code>

mapAnalysis*Generic analysis for map objects***Description**

This is the workhorse function that runs any analyses described in `map@analyses`. It uses hashing, and will not rerun any analysis that already ran on identical inputs.

Usage

```
mapAnalysis(
  map,
  functionName = NULL,
  purgeAnalyses = NULL,
  useParallel = getOption("map.useParallel", FALSE),
  ...
)
```

Arguments

<code>map</code>	Optional map object. If not provided, then one will be created. If provided, then the present object or options passed to <code>prepInputs</code> e.g., <code>url</code> , will be appended to this <code>map</code> .
<code>functionName</code>	A function name that will be run on combinations of inputs in the <code>map</code> object. See details.
<code>purgeAnalyses</code>	A character string indicating which analysis group combination or part thereof (e.g., the name entered into the row under <code>analysisGroup2</code> column of the <code>map@metadata</code> or a <code>functionName</code> .
<code>useParallel</code>	Logical. If TRUE, then if there is more than one calculation to do at any stage, it will create and use a parallel cluster via <code>makeOptimalCluster</code> . If running analyses in parallel, it may be useful to pass a function (via <code>.clInit</code>) to be run on each of the nodes immediately upon cluster creation (e.g., to set options).
...	Additonal arguments passed to <code>reproducible::postProcess()</code> , <code>reproducible::projectInputs()</code> , <code>reproducible::fixErrors()</code> , and <code>reproducible::prepInputs()</code> .

Details

This function will do a sequence of things. First, it will run `expand.grid` on any columns whose names start with `analysisGroup`, creating a factorial set of analyses as described by these columns. It will assess the combinations against the arguments used by the `functionName`. For any `analysisGroup` that does not provide the correct arguments for the `functionName`, these `analysisGroups` will be omitted for that particular function. For efficiency, the function will then assess if any of these has already been run. For those that have not been run, it will then run the `functionName` on arguments that it finds in the `metadata` slot of the `map` object, as well as any arguments passed in here in the `...`. In general, the arguments being passed in here should be fixed across all analyses, while any that vary by analysis should be entered into the `metadata` table at the time of adding the layer to the `map`, via `mapAdd`.

Value

TODO

`mapRm`

Remove objects from a map

Description

Remove objects from a map

Usage

```
mapRm(map, layer, ask = TRUE, ...)
## Default S3 method:
mapRm(map = NULL, layer = NULL, ask = TRUE, ...)
```

Arguments

<code>map</code>	TODO: document this
<code>layer</code>	TODO: document this
<code>ask</code>	TODO: document this
<code>...</code>	TODO: document this

See Also

Other mapMethods: [area](#), [map-method](#), [crs](#), [map-method](#), [rasterToMatch](#), [map-method](#), [rasters\(\)](#), [studyAreaName\(\)](#), [studyArea\(\)](#)

Other mapMethods: [area](#), [map-method](#), [crs](#), [map-method](#), [rasterToMatch](#), [map-method](#), [rasters\(\)](#), [studyAreaName\(\)](#), [studyArea\(\)](#)

Examples

```
if (require("SpaDES.tools", quietly = TRUE)) {
  p <- terra::vect(cbind(-120, 60), crs = "epsg:4326") |>
    SpaDES.tools::randomPolygon(area = 1e5) |>
    sf::st_as_sf() |>
    sf::as_Spatial()
  m <- mapAdd(p, layerName = "p")
  m

  m <- mapRm(m, "p")
  m
}
```

metadata

Extract the metadata obj

Description

Methods for specific classes exist.

Usage

```
metadata(x)

## S3 method for class 'Raster'
metadata(x)

## S3 method for class 'map'
metadata(x)
```

Arguments

x	TODO: description needed
---	--------------------------

rasters

Extract rasters in the map object

Description

This will extract all objects in or pointed to within the map.

Usage

```
rasters(map)

## S3 method for class 'map'
rasters(map)

sp(map)

## S3 method for class 'map'
sp(map)

sf(map)

## S3 method for class 'map'
sf(map)

spatialPolygons(map)

spatialPoints(map)

maps(map, class = NULL, layerName = NULL)
```

Arguments

<code>map</code>	A map class obj
<code>class</code>	If supplied, this will be the class of objects returned. Default is <code>NULL</code> which is "all", meaning all objects in the <code>map</code> object.
<code>layerName</code>	TODO: description needed

Value

A list of maps (i.e., `sp`, `raster`, or `sf` objects) of class `class`

See Also

- Other mapMethods: [area](#), [map-method](#), [crs](#), [map-method](#), [mapRm\(\)](#), [rasterToMatch](#), [map-method](#), [studyAreaName\(\)](#), [studyArea\(\)](#)
- Other mapMethods: [area](#), [map-method](#), [crs](#), [map-method](#), [mapRm\(\)](#), [rasterToMatch](#), [map-method](#), [studyAreaName\(\)](#), [studyArea\(\)](#)
- Other mapMethods: [area](#), [map-method](#), [crs](#), [map-method](#), [mapRm\(\)](#), [rasterToMatch](#), [map-method](#), [studyAreaName\(\)](#), [studyArea\(\)](#)
- Other mapMethods: [area](#), [map-method](#), [crs](#), [map-method](#), [mapRm\(\)](#), [rasterToMatch](#), [map-method](#), [studyAreaName\(\)](#), [studyArea\(\)](#)
- Other mapMethods: [area](#), [map-method](#), [crs](#), [map-method](#), [mapRm\(\)](#), [rasterToMatch](#), [map-method](#), [studyAreaName\(\)](#), [studyArea\(\)](#)
- Other mapMethods: [area](#), [map-method](#), [crs](#), [map-method](#), [mapRm\(\)](#), [rasterToMatch](#), [map-method](#), [studyAreaName\(\)](#), [studyArea\(\)](#)

rasterToMatch, map-method

Extract the rasterToMatch(s) from a x

Description

If layer is not provided and there is more than one studyArea, then this will extract the last one added.

Usage

```
## S4 method for signature 'map'  
rasterToMatch(x, layer = 1)
```

Arguments

x	TODO: describe this
layer	TODO: describe this

See Also

Other mapMethods: [area](#), [map-method](#), [crs](#), [map-method](#), [mapRm\(\)](#), [rasters\(\)](#), [studyAreaName\(\)](#), [studyArea\(\)](#)

rbindlistAG

Utility functions for grouping analyses in a map object

Description

Utility functions for grouping analyses in a map object

Usage

```
rbindlistAG(map, functionName, analysisGroups)
```

Arguments

map	Optional map object. If not provided, then one will be created. If provided, then the present object or options passed to prepInputs e.g., url, will be appended to this map.
functionName	TODO: description needed
analysisGroups	A character (length 1 currently), indicating which analysis group (e.g., "analysisGroup1") should be used to rbindlist. Can also specify "all" which will rbindlist all outputs.

Value

A list of `data.tables`.

`runMapAnalyses`

`runMapAnalyses`

Description

TODO: description needed

Usage

```
runMapAnalyses(
  map,
  purgeAnalyses = NULL,
  useParallel = getOption("map.useParallel", FALSE),
  ...
)
```

Arguments

<code>map</code>	TODO
<code>purgeAnalyses</code>	TODO
<code>useParallel</code>	TODO
...	TODO

Value

TODO

`show, map-method`

Show method for map class objects

Description

Show method for map class objects

Usage

```
## S4 method for signature 'map'
show(object)
```

Arguments

<code>object</code>	TODO: describe this
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studyArea	<i>Extract the studyArea(s) from a map</i>
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Description

If layer is not provided and there is more than one studyArea, then this will extract the last one added.

Usage

```
studyArea(map, layer = NA, sorted = FALSE)

## S4 method for signature 'ANY'
studyArea(map, layer = NA, sorted = FALSE)

## S4 method for signature 'map'
studyArea(map, layer = NA, sorted = FALSE)

studyArea(map, layer = NA) <- value

## S4 replacement method for signature 'map'
studyArea(map, layer = NA) <- value
```

Arguments

map	TODO: document this
layer	TODO: document this
sorted	Logical. Should the numeric layer be referring to geographic area of the area or the order that the studyArea were placed into map object
value	The value to assign to the object.

See Also

Other mapMethods: [area](#), [map-method](#), [crs](#), [map-method](#), [mapRm\(\)](#), [rasterToMatch](#), [map-method](#), [rasters\(\)](#), [studyAreaName\(\)](#)

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studyAreaName	<i>Map class methods</i>
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Description

Tools for getting objects and metadata in and out of a `map` class.

Usage

```
studyAreaName(x, layer)

## S3 method for class 'map'
studyAreaName(x, layer = 1)

## S3 method for class 'data.table'
studyAreaName(x, layer = 1)
```

Arguments

x	TODO: document this
layer	TODO: document this

See Also

Other mapMethods: [area](#), [map-method](#), [crs](#), [map-method](#), [mapRm\(\)](#), [rasterToMatch](#), [map-method](#), [rasters\(\)](#), [studyArea\(\)](#)

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