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Description Producing probabilistic projections of net migration rate for all countries of the world or for subnational units using a Bayesian hierarchical model by Azose an Raftery (2015) <doi:10.1007/s13524-015-0415-0>.

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bayesMig-package	<i>Bayesian Projection of Migration</i>
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Description

Collection of functions for making probabilistic projections of net migration rate for all countries of the world, using a Bayesian hierarchical model (BHM) and the United Nations demographic time series. The model can be also applied to user-defined data for other locations, such as subnational units. Methodological details are provided in Azose & Raftery (2015). The projected rates can be used as input to population projections generated via the **bayesPop** package.

Details

The package is implemented in a similar way as the **bayesTFR** package and thus, many functions have their equivalents in **bayesTFR**. The main functions of the package are:

- `run.mig.mcmc`: Runs a Markov Chain Monte Carlo (MCMC) simulation. It results in posterior samples of the model parameters.
- `mig.predict`: Using the posterior parameter samples, trajectories of future net migration rates are generated for all countries or given locations.

The following functions can be used to analyze results:

- `mig.trajectories.plot`: Shows the posterior trajectories for a given location, including the median and given probability intervals.
- `mig.trajectories.table`: Shows a tabular form of the posterior trajectories for a given location.
- `mig.map`, `mig.ggmap` and `mig.map.gvis`: Show a world map of migration rates for a given projection or observed period, or for country-specific parameter estimates.
- `mig.partraces.plot` and `mig.partraces.cs.plot`: Plot the MCMC traces of country-independent parameters and country-specific parameters, respectively.

- `mig.pardensity.plot` and `mig.pardensity.cs.plot`: Plot the posterior density of the country-independent parameters and country-specific parameters, respectively.
- `summary.bayesMig.mcmc.set`: Summary method for the MCMC results.
- `summary.bayesMig.prediction`: Summary method for the prediction results.

For MCMC diagnostics, function `mig.coda.list.mcmc` creates an object of type “mcmc.list” that can be used with the **coda** package. Furthermore, function `mig.diagnose` analyzes the MCMCs using the Raftery diagnostics implemented in the **coda** package and gives information about parameters that did not converge.

Existing results can be accessed using the `get.mig.mcmc` (estimation) and `get.mig.prediction` (prediction) functions. Existing convergence diagnostics can be accessed using the `get.mig.convergence` and `get.mig.convergence.all` functions.

Historical data on migration rates are taken from the **wpp2019** (default), **wpp2022** or **wpp2017** package, depending on users settings. Alternatively, users can input their own data. These can be either 5-year or annual time series. An example file with historical annual US migration rates is included in the package. Its usage is shown in the Example of `mig.predict`.

Note

As this package has been designed for simulating migration on a national level, many functions use arguments and terminology related to countries. However, a “country” is to be interpreted as any location included in the simulation.

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References

Azose, J. J., & Raftery, A. E. (2015). Bayesian probabilistic projection of international migration. *Demography*, 52(5), 1627-1650. doi:10.1007/s1352401504150.

Azose, J.J., Ševčíková, H., Raftery, A.E. (2016): Probabilistic population projections with migration uncertainty. *Proceedings of the National Academy of Sciences* 113:6460–6465. doi:10.1073/pnas.1606119113.

Examples

```
# Run a real simulation (can take long time)
sim.dir <- tempfile()
m <- run.mig.mcmc(nr.chains = 4, iter = 10000, thin = 10, output.dir = sim.dir,
  verbose.iter = 1000)

# Prediction for all countries
# (use argument save.as.ascii for passing predictions into bayesPop)
pred <- mig.predict(sim.dir = sim.dir, nr.traj = 1000, burnin = 1000)

# Explore results
summary(pred, country = "Germany")
```

```
mig.trajectories.plot(pred, country = "Germany", nr.traj = 50)

# Check convergence diagnostics
mig.diagnose(sim.dir, burnin = 4000, thin = 1)

unlink(sim.dir, recursive = TRUE)
# For annual projections on sub-national level, see ?mig.predict.
```

get.mig.convergence *Accessing Convergence Diagnostics Object*

Description

The function retrieves results of convergence diagnostics (created by [mig.diagnose](#)) from disk.

Usage

```
get.mig.convergence(sim.dir, thin = 225, burnin = 10000)

get.mig.convergence.all(sim.dir)
```

Arguments

sim.dir	Simulation directory used for computing the diagnostics.
thin	Thinning interval used with this diagnostics.
burnin	Burn-in used for computing the diagnostics.

Details

Function `get.mig.convergence` loads an object of class [bayesMig.convergence](#) for the specific `thin` and `burnin` used in [mig.diagnose](#) to generate this object. Function `get.mig.convergence.all` loads all [bayesMig.convergence](#) objects available in `sim.dir`.

Value

`get.mig.convergence` returns an object of class [bayesMig.convergence](#);
`get.mig.convergence.all` returns a list of objects of class [bayesMig.convergence](#).

See Also

[mig.diagnose](#), [summary.bayesMig.convergence](#)

Examples

```
# Run a real simulation (can take long time)
sim.dir <- tempfile()
m <- run.mig.mcmc(nr.chains = 2, iter = 10000, thin = 10, output.dir = sim.dir)

# Run convergence diagnostics with different burning and thin
mig.diagnose(sim.dir, burnin = 1000, thin = 2)
mig.diagnose(sim.dir, burnin = 500, thin = 1)

diags <- get.mig.convergence.all(sim.dir)
for(i in 1:length(diags))
  print(summary(diags[[i]]))

unlink(sim.dir, recursive = TRUE)
```

get.mig.mcmc

Access MCMC results

Description

Function `get.mig.mcmc` retrieves results of an MCMC simulation and creates an object of class `bayesMig.mcmc.set`. Function `has.mig.mcmc` checks the existence of such results.

Usage

```
get.mig.mcmc(
  sim.dir,
  chain.ids = NULL,
  low.memory = TRUE,
  burnin = 0,
  verbose = FALSE
)

has.mig.mcmc(sim.dir)
```

Arguments

<code>sim.dir</code>	Directory where simulation results are stored.
<code>chain.ids</code>	Chain identifiers in case only specific chains should be included in the resulting object. By default, all available chains are included.
<code>low.memory</code>	Logical. If FALSE full MCMC traces are loaded into memory.
<code>burnin</code>	Burn-in used for loading traces. Only relevant, if <code>low.memory=FALSE</code> .
<code>verbose</code>	Logical value. Switches log messages on and off.

Value

get.mig.mcmc returns an object of class `bayesMig.mcmc.set`.

has.mig.mcmc returns a logical value indicating if a migration simulation exists in the given directory.

See Also

[run.mig.mcmc](#)

Examples

```
# Toy simulation
sim.dir <- tempfile()
m <- run.mig.mcmc(nr.chains = 1, iter = 10, output.dir = sim.dir)

# can be later accessed via
m <- get.mig.mcmc(sim.dir)
summary(m)

has.mig.mcmc(sim.dir) # should be TRUE

unlink(sim.dir, recursive = TRUE)
```

get.mig.parameter.traces

Accessing MCMC Parameter Traces

Description

Functions for accessing traces of the MCMC parameters, either country-independent or country-specific.

Usage

```
get.mig.parameter.traces(
  mcmc.list,
  par.names = NULL,
  burnin = 0,
  thinning.index = NULL,
  thin = NULL
)

get.mig.parameter.traces.cs(
  mcmc.list,
  country.obj,
  par.names = NULL,
```

```

    burnin = 0,
    thinning.index = NULL,
    thin = NULL
  )

```

Arguments

mcmc.list	List of <code>bayesMig.mcmc</code> objects.
par.names	Names of country-independent parameters (in case of <code>get.mig.parameter.traces</code>) or country-specific parameters (in case of <code>get.mig.parameter.traces.cs</code>) to be included. By default all parameters are included, given either by <code>mig.parameter.names()</code> (for global parameters) or <code>mig.parameter.names.cs()</code> (for location-specific parameters).
burnin	Burn-in indicating how many iterations should be removed from the beginning of each chain.
thinning.index	Index of the traces for thinning. If it is NULL, <code>thin</code> is used. <code>thinning.index</code> does not include <code>burnin</code> and should be flattened over all chains. For example, if there are two MCMC chains of length 1000, <code>burnin=200</code> and we want an equidistantly spaced sample of length 400, then the value should be <code>thinning.index = seq(1, 1600, length = 400)</code> .
thin	An integer value for thinning. It is an alternative to <code>thinning.index</code> . The above example is equivalent to <code>thin=4</code> .
country.obj	Country object (see <code>get.country.object</code>).

Value

Both functions return a matrix with columns being the parameters and rows being the MCMC values, attached to one another in case of multiple chains. `get.mig.parameter.traces` returns country-independent parameters, `get.mig.parameter.traces.cs` returns country-specific parameters.

See Also

`mig.coda.list.mcmc` for another way of retrieving parameter traces; `mig.parameter.names` and `mig.parameter.names.cs` for parameter names.

Examples

```

# Toy simulation for US states
us.mig.file <- file.path(find.package("bayesMig"), "extdata", "USmigrates.txt")
sim.dir <- tempfile()
m <- run.mig.mcmc(nr.chains = 2, iter = 30, thin = 1, my.mig.file = us.mig.file,
  output.dir = sim.dir, present.year = 2017, annual = TRUE)
# obtain traces of hierarchical parameters
par.values <- get.mig.parameter.traces(m$mcmc.list, burnin = 5)
dim(par.values) # matrix 50 x 4
hist(par.values[, "mu_global"], main = "mu")

# obtain traces of location-specific traces for California

```

```

mig.parameter.names.cs() # allowed parameter names
par.values.cs <- get.mig.parameter.traces.cs(m$mcmc.list,
      country.obj = get.country.object("California", meta = m$meta),
      burnin = 5, par.names = "phi_c")
dim(par.values.cs) # matrix 50 x 1
hist(par.values.cs, main = colnames(par.values.cs))
unlink(sim.dir, recursive = TRUE)

```

get.mig.prediction *Access Prediction Object*

Description

Function `get.mig.prediction` retrieves results of a prediction and creates an object of class `bayesMig.prediction`. Function `has.mig.prediction` checks an existence of such results.

Usage

```
get.mig.prediction(mcmc = NULL, sim.dir = NULL, mcmc.dir = NULL)
```

```
has.mig.prediction(mcmc = NULL, sim.dir = NULL)
```

Arguments

<code>mcmc</code>	Object of class <code>bayesMig.mcmc.set</code> used to make the prediction. If it is <code>NULL</code> , the prediction is loaded from directory given by <code>sim.dir</code> .
<code>sim.dir</code>	Directory where the prediction is stored.
<code>mcmc.dir</code>	Optional argument to be used only in a special case when the <code>mcmc</code> object contained in the prediction object was estimated in different directory than in the one to which it points to (for example due to moving or renaming the original directory). The argument causes that the <code>mcmc</code> is redirected to the given directory. It can be set to <code>NA</code> if no loading of the <code>mcmc</code> object is desired.

Details

If `mcmc` is not `NULL`, the search directory is set to `mcmc$meta$output.dir`. This approach assumes that the prediction was stored in the same directory as the MCMC simulation, i.e. the `output.dir` argument of the `mig.predict` function was set to `NULL`. If it is not the case, the argument `mcmc.dir` should be used.

Value

Function `get.mig.prediction` returns an object of class `bayesMig.prediction`.

Function `has.mig.prediction` returns a logical indicating if a prediction exists.

mig.coda.list.mcmc *Conversion to coda-formatted objects*

Description

The functions convert MCMC traces (simulated using `run.mig.mcmc`) into objects that can be used with the **coda** package.

Usage

```

mig.coda.list.mcmc(
  mcmc.list = NULL,
  country = NULL,
  chain.ids = NULL,
  sim.dir = NULL,
  par.names = NULL,
  par.names.cs = NULL,
  low.memory = FALSE,
  ...
)

```

Arguments

<code>mcmc.list</code>	A list of objects of class <code>bayesMig.mcmc</code> , or an object of class <code>bayesMig.mcmc.set</code> or <code>bayesMig.prediction</code> . If <code>NULL</code> , the MCMCs are loaded from <code>sim.dir</code> . Either <code>mcmc</code> or <code>sim.dir</code> must be given.
<code>country</code>	Location name or code. Used in connection with the <code>par.names.cs</code> argument (see below).
<code>chain.ids</code>	Vector of chain identifiers. By default, all chains available in the <code>mcmc.list</code> object are included.
<code>sim.dir</code>	Directory with the MCMC simulation results. Only used if <code>mcmc.list</code> is <code>NULL</code> .
<code>par.names</code>	Names of country-independent parameters to be included. Default names are those returned by the <code>mig.parameter.names</code> function, which includes all country-independent parameters in the BHM.
<code>par.names.cs</code>	Names of country-specific parameters to be included. The argument <code>country</code> is used to filter out traces that correspond to a specific location. If <code>country</code> is not given, traces of each parameter are given for all countries. Default names are those returned by <code>mig.parameter.names.cs()</code> , which includes all country-specific parameters in the BHM.
<code>low.memory</code>	Logical indicating if the function should run in a memory-efficient mode.
<code>...</code>	Additional arguments passed to the coda 's <code>mcmc</code> function, such as <code>burnin</code> and <code>thin</code> .

Value

Returns an object of class `mcmc.list` defined in the **coda** package.

mig.diagnose *MCMC convergence diagnostics*

Description

Runs convergence diagnostics of existing migration Markov chains using the `raftery.diag` function from the `coda` package.

Usage

```

mig.diagnose(
  sim.dir,
  thin = 80,
  burnin = 2000,
  express = FALSE,
  country.sampling.prop = NULL,
  keep.thin.mcmc = FALSE,
  verbose = TRUE
)

mig.raftery.diag(
  mcmc = NULL,
  sim.dir = NULL,
  burnin = 0,
  country = NULL,
  par.names = NULL,
  par.names.cs = NULL,
  country.sampling.prop = 1,
  verbose = TRUE,
  ...
)

estimate.a.hw(mcmc, burnin = 0, thin = NULL)

```

Arguments

<code>sim.dir</code>	Directory with MCMC simulation results.
<code>thin</code>	Thinning interval.
<code>burnin</code>	Number of iterations to discard from the beginning of the parameter traces.
<code>express</code>	Logical. If TRUE, the convergence diagnostic is run only on the country-independent parameters. If FALSE, the country-specific parameters are included in the diagnostics. The number of countries can be controlled by <code>country.sampling.prop</code> .
<code>country.sampling.prop</code>	Proportion of countries to include in the diagnostics. If it is NULL and <code>express=FALSE</code> , all countries are included. Setting a number between 0 and 1 will determine the proportion of countries to be randomly sampled. For long Markov chains, this argument may significantly influence the runtime of this function.

keep.thin.mcmc	Logical. If TRUE, the thinned traces used for computing the diagnostics are stored on disk.
verbose	Logical value. Switches log messages on and off.
mcmc	A bayesMig.mcmc or bayesMig.mcmc.set object. If not given, the object is loaded from the simulation directory given by <code>sim.dir</code> .
country	Name or code of a country. If it is given, only country-specific parameters parameters of that country are considered.
par.names	Names of country-independent parameters for which the Raftery diagnostics should be computed. By default all parameters are used.
par.names.cs	Names of country-specific parameters for which the Raftery diagnostics should be computed. By default all parameters are used.
...	Additional arguments passed to the mig.coda.list.mcmc function.

Details

The `mig.diagnose` function invokes the [mig.raftery.diag](#) function separately for country-independent parameters and for country-specific parameters. It results in two possible states: red, i.e. it did not converge, and green, i.e. it converged. The resulting object is stored in `{sim.dir}/diagnostics/bayesMig.convergence_` and can be accessed using the function [get.mig.convergence](#).

Function [has.mcmc.converged](#) from the **bayesTFR** package can be used to check if the existing diagnostics converged.

For details on the `mig.raftery.diag` function, see [tfr.raftery.diag](#).

The `estimate.a.hw` function estimates an optimal value for the `a.half.width` argument in [run.mig.mcmc](#).

Value

`mig.diagnose` returns an object of class `bayesMig.convergence` containing summaries of the convergence check inputs and outputs. It has the same structure as [bayesTFR.convergence](#). In addition it has an element `a.hw.est` which is the estimated value for the `a.half.width` argument in [run.mig.mcmc](#).

See Also

[tfr.raftery.diag](#), [raftery.diag](#), [get.mig.convergence](#)

Examples

```
# See examples in ?bayesMig and ?get.mig.convergence
```

 mig.map

World Map of Net Migration Rate

Description

Generates a world map of the net migration rate for given quantile and time period, which can be either projection or estimation time period, using different techniques: `mig.map` and `mig.map.all` use **rworldmap**, `mig.ggmap` uses **ggplot2**, and `mig.map.gvis` creates an interactive map via **Google-Vis**. A map of country-specific model parameters is also supported.

Usage

```

mig.map(pred, ...)

mig.ggmap(pred, ...)

mig.map.gvis(pred, ...)

mig.map.all(
  pred,
  output.dir,
  output.type = "png",
  mig.range = NULL,
  nr.cats = 50,
  same.scale = TRUE,
  quantile = 0.5,
  file.prefix = "migwrldmap_",
  ...
)

get.mig.map.parameters(
  pred,
  mig.range = NULL,
  nr.cats = 50,
  same.scale = TRUE,
  quantile = 0.5,
  palette = "Blue-Red",
  ...
)

```

Arguments

<code>pred</code>	Object of class <code>bayesMig.prediction</code> . Note that location codes must correspond to the UN country codes in order to generate a world map.
<code>...</code>	In <code>mig.map</code> , <code>...</code> are all arguments that can be passed to <code>tfr.map</code> , such as <code>quantile</code> , <code>year</code> , <code>projection.index</code> , <code>par.name</code> , <code>adjusted</code> , <code>device</code> , <code>main</code> , <code>device.args</code> , and <code>data.args</code> . In <code>mig.map.gvis</code> , <code>...</code> are all arguments that can be passed to

	<code>tfr.map.gvis</code> . In <code>e0.ggmap, ...</code> are arguments that can be passed to <code>tfr.ggmap</code> . In addition, functions that use the rworldmap package accept arguments passed to the <code>mapCountryData</code> function of the rworldmap package.
<code>output.dir</code>	Directory into which resulting maps are stored.
<code>output.type</code>	Type of the resulting files. It can be “png”, “pdf”, “jpeg”, “bmp”, “tiff”, or “postscript”.
<code>mig.range</code>	Range of the migration rate to be displayed. It is of the form <code>c(mig.min, mig.max)</code> . By default, the whole available range is considered. Note that countries with values outside of the given range will appear white.
<code>nr.cats</code>	Number of color categories.
<code>same.scale</code>	Logical controlling if maps for all years of this prediction object should be on the same color scale.
<code>quantile</code>	Quantile for which the map should be generated. It must be equal to one of the values in <code>dimnames(pred\$quantiles)[[2]]</code> , i.e. 0, 0.025, 0.05, 0.1, 0.2, 0.25, 0.3, 0.4, 0.5, 0.6, 0.7, 0.75, 0.8, 0.9, 0.95, 0.975, 1. Value 0.5 corresponds to the median.
<code>file.prefix</code>	Prefix for file names.
<code>palette</code>	Color palette to use.

Details

The functions only work for national simulations where location codes correspond to the countries' UN codes.

`mig.map` creates a single map for the given time period and quantile. `mig.map.all` generates a sequence of maps, namely one for each projection period. If the package **fields** is installed, a color bar legend at the bottom of the map is created.

Function `get.mig.map.parameters` can be used in combination with `mig.map`. (Note that `get.mig.map.parameters` is called from inside of `mig.map.all`.) It sets breakpoints for the color scheme.

Function `mig.ggmap` is similar to `mig.map`, but used the **ggplot2** package in combination with the `geom_sf` function.

Function `mig.map.gvis` creates an interactive map using the **googleVis** package and opens it in an internet browser. It also generates a table of the mapped values that can be sorted by columns interactively in the browser.

By default, `mig.map`, `mig.ggmap` and `mig.map.gvis` produce maps of net migration rates. Alternatively, the functions can be used to plot country-specific MCMC parameters into a world map. They are given by the argument `par.name`. One can pass any value from `mig.parameter.names.cs()`.

Value

`get.mig.map.parameters` returns a list with elements:

pred The `bayesMig.prediction` object used in the function.

quantile Value of the argument `quantile`.

catMethod If the argument `same.scale` is TRUE, this element contains breakpoints for categorization generated using the quantiles. Otherwise, it is NULL.

numCats Number of categories.

coulourPalette The color palette.

See Also

[tfr.map](#)

`mig.parameter.names` *Accessing Parameter Names*

Description

Functions for accessing names of the MCMC parameters, either country-independent or country-specific.

Usage

```
mig.parameter.names()
```

```
mig.parameter.names.cs(country.code = NULL)
```

Arguments

`country.code` Location code. If it is given, the country-specific parameter names contain the suffix `'_countryX'` where `X` is the `country.code`.

Value

`mig.parameter.names` returns names of the world parameters.

`mig.parameter.names.cs` returns names of the country-specific parameters.

Examples

```
mig.parameter.names()
```

```
mig.parameter.names.cs()
```

 mig.pardensity.plot *Plotting MCMC Parameter Density*

Description

Functions for plotting the density of the posterior distribution of the MCMC parameters from the migration model.

Usage

```

mig.pardensity.plot(
  mcmc.list = NULL,
  sim.dir = NULL,
  chain.ids = NULL,
  par.names = mig.parameter.names(),
  burnin = NULL,
  dev.ncol = 2,
  low.memory = TRUE,
  ...
)

mig.pardensity.cs.plot(
  country,
  mcmc.list = NULL,
  sim.dir = NULL,
  chain.ids = NULL,
  par.names = mig.parameter.names.cs(),
  burnin = NULL,
  dev.ncol = 3,
  low.memory = TRUE,
  ...
)

```

Arguments

mcmc.list	List of bayesMig.mcmc objects, or an object of class bayesMig.mcmc.set or of class bayesMig.prediction . If it is NULL, the values are loaded from <code>sim.dir</code> .
sim.dir	Directory with the MCMC simulation results. It is only used if <code>mcmc.list</code> is NULL.
chain.ids	List of MCMC identifiers to be plotted. If it is NULL, all chains found in <code>mcmc.list</code> or <code>sim.dir</code> are plotted.
par.names	Names of parameters for which density should be plotted. By default all country-independent parameters are plotted if used within <code>mig.pardensity.plot</code> , or country-specific parameters are plotted if used within <code>mig.pardensity.cs.plot</code> .
burnin	Number of iterations to be discarded from the beginning of each chain before computing the density.

dev.ncol	Number of column for the graphics device. If the number of parameters is smaller than dev.ncol, the number of columns is automatically decreased.
low.memory	Logical indicating if the processing should run in a low-memory mode. If it is FALSE, traces of all available parameters are loaded into memory. Otherwise, parameters are loaded as they are needed.
...	Further arguments passed to the density function.
country	Name or numerical code of a country. It can also be given as ISO-2 or ISO-3 characters.

Details

The functions plot the density of the posterior distribution either for country-independent parameters (`mig.pardensity.plot` or for country-specific parameters (`mig.pardensity.cs.plot`, one graph per parameter. One can restrict it to specific chains by setting the `chain.ids` argument and to specific parameters by setting the `par.names` argument.

If `mcmc.list` is an object of class `bayesMig.prediction` and if this object contains thinned traces, they are used instead of the full chains. In such a case, `burnin` and `chain.ids` cannot be modified - their value is set to the one used when the thinned traces were created, namely when running `mig.predict`. In a situation with long MCMC chains, this approach can significantly speed-up creation of the density plots.

Value

No return value.

<code>mig.partraces.plot</code>	<i>Plotting MCMC Parameter Traces</i>
---------------------------------	---------------------------------------

Description

Functions for plotting the MCMC parameter traces from the migration model.

Usage

```

mig.partraces.plot(
  mcmc.list = NULL,
  sim.dir = NULL,
  chain.ids = NULL,
  par.names = mig.parameter.names(),
  nr.points = NULL,
  dev.ncol = 2,
  ...
)

mig.partraces.cs.plot(
  country,

```



```

    mcmc.list = NULL,
    sim.dir = NULL,
    chain.ids = NULL,
    par.names = mig.parameter.names.cs(),
    nr.points = NULL,
    dev.ncol = 3,
    ...
)

```

Arguments

mcmc.list	List of <code>bayesMig.mcmc</code> objects, or an object of class <code>bayesMig.mcmc.set</code> or of class <code>bayesMig.prediction</code> . If it is <code>NULL</code> , the traces are loaded from <code>sim.dir</code> .
sim.dir	Directory with the MCMC simulation results. It is only used if <code>mcmc.list</code> is <code>NULL</code> .
chain.ids	List of MCMC identifiers to be plotted. If it is <code>NULL</code> , all chains found in <code>mcmc.list</code> or <code>sim.dir</code> are plotted.
par.names	Names of parameters for which traces should be plotted. By default all country-independent parameters are plotted if used within <code>mig.partraces.plot</code> , or country-specific parameters are plotted if used within <code>mig.partraces.cs.plot</code> .
nr.points	Number of points to be plotted. If <code>NULL</code> , all points are plotted, otherwise the traces are thinned evenly.
dev.ncol	Number of column for the graphics device. If the number of parameters is smaller than <code>dev.ncol</code> , the number of columns is automatically decreased.
...	Additional graphical parameters.
country	Name or numerical code of a country. It can also be given as ISO-2 or ISO-3 characters.

Details

The functions plot MCMC traces either for country-independent parameters (`mig.partraces.plot` or for country-specific parameters (`mig.partraces.cs.plot`, one graph per parameter. One can restrict it to specific chains by setting the `chain.ids` argument, and to specific parameters by setting the `par.names` argument.

Value

No return value.

 mig.predict

 Generate posterior trajectories of net migration rates

Description

Using the posterior parameter samples simulated by `run.mig.mcmc`, generate posterior trajectories for the net migration rates for all countries of the world, or all locations included in the estimation. This code *does not* adjust trajectories to ensure that net migration counts over all countries sum to zero.

Usage

```

mig.predict(
  mcmc.set = NULL,
  end.year = 2100,
  sim.dir = NULL,
  replace.output = FALSE,
  start.year = NULL,
  nr.traj = NULL,
  thin = NULL,
  burnin = 20000,
  use.cummulative.threshold = FALSE,
  ignore.gcc.in.threshold = FALSE,
  post.last.observed = c("obsdata", "alldata", "impute"),
  save.as.ascii = 0,
  output.dir = NULL,
  seed = NULL,
  verbose = TRUE,
  ...
)

```

Arguments

<code>mcmc.set</code>	Object of class <code>bayesMig.mcmc.set</code> corresponding to sampled parameter values for net migration model. If it is <code>NULL</code> , the object is loaded from the directory specified in <code>sim.dir</code>
<code>end.year</code>	End year of the prediction
<code>sim.dir</code>	Directory with MCMC simulation results. It should be the same as the <code>output.dir</code> argument in <code>run.mig.mcmc</code>
<code>replace.output</code>	Logical value. If <code>TRUE</code> , existing predictions in <code>output.dir</code> will be replaced by results of this run.
<code>start.year</code>	Start year of the prediction, i.e. the first predicted year. By default the prediction is started at the next time period after <code>present.year</code> set in the estimation step. If <code>start.year</code> is smaller than the default, the behavior is controlled by the <code>post.last.observed</code> argument: Either data post <code>start.year</code> is ignored (default) or the projection is set to the available data (<code>post.last.observed = "a"</code>).

nr.traj	Number of trajectories to be generated. If NULL, the argument thin is taken to determine the number of trajectories. If both are NULL, the number of trajectories corresponds to the size of the parameter sample.
thin	Thinning interval used for determining the number of trajectories. Only relevant if nr.traj is NULL.
burnin	Number of iterations to be discarded from the beginning of the parameter traces.
use.cummulative.threshold	If TRUE historical cummulative thresholds are applied to avoid sampling rates that are too extreme. The thresholds are derived over prior rates of all locations. As a time span for deriving the limits on projected rates, at each projected time point, six prior time periods are used in a 5-year simulation, corresponding to 30 years in an annual simulation. In a national simulation, prior rates of GCC countries (plus Western Sahara and Djibouti) are excluded when deriving thresholds for non-GCC countries. If this option is used in a non-country simulation, e.g. in a sub-national settings, set the ignore.gcc.in.threshold argument to TRUE.
ignore.gcc.in.threshold	If use.cummulative.threshold is TRUE, by default the GCC countries (plus Western Sahara and Djibouti) identified by numerical codes of the countries are excluded from computing the historical cummulative thresholds for non-GCC countries. If this argument is TRUE, this distinction is not made. It is important to set it to TRUE in a sub-national simulation to avoid any random overlaps of UN codes and user-defined codes.
post.last.observed	If a user-specific data file was used during estimation and the data contained the "last.observed" column, this argument determines how to treat the time periods between the last observed point and the start year of the prediction, for locations where there is a gap between them, or if short-term predictions were included in the file. It is also relevant if start.year is set to a smaller value than present.year in the estimation. Possible values are: <ul style="list-style-type: none"> • "obsdata" or "o" (default) uses any non-missing observed data provided in the data file during estimation, up to the time point defined by the argument start.year (excluding the start year itself). • "alldata" or "a" would similarly use the provided data but would use all data, even if it goes beyond the start year. This allows to use short-term deterministic projections for locations where it is available. • "impute" or "i" would ignore all data beyond the last observed data point and impute the missing time periods.
save.as.ascii	Either a number determining how many trajectories should be converted into an ASCII file, or 'all' in which case all trajectories are converted. It should be set to 0 if no conversion is desired. If this argument is larger than zero, the resulting file can be used as input into population projection via bayesPop , see Details.
output.dir	Directory into which the resulting prediction object and the trajectories are stored. If it is NULL, it is set to either sim.dir, or to output.dir of mcmc.set\$meta if mcmc.set is given.
seed	Seed of the random number generator. If NULL no seed is set. Can be used to generate reproducible projections.

verbose Logical value. Switches log messages on and off.
 ... Further arguments passed to the underlying functions.

Details

The trajectories of net migration rates for each location are generated using the model of Azose & Raftery (2015). Parameter samples simulated via `run.mig.mcmc` are used from all chains, from which the given `burnin` was discarded. They are evenly thinned to match `nr.traj` or using the `thin` argument. Such thinned parameter traces, collapsed into one chain, if they do not already exist, are stored on disk into the sub-directory ‘`thinned_mcmc_t_b`’ where t is the value of `thin` and b the value of `burnin`.

The projection is run for all missing values before the present year, if any. Medians over the trajectories are used as imputed values and the trajectories are discarded. The process then continues by projecting the future values where all generated trajectories are kept.

A special case is when the argument `start.year` is given that is smaller than or equal to the present year. In such a case, imputed missing values before present year are treated as ordinary predictions (trajectories are kept). If `post.last.observed` is “a”, all historical data between start year and present year are used as projections.

The resulting prediction object is saved into ‘`{output.dir}/predictions`’. Trajectories for all locations are saved into the same directory in a binary format, one file per location. At the end of the projection, if `save.as.ascii` is larger than 0, the function converts the given number of trajectories into a CSV file, called ‘`ascii_trajectories.csv`’ also located in the ‘`predictions`’ directory. The converted trajectories are selected by equal spacing. In addition to the converted trajectories, two summary files are created: one in a user-friendly format, the other using a UN-specific coding, as described in `mig.write.projection.summary`.

If it is desired to use these predictions as input to population projections in **bayesPop**, enter the full file path of the ‘`ascii_trajectories.csv`’ file into the `inputs` argument of `bayesPop::pop.predict` as item `migtraj` and set the argument `mig.is.rate` appropriately.

Value

Object of class `bayesMig.prediction` which is a list with components containing details of the prediction. Key result component is an array of quantiles with dimensions (number of locations) x (number of computed quantiles) x (number of projected time points). First time point in the sequence is not a projection, but the last observed time period.

Other key result components include `traj.mean.sd`, a summary of means and standard deviations for each country at each time point. See `bayesTFR.prediction` for more detail.

References

- Azose, J. J., & Raftery, A. E. (2015). Bayesian probabilistic projection of international migration. *Demography*, 52(5), 1627-1650. doi:10.1007/s1352401504150.
- Azose, J.J., Ševčíková, H., Raftery, A.E. (2016): Probabilistic population projections with migration uncertainty. *Proceedings of the National Academy of Sciences* 113:6460–6465. doi:10.1073/pnas.1606119113.

Examples

```
# Toy simulation for US states
us.mig.file <- file.path(find.package("bayesMig"), "extdata", "USmigrates.txt")
sim.dir <- tempfile()
m <- run.mig.mcmc(nr.chains = 2, iter = 30, thin = 1, my.mig.file = us.mig.file,
                 output.dir = sim.dir, present.year = 2017, annual = TRUE)

# Prediction
pred <- mig.predict(sim.dir = sim.dir, burnin = 5, end.year = 2050)
# here unrealistic results since this is a toy simulation
mig.trajectories.plot(pred, "Hawaii", pi = 80, ylim = c(-0.02, 0.02))
mig.trajectories.table(pred, "Hawaii")
summary(pred, "California")

# view locations included in the simulation
get.countries.table(pred)

unlink(sim.dir, recursive = TRUE)
# For projections on national level, see ?bayesMig.
```

`mig.trajectories.plot` *Output of posterior distribution of migration trajectories*

Description

The functions `plot`/`tabulate` the posterior distribution of trajectories of net migration rates for a given location, or for all locations, including their median and given probability intervals.

Usage

```
mig.trajectories.plot(
  mig.pred,
  country,
  pi = c(80, 95),
  nr.traj = 50,
  mark.estimation.points = FALSE,
  xlim = NULL,
  ylim = NULL,
  type = "b",
  xlab = "Year",
  ylab = "Migration rate",
  main = NULL,
  lwd = c(2, 2, 2, 2, 1),
  col = c("black", "green", "red", "red", "#00000020"),
  show.legend = TRUE,
  add = FALSE,
  scale = FALSE,
  ...
```

```

)

mig.trajectories.plot.all(
  mig.pred,
  output.dir = NULL,
  output.type = "png",
  verbose = FALSE,
  ...
)

mig.trajectories.table(mig.pred, country, pi = c(80, 95), ...)

```

Arguments

<code>mig.pred</code>	Prediction object of class <code>bayesMig.prediction</code> .
<code>country</code>	Name or numerical code of a location. If it is a country, it can also be given as ISO-2 or ISO-3 characters.
<code>pi</code>	Probability interval (as percentage) to be included in the output. It can be a single number or a vector.
<code>nr.traj</code>	Number of trajectories to be plotted. If <code>NULL</code> , all trajectories are plotted, otherwise they are thinned evenly.
<code>mark.estimation.points</code>	Logical. If <code>TRUE</code> , points that were not used in the estimation are shown in a lighter color.
<code>xlim, ylim, type, xlab, ylab</code>	Graphical parameters passed to the <code>plot</code> function.
<code>main</code>	Main title for the plot(s). In <code>mig.trajectories.plot.all</code> any occurrence of the string “XXX” is replaced by the name of the appropriate country.
<code>lwd, col</code>	Vector of five elements giving the line width and color for: 1. observed data, 2. imputed values, 3. median, 4. quantiles, 5. trajectories.
<code>show.legend</code>	Logical controlling whether a legend should be drawn.
<code>add</code>	Logical controlling whether the trajectories should be plotted into a new graphic device (<code>FALSE</code>) or into an existing device (<code>TRUE</code>). One can use this argument to plot trajectories from multiple countries into one graphics.
<code>scale</code>	Logical. If <code>TRUE</code> , values are scaled to be “per population”, i.e. they are divided by <code>pop.denom</code> passed to <code>run.mig.mcmc</code> .
<code>...</code>	Additional graphical parameters. In addition, for <code>mig.trajectories.plot.all</code> any of the arguments of <code>tfr.trajectories.plot</code> can be passed here.
<code>output.dir</code>	Directory into which resulting plots are written. By default, the plots are saved into directory <code>sim.dir/predictions/migTrajectories</code> .
<code>output.type</code>	Type of the resulting plot files. Can be “png”, “pdf”, “jpeg”, “bmp”, “tiff”, or “postscript”.
<code>verbose</code>	Logical value. Switches log messages on and off.

Details

mig.trajectories.plot plots posterior distribution of trajectories of net migration rates for a given location. mig.trajectories.table gives the same output as a table. mig.trajectories.plot.all creates a set of graphs (one per location) that are stored in output.dir.

The median and given probability intervals are computed using all available trajectories. Thus, nr.traj does not influence those values - it is used only to control the number of trajectories in the graphs.

Value

No return value.

See Also

[mig.predict](#), [summary.bayesMig.prediction](#)

Examples

```
# See example in ?mig.predict
```

```
mig.write.projection.summary
```

Writing Projection Summary Files

Description

The function creates two files containing projection summaries, such as the median, the lower and upper bound of the 80 and 90% probability intervals, respectively, and the constant variant. One file is in a user-friendly format, whereas the other is in a UN-specific format with internal coding of the time and the variants.

Usage

```
mig.write.projection.summary(pred, output.dir)
```

Arguments

pred	Object of class bayesMig.prediction.
output.dir	Directory where output is written.

Value

No return value.

See Also

[write.projection.summary](#)

run.mig.mcmc	<i>Run Markov chain Monte Carlo for parameters of net migration rate model</i>
--------------	--

Description

Runs MCMCs for simulating the net migration rate of all countries of the world or for locations specified by users, using the Bayesian hierarchical model of Azose & Raftery (2015).

Usage

```
run.mig.mcmc(
  output.dir,
  nr.chains = 3,
  iter = 50000,
  thin = 1,
  replace.output = FALSE,
  annual = FALSE,
  start.year = 1950,
  present.year = 2020,
  wpp.year = 2019,
  my.mig.file = NULL,
  sigma.c.min = 1e-04,
  a.ini = NULL,
  a.half.width = NULL,
  mu.ini = NULL,
  exclude.from.world = NULL,
  pop.denom = 1,
  seed = NULL,
  parallel = FALSE,
  nr.nodes = nr.chains,
  buffer.size = 1000,
  verbose = TRUE,
  verbose.iter = 10,
  ...
)
```

Arguments

output.dir	A file path pointing to the directory in which to store results.
nr.chains	An integer number of independent Markov chains to run.
iter	The number of iterations to run per Markov chain.
thin	Thinning interval. A chain with 1000 iterations thinned by 20 will return a final count of 50 iterations.
replace.output	If the specified output directory already exists, should it be overwritten?
annual	If TRUE, the model assumes the underlying data is on annual time scale.

start.year	Start year for using historical data.
present.year	End year for using historical data.
wpp.year	Year for which WPP data is used if no user data is provided via my.mig.file. In such a case, the function loads a package called wppx where x is the wpp.year and generates historical migration rates using the migration and pop datasets.
my.mig.file	File name containing user-specified historical time series of migration rates for all locations that should be included in the simulation. It should be a tab-separated file. For structure, see Details below.
sigma.c.min, a.ini, mu.ini	Settings for the parameters of the model (see Azose & Raftery 2015), such as minimum value and initial values. Initial values (*.ini) can be given as a vector of length nr.chains, giving one initial value per chain. By default the initial values are equidistantly spread between their respective ranges.
a.half.width	Half width for Metropolis proposals of the a parameter. This argument can greatly influence the convergence and it is dependent on the scale of the data. By default it is set to 0.01 for 5-year data defined as rate per population; to 0.03 for 5-year data defined as per 1000; to 0.3 for annual data per population; to 0.5 for annual data per 1000. If the default does not yield satisfactory results, use the function estimate.a.hw to estimate an appropriate value, based on an existing simulation. Also it is important to set the pop.denom argument correctly.
exclude.from.world	Vector of location codes that should be excluded from estimating the hyperparameters. These would be for example small locations or locations with unusual patterns. Note that location-specific parameters are generated for all locations, regardless of this setting.
pop.denom	Denominator used to generate the input migration rates. It is used to derive an appropriate scaler for the priors and conditional distributions. Typically, this will be either 1 (default) if the rates are defined as per population, or 1000, if the rates are per 1000 population. Use this argument only if user-specified rates are supplied via the my.mig.file argument.
seed	Seed of the random number generator. If NULL no seed is set. It can be used to generate reproducible results.
parallel	Whether to run code in parallel.
nr.nodes	Relevant only if parallel is TRUE. It gives the number of nodes for running the simulation in parallel. By default it equals to the number of chains.
buffer.size	Buffer size (in number of iterations) for keeping data in the memory before flushing to disk.
verbose	Whether or not to print status updates to console window while the code is running.
verbose.iter	If verbose is TRUE, the number of iterations to wait between printing updates.
...	Additional parameters to be passed to the function performParallel , if parallel is TRUE.

Details

The function creates an object of class `bayesMig.mcmc.meta` and stores it in `output.dir`. It launches `nr.chains` MCMCs, either sequentially or in parallel. Parameter traces of each chain are stored as ASCII files in a subdirectory of `output.dir`, called `mcx` where x is the identifier of that chain. There is one file per parameter, named after the parameter with the suffix “.txt”. Location-specific parameters have the suffix `_countryc` where c is the location code. In addition to the trace files, each `mcx` directory contains the object `bayesMig.mcmc` in binary format. All chain-specific files are written onto disk after the first, last and each i -th (thinned) iteration, where i is given by the argument `buffer.size`.

By default (if no data is passed via the `my.mig.file` argument), the function loads observed data (further denoted as WPP dataset), from the `migration` and `pop` datasets in the `wppx` package where x is the `wpp.year`. Net migration rates are computed as $\text{migration}(t) / (\text{population}(t_e) - \text{migration}(t))$ where t_e means the end of time period t . For an annual simulation and `wpp.year` set to 2022, $t = t_e$ because the population in year t is considered at the end of the year. If `wpp.year` is smaller than 2022 and `annual` is TRUE the default dataset is interpolated from 5-year data.

The argument `my.mig.file` can be used to overwrite the default data. It should be a tab-separated file. If it is used, it should contain net migration rates for all locations to be used in the simulation, as no WPP data is used in such a case. The structure of the file has the same format as the `migration` dataset, but the values should be rates (instead of counts). Use the argument `pop.denom` to define the scale of the denominator in these rates, i.e. if the rates are to be interpreted as per population (default) or some other scale. Each row in the `my.mig.file` file corresponds to a location. It does not have to be necessarily a country - it can be for example a subnational unit. It must contain columns “country_code” or “code” (unique identifier of the location), “name”, and columns representing 5-year time intervals (if `annual` is FALSE), e.g., “1995-2000”, “2000-2005” etc., or single years (if `annual` is TRUE). An example dataset of annual net migration rates for US states is included in the package, see example below.

Optionally, the `my.mig.file` can contain columns called “first.observed” and/or “last.observed”, containing for each location the year of the first and last observation, respectively. In such a case, any data before and after those time points will be ignored. Furthermore, the function `mig.predict` fills in the missing values after the last observation, using the median of the BHM procedure.

If there are countries or locations that should be excluded from influencing the hyperparameters, for example small countries or locations with unique migration patterns, their codes should be included in the argument `exclude.from.world`. These locations will still get their parameters simulated and thus, will be included in a projection. Alternatively if `my.mig.file` is used, these locations can be determined using an additional column, called “include_code”. Value 2 means the location is included in the BHM; value 1 means it’s excluded but location-specific parameters are generated; value 0 means the location is ignored.

Value

An object of class `bayesMig.mcmc.set` which is a list with two components:

<code>meta</code>	An object of class <code>bayesMig.mcmc.meta</code> . It contains information that is common to all chains. Most items are the same as in <code>bayesTFR.mcmc.meta</code> . In addition, <code>mig.rates</code> is a matrix of the observed migration rates with NAs in spots that were not used for estimation. <code>mig.rates.all</code> is a similar matrix but contains all data, regardless if used for estimation or not. Item <code>user.data</code> is a
-------------------	--

logical indicating if the migration rates are given by the user (TRUE) or are taken from a **wpp** package (FALSE).

mcmc.list A list of objects of class bayesMig.mcmc, one for each MCMC. Information stored here is specific to each MCMC chain, similarly to [bayesTFR.mcmc](#).

References

Azose, J. J., & Raftery, A. E. (2015). Bayesian probabilistic projection of international migration. *Demography*, 52(5), 1627-1650.

See Also

[get.mig.mcmc](#), [summary.bayesMig.mcmc.set](#), [mig.partraces.plot](#), [mig.pardensity.plot](#), [mig.predict](#)

Examples

```
# Toy simulation for US states
us.mig.file <- file.path(find.package("bayesMig"), "extdata", "USmigrates.txt")
sim.dir <- tempfile()
m <- run.mig.mcmc(nr.chains = 3, iter = 100, thin = 1, my.mig.file = us.mig.file,
                 annual = TRUE, output.dir = sim.dir)
summary(m)
summary(m, "Washington")

mig.partraces.plot(m)
mig.partraces.cs.plot("California", m)

# later one can access the object from disk
m <- get.mig.mcmc(sim.dir)

unlink(sim.dir, recursive = TRUE)
# For a country-level simulation, see example in ?bayesMig.
```

summary.bayesMig.convergence

Summary of Convergence Diagnostics

Description

Summary of an object of class [bayesMig.convergence](#) created using the [mig.diagnose](#) function. It gives an overview about parameters that did not converge.

Usage

```
## S3 method for class 'bayesMig.convergence'
summary(object, expand = FALSE, ...)
```

Arguments

object	Object of class bayesMig.prediction .
expand	By default, the function does not show country-specific parameters for which there was no convergence (only country-independent parameters), if the status is 'red'. This argument can switch that option on.
...	Not used.

Value

List with items that summarize an object of class [bayesMig.convergence](#).

summary.bayesMig.mcmc *Summary Statistics for Migration Markov Chain Monte Carlo*

Description

Summary of an object [bayesMig.mcmc.set](#) or [bayesMig.mcmc](#), computed via [run.mig.mcmc](#). It can be obtained either for all locations or for a specific location, and either for all parameters or for specific parameters. The function uses the [summary.mcmc](#) function of the **coda** package.

Usage

```
## S3 method for class 'bayesMig.mcmc'
summary(
  object,
  country = NULL,
  par.names = NULL,
  par.names.cs = NULL,
  thin = 1,
  burnin = 0,
  ...
)

## S3 method for class 'bayesMig.mcmc.set'
summary(
  object,
  country = NULL,
  chain.id = NULL,
  par.names = NULL,
  par.names.cs = NULL,
  meta.only = FALSE,
  thin = 1,
  burnin = 0,
  ...
)
```

Arguments

object	Object of class <code>bayesMig.mcmc.set</code> or <code>bayesMig.mcmc</code> .
country	Location name or code if a location-specific summary is desired. The code can be either numeric or (if locations are countries) ISO-2 or ISO-3 characters. By default, summary for all locations is generated.
par.names	Country independent parameters (hyperparameters) to be included in the summary. The default names are given by <code>mig.parameter.names()</code> .
par.names.cs	Location-specific parameters to be included in the summary. The default names are given by <code>mig.parameter.names.cs()</code> .
thin	Thinning interval. Only used if larger than the <code>thin</code> argument used in <code>run.mig.mcmc</code> .
burnin	Number of iterations to be discarded from the beginning of each chain before computing the summary.
...	Additional arguments passed to the <code>summary.mcmc</code> function of the <code>coda</code> package.
chain.id	Identifiers of MCMC chains. By default, all chains are considered.
meta.only	Logical. If it is TRUE, only meta information of the simulation is included.

Value

Return list with elements:

meta contains meta information about the object.

results contains result of `summary.mcmc`.

country.name optional; available if country is provided as argument.

Examples

```
# See example in ?run.mig.mcmc
```

```
summary.bayesMig.prediction
```

Summary of Prediction of Net Migration Rate

Description

Summary of an object of class `bayesMig.prediction`, created using the function `mig.predict`. The summary contains the mean, standard deviation and several commonly used quantiles of the simulated trajectories.

Usage

```
## S3 method for class 'bayesMig.prediction'
summary(object, country = NULL, compact = TRUE, ...)
```

```
## S3 method for class 'summary.bayesMig.prediction'
print(x, digits = 3, ...)
```

Arguments

<code>object</code>	Object of class <code>bayesMig.prediction</code> .
<code>country</code>	Location name or code if a location-specific summary is desired. The code can be either numeric or (if locations are countries) ISO-2 or ISO-3 characters. If it is NULL, only prediction meta info is included.
<code>compact</code>	Logical switching between a smaller and larger number of displayed quantiles.
<code>...</code>	A list of further arguments.
<code>x</code>	A result of the <code>summary</code> function.
<code>digits</code>	Minimal number of significant digits.

Value

`summary` returns a list with objects `burnin`, `nr.traj`, `projection.years`, `country.name` containing the MCMC burn-in, number of trajectories, projected years and name of the location, respectively. The projection results are stored in the item `projections` which is a matrix with rows being the years and columns being the mean and various quantiles.

Examples

```
# See example in ?mig.predict
```

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