Package ‘reems’

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Title Estimating Effective Migration Surfaces from Single Nucleotide Polymorphism Data

Version 0.1.0

Description Wrapper and plotting utilities for the spatial population genetics tool 'EEMS' (Estimated Effective Migration Surfaces) for SNP (Single Nucleotide Polymorphism) data, originally provided as a command-line tool written in 'C++' together with an accompanying 'R' package for plotting the output of the 'EEMS' tool itself (<`https://github.com/dipetkov/eems/`>). There are four main motivations for offering this to 'R' users as a package. Firstly, to remove the installation and configuration burden for the 'EEMS' command-line tool, which relies on manually installed 'Boost' and 'Eigen' system libraries and configuring their location; secondly, to streamline the workflow by having a singe environment (the 'R' system) for the entire analysis rather than a file-based command-line executable whose output files are then to be imported and analysed by a separate 'R' script; thirdly, to make the input formats compatible with other, 'R'-based spatial population genetics tools such as the 'ConStruct' package; and lastly, to allow for easily running several chains in parallel and combining them for plotting and further analysis. The package also adds more intuitive, streamlined tooling around creating more complex habitats. The method of estimating effective migration surfaces was first described by Petkova, D., Novembre, J. & Stephens, M. (2016) <doi:10.1038/ng.3464>.

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`eems` *Run an EEMS analysis from data in R format*

Description

This function runs an EEMS analysis with given parameters in the input format for `conStruct`, which include R matrices for allele frequency data and coordinates. In addition to taking R objects as inputs, it also provides additional default values over the original `EEMS` command-line utility. Furthermore, it allows for running more than one chain, either in parallel or sequentially, and returns a vector of output directories as input to `eems.plots()`.

Usage

```
eems(
  seed = unclass(Sys.time()),
  coords,
  freqs,
  outer = NULL,
  buffer = NULL,
  mcmcpath,
  demes = NULL,
  edges = NULL,
  prevpath = "",
  nChains = 1,
  parallel = FALSE,
  nWorkers = NULL,
  nDemes = NULL,
  diploid = TRUE,
  distance = "greatcircle",
  numMCMCIter = 2e+06,
  numBurnIter = 1e+06,
  numThinIter = 9999,
  mSeedsProposalS2 = 0.01,
  qSeedsProposalS2 = 0.1,
  mEffctProposalS2 = 0.1,
  qEffctProposalS2 = 0.001,
  mrateMuProposalS2 = 0.01,
  qVoronoiPr = 0.25,
  qrateShape = 0.001,
  mrateShape = 0.001,
  sigmaShape = 0.001,
  qrateScale = 1,
  mrateScale = 1,
  sigmaScale = 1,
  negBiProb = 0.67,
  negBiSize = 10
)
```

Arguments

`seed`	The random seed. Defaults to the current system time in seconds.
`coords`	The coordinate matrix, a two-column matrix with a line for every sample.
`freqs`	An allele frequency matrix in `conStruct` format, with a column for every site and a row for every sample. Choosing one main allele, it tabulates the average genotypes of the sample at that locus.
`outer`	Matrix of coordinates of the outer polygon. Defaults to a polygon larger than the convex hull of the supplied coordinates to mitigate EEMS boundary effects, which is created by `outer.buffered()`.

`buffer`	The rough distance of the boundary from the convex hull. Defaults to 0.2 times the length of the hull. Unused if `outer` is specified.
`mcmcpath`	Full path to a filename prefix in an output directory with write permission.
`demes`	Matrix of coordinates of demes; optional, and usually unnecessary. Only in conjunction with `edges`.
`edges`	Matrix of custom input grid; optional, and usually unnecessary. Only in conjunction with `demes`.
`prevpath`	Full path to previous output directory, i.e., the mcmcpath in a previous EEMS run. Optional.
`nChains`	Number of chains to be run. Defaults to 1.
`parallel`	Logical values that indicates whether chains should be run in parallel. Defaults to FALSE.
`nWorkers`	If `parallel` is TRUE, then the number of workers used is the minimum of `nChains` and `nWorkers`. Defaults to the number of available cores.
`nDemes`	Number of demes, roughly. EEMS constructs a regular triangular grid with circa nDemes vertices. Defaults to 6 times the number of individuals, aiming for sufficient resolution.
`diploid`	Logical value that indicates whether the species is diploid (TRUE) or haploid (FALSE). Defaults to TRUE.
`distance`	Distance metric. Either `euclidean` or `greatcirc`, that is, great circle distance. Defaults to 'greatcirc', which is more accurate at larger scales.
`numMCMCIter`	Number of Markov Chain Monte Carlo iterations. Defaults to 2000000.
`numBurnIter`	Number of burn-in iterations to be discarded before sampling from posterior. Defaults to 1000000.
`numThinIter`	Number of thinning iterations to be discarded between sampling from posterior. Defaults to 9999.
`mSeedsProposalS2`	Variance of normal proposals to update the seeds of the migration tiles. Defaults to 0.01.
`qSeedsProposalS2`	Variance of normal proposals to update the seeds of the diversity tiles. Defaults to 0.1.
`mEffctProposalS2`	Variance of normal proposals to update the log10 rates of the migration tiles. Defaults to 0.1.
`qEffctProposalS2`	Variance of normal proposals to update the log10 rates of the diversity tiles. Defaults to 0.001.
`mrateMuProposalS2`	Variance of normal proposals to update the overall mean migration rate, on the log10 scale. Defaults to 0.01.
`qVoronoiPr`	With probability qVoronoiPr, update diversity Voronoi; with probability 1-qVoronoiPr, update migration Voronoi. Defaults to 0.25.

`qrateShape`	Shape hyperparameter for the diversity rates variance, qrateS2 ~ invgamma(qrateShape, qrateScale). Defaults to 0.001
`mrateShape`	Shape hyperparameter for the migration rates variance, mrateS2 ~ invgamma(mrateShape, mrateScale). Defaults to 0.001.
`sigmaShape`	Shape hyperparameter for the scaling factor sigma^2 ~ invgamma(sigmaShape, sigmaScale). Defaults to 0.001.
`qrateScale`	Scale hyperparameter for the diversity rates variance, qrateS2 ~ invgamma(qrateShape, qrateScale). Defaults to 1.0.
`mrateScale`	Scale hyperparameter for the migration rates variance, mrateS2 ~ invgamma(mrateShape, mrateScale). Defaults to 1.0.
`sigmaScale`	Scale hyperparameter for the scaling factor sigma^2 ~ invgamma(sigmaShape, sigmaScale). Defaults to 1.0.
`negBiProb`	Success probability for the number of Voronoi tiles ~ negbinom(negBiSize, negBiProb). Defaults to 0.67.
`negBiSize`	Size for the number of Voronoi tiles ~ negbinom(negBiSize, negBiProb). Defaults to 10.

Value

A vector of output directories which can be given as input to `eems.plots()`.

References

Petkova, D., Novembre, J. & Stephens, M. Visualizing spatial population structure with estimated effective migration surfaces. Nat Genet 48, 94–100 (2016). https://doi.org/10.1038/ng.3464

See Also

`eems.plots`, `eems.from.files`

Examples

```
# The example puts the output in a temporary directory.
mcmcdir <- file.path(tempdir(), "eems_out")
dir.create(mcmcdir, showWarnings = FALSE)
mcmcpath <- file.path(mcmcdir,"example")

# Run an example EEMS analysis with a small number of iterations to ensure quick termination.

eems(
  freqs = ex.freqs,
  coords = ex.coords,
  mcmcpath = mcmcpath,
  numMCMCIter = 200,
  numBurnIter = 100,
  numThinIter = 99,
)
# Delete the output directory to tidy up.
unlink(mcmcdir, recursive = TRUE, force = TRUE)
```

`eems.from.files` *Run an EEMS analysis*

Description

This function runs an EEMS analysis with given parameters, which include file paths for retrieving the input files (datapath.coord, datapath.diffs and datapath.outer) and writing the output files. It is an exact replicate of the original EEMS command-line function.

Usage

```
eems.from.files(
  seed = unclass(Sys.time()),
  datapath,
  mcmcpath,
  prevpath = "",
  gridpath = "",
  nDemes,
  nIndiv,
  nSites,
  diploid = TRUE,
  distance = "euclidean",
  numMCMCIter,
  numBurnIter,
  numThinIter,
  mSeedsProposalS2 = 0.01,
  qSeedsProposalS2 = 0.1,
  mEffctProposalS2 = 0.1,
  qEffctProposalS2 = 0.001,
  mrateMuProposalS2 = 0.01,
  qVoronoiPr = 0.25,
  qrateShape = 0.001,
  mrateShape = 0.001,
  sigmaShape = 0.001,
  qrateScale = 1,
  mrateScale = 1,
  sigmaScale = 1,
  negBiProb = 0.67,
  negBiSize = 10
)
```

Arguments

`seed`	The random seed. Defaults to the current system time in seconds.
`datapath`	Full path to a set of three files: datapath.coord, datapath.diffs and datapath.outer.
`mcmcpath`	Full path to a filename prefix in an output directory with write permission.

`prevpath`	Full path to previous output directory, i.e., the mcmcpath in a previous EEMS run. Optional.
`gridpath`	Full path to a set of two files: gridpath.demes and gridpath.edges. Optional.
`nDemes`	Number of demes, roughly. EEMS constructs a regular triangular grid with circa nDemes vertices.
`nIndiv`	Number of samples. Should match the size of the dissimilarity matrix in datapath.diffs.
`nSites`	Number of SNPs used to compute the observed dissimilarity matrix in datapath.diffs.
`diploid`	Logical value that indicates whether the species is diploid (TRUE) or haploid (FALSE). Defaults to TRUE.
`distance`	Distance metric. Either `euclidean` or `greatcirc`, that is, great circle distance. Defaults to 'euclidean'.
`numMCMCIter`	Number of Markov Chain Monte Carlo iterations.
`numBurnIter`	Number of burn-in iterations to be discarded before sampling from posterior.
`numThinIter`	Number of thinning iterations to be discarded between sampling from posterior.
`mSeedsProposalS2`	Variance of normal proposals to update the seeds of the migration tiles. Defaults to 0.01.
`qSeedsProposalS2`	Variance of normal proposals to update the seeds of the diversity tiles. Defaults to 0.1.
`mEffctProposalS2`	Variance of normal proposals to update the log10 rates of the migration tiles. Defaults to 0.1.
`qEffctProposalS2`	Variance of normal proposals to update the log10 rates of the diversity tiles. Defaults to 0.001.
`mrateMuProposalS2`	Variance of normal proposals to update the overall mean migration rate, on the log10 scale. Defaults to 0.01.
`qVoronoiPr`	With probability qVoronoiPr, update diversity Voronoi; with probability 1-qVoronoiPr, update migration Voronoi. Defaults to 0.25.
`qrateShape`	Shape hyperparameter for the diversity rates variance, qrateS2 ~ invgamma(qrateShape, qrateScale). Defaults to 0.001
`mrateShape`	Shape hyperparameter for the migration rates variance, mrateS2 ~ invgamma(mrateShape, mrateScale). Defaults to 0.001.
`sigmaShape`	Shape hyperparameter for the scaling factor sigma^2 ~ invgamma(sigmaShape, sigmaScale). Defaults to 0.001.
`qrateScale`	Scale hyperparameter for the diversity rates variance, qrateS2 ~ invgamma(qrateShape, qrateScale). Defaults to 1.0.
`mrateScale`	Scale hyperparameter for the migration rates variance, mrateS2 ~ invgamma(mrateShape, mrateScale). Defaults to 1.0.

`sigmaScale`	Scale hyperparameter for the scaling factor sigma^2 ~ invgamma(sigmaShape, sigmaScale). Defaults to 1.0.
`negBiProb`	Success probability for the number of Voronoi tiles ~ negbinom(negBiSize, negBiProb). Defaults to 0.67.
`negBiSize`	Size for the number of Voronoi tiles ~ negbinom(negBiSize, negBiProb). Defaults to 10.

Value

None

References

Petkova, D., Novembre, J. & Stephens, M. Visualizing spatial population structure with estimated effective migration surfaces. Nat Genet 48, 94–100 (2016). https://doi.org/10.1038/ng.3464

See Also

`eems.plots`, `eems`

Examples

```
# We use example input from Petkova et al. (2016), found in the '/extdata' directory
data_path <- system.file("extdata", package = "reems")
input <- file.path(data_path, "barrier-schemeX-nIndiv300-nSites3000")
# The example puts the output in a temporary directory.
mcmcdir <- file.path(tempdir(), "eems_out")
dir.create(mcmcdir, showWarnings = FALSE)


# Run an example EEMS analysis with a small number of iterations to ensure quick termination.

eems.from.files(
  datapath = input,
  mcmcpath = mcmcdir,
  nDemes = 200,
  nIndiv = 300,
  nSites = 3000,
  diploid = FALSE,
  numMCMCIter = 200,
  numBurnIter = 100,
  numThinIter = 99,
)
# Delete the output directory to tidy up.
unlink(mcmcdir, recursive = TRUE, force = TRUE)
```

`eems.plots` *A function to plot effective migration and diversity surfaces from EEMS output*

Description

Given a vector of EEMS output directories, this function generates several figures to visualize EEMS results. It is a good idea to examine all these figures, which is why they are generated by default.

- `plotpath-mrates01`: effective migration surface. This contour plot visualizes the estimated effective migration rates `m`, on the log10 scale after mean centering.
- `plotpath-mrates02`: posterior probabilities `P(m > 0 | diffs)` and `P(m < 0 | diffs)` for each location in the habitat. Since migration rates are visualized on the log10 scale after mean centering, 0 corresponds to the overall mean migration rate. This contour plot emphasizes regions with effective migration that is significantly higher/lower than the overall average.
- `plotpath-qrates01`: effective diversity surface. This contour plot visualizes the estimated effective diversity rates `q`, on the log10 scale after mean centering.
- `plotpath-qrates02`: posterior probabilities `P(q > 0 | diffs)` and `P(q < 0 | diffs)`. Similar to `plotpath-mrates02` but applied to the effective diversity rates.
- `plotpath-rdist01`: scatter plot of the observed vs the fitted between-deme component of genetic dissimilarity, where one point represents a pair of sampled demes.
- `plotpath-rdist02`: scatter plot of the observed vs the fitted within-deme component of genetic dissimilarity, where one point represents a sampled deme.
- `plotpath-rdist03`: scatter plot of observed genetic dissimilarities between demes vs observed geographic distances between demes.
- `plotpath-pilogl01`: posterior probability trace

The `mrates` and `qrates` figures visualize (properties of) the effective migration and diversity rates across the habitat. The other figures can help to check that the MCMC sampler has converged (the trace plot `pilogl`) and that the EEMS model fits the data well (the scatter plots of genetic dissimilarities `rdist`).

Usage

```
eems.plots(
  mcmcpath,
  plotpath,
  longlat,
  plot.width = 10,
  plot.height = 10,
  out.png = NULL,
  res = 600,
  xpd = TRUE,
  add.grid = FALSE,
```

```
  col.grid = "gray80",
  lwd.grid = 1,
  add.demes = FALSE,
  col.demes = "black",
  pch.demes = 19,
  min.cex.demes = 1,
  max.cex.demes = 3,
  add.outline = FALSE,
  col.outline = "gray90",
  lwd.outline = 2,
  projection.in = NULL,
  projection.out = NULL,
  add.map = FALSE,
  col.map = "gray60",
  lwd.map = 2,
  eems.colors = NULL,
  prob.levels = c(0.9, 0.95),
  add.colbar = TRUE,
  m.colscale = NULL,
  q.colscale = NULL,
  remove.singletons = TRUE,
  add.abline = FALSE,
  add.r.squared = FALSE,
  add.title = TRUE,
  m.plot.xy = NULL,
  q.plot.xy = NULL,
  xy.coords = NULL
)
```

Arguments

`mcmcpath`	A vector of EEMS output directories, for the same dataset. Warning: There is minimal checking that the given directories are for the same dataset.
`plotpath`	The full path and the file name for the graphics to be generated.
`longlat`	A logical value indicating whether the coordinates are given as pairs (longitude, latitude) or (latitude, longitude).
`plot.width`	The width of the graphics region for the two rate contour plots, in inches. The default value is 10.
`plot.height`	The height of the graphics region, in inches. The default value is 10.
`out.png`	A logical value which, if set, forces output graphics to be generated as PNGs (if `TRUE`) or PDFs (if `FALSE`). If left unset, the format depends on the nature of the plot.
`res`	Resolution, in dots per inch; used only for PNG images. The default is 600.
`xpd`	A logical value indicating whether to clip plotting to the figure region (`xpd` = TRUE, which is the default) or clip plotting to the plot region (`xpd` = FALSE).
`add.grid`	A logical value indicating whether to add the population grid or not.

`col.grid`	The color of the population grid. Defaults to `gray80`.
`lwd.grid`	The line width of the population grid. Defaults to 1.
`add.demes`	A logical value indicating whether to add the observed demes or not.
`col.demes`	The color of the demes. Defaults to `black`.
`pch.demes`	The symbol, specified as an integer, or the character to be used for plotting the demes. Defaults to 19.
`min.cex.demes`	The minimum size of the deme symbol/character.
`max.cex.demes`	The maximum size of the deme symbol/character. Defaults to 1 and 3, respectively. If `max.cex.demes` > `min.cex.demes`, then demes with more samples also have bigger size: the deme with the fewest samples has size `min.cex.demes` and the deme with the most samples has size `max.cex.demes`.
`add.outline`	A logical value indicating whether to add the habitat outline or not.
`col.outline`	The color of the habitat outline. Defaults to `white`.
`lwd.outline`	The line width of the habitat outline. Defaults to 2.
`projection.in`	The input cartographic projection, specified as a PROJ.4 string.
`projection.out`	The output cartographic projection, specified as a PROJ.4 string.
`add.map`	A logical value indicating whether to add a high-resolution geographic map. Requires the `rworldmap` and `rworldxtra` packages. It also requires that `projection.in` is specified.
`col.map`	The color of the geographic map. Default is `gray60`.
`lwd.map`	The line width of the geographic map. Defaults to 2.
`eems.colors`	The EEMS color scheme as a vector of colors, ordered from low to high. Defaults to a DarkOrange to Blue divergent palette with six orange shades, white in the middle, six blue shades. Acknowledgement: The default color scheme is adapted from the `dichromat` package.
`prob.levels`	A vector of probabilities for plotting the posterior probability contours of `P(m > 0 | diffs)` and `P(m < 0 | diffs)`. Defaults to `c(0.9, 0.95)`.
`add.colbar`	A logical value indicating whether to add the color bar (the key that shows how colors map to rates) to the right of the plot. Defaults to TRUE.
`m.colscale`	A fixed range for log10-transformed migration rates. If the estimated rates fall outside the specified range, then the color scale is ignored. By default, no range is specified for either type of rates.
`q.colscale`	A fixed range for log10-transformed diversity rates.
`remove.singletons`	Remove demes with a single observation from the diagnostic scatter plots. Defaults to TRUE.
`add.abline`	Add the line `y = x` to the diagnostic scatter plots of observed vs fitted genetic dissimilarities.
`add.r.squared`	Add the R squared coefficient to the diagnostic scatter plots of observed vs fitted genetic dissimilarities.
`add.title`	A logical value indicating whether to add the main title in the contour plots. Defaults to TRUE.

`m.plot.xy`	Statements which add graphical elements (e.g. points) on top of the migration sufrace.
`q.plot.xy`	Statements which add graphical elements (e.g. points) on top of the diversity surface.
`xy.coords`	Additional coordinates at which to estimate the migration and diversity rates.

Details

The function `eems.plots` will work given the results from a single EEMS run (one directory in `mcmcpath`) but it is better to run EEMS several times, randomly initializing the MCMC chain each time. In other words, simulate several realizations of the Markov chain and let each realization start from a different state in the parameter space (by using a different random seed).

Detail about the within-deme and between-deme components of genetic dissimilarity: Let `D(a,b)` be the dissimilarity between one individual from deme `a` and another individual from deme `b`. Then the within-deme component for `a` and `b` is simply `D(a,a)` and `D(b, b)`, respectively. The between-deme component is `D(a,b) - [D(a,a) + D(b,b)] / 2` and it represents dissimilarity that is due to the spatial structure of the population and is not a consequence of the local diversity in the two demes.

Value

None

References

Light A and Bartlein PJ (2004). The End of the Rainbow? Color Schemes for Improved Data Graphics. EOS Transactions of the American Geophysical Union, 85(40), 385.

See Also

`eems.voronoi.samples`, `eems.posterior.draws`, `eems.population.grid`

Examples

```
# Use the provided example or supply the path to your own EEMS run.
extdata_path <- system.file("extdata", package = "reems")
eems_results <- file.path(extdata_path, "EEMS-example")
# Create a temporary output directory for the sake of the example
outdir <- file.path(tempdir(), "plot_out")
dir.create(outdir, showWarnings = FALSE)
name_figures <- file.path(outdir, "EEMS-example")

# Produce the set of EEMS figures, with default values for all optional parameters.
eems.plots(
  mcmcpath = eems_results,
  plotpath = paste0(name_figures, "-default"),
  longlat = TRUE,
  out.png = FALSE
)
```

```
# Delete the temporary output directory to tidy up.
unlink(outdir, recursive = TRUE, force = TRUE)
```

`eems.population.grid` *A function to plot the constructed population grid and optionally the initial sampling locations*

Description

Given an EEMS output directory, this function generates one figure to visualize the EEMS population grid. All edges are shown in the same color to visualize the grid before estimating migration and diversity rates. This can be helpful if EEMS exits with the error message "The population grid is not connected".

Usage

```
eems.population.grid(
  mcmcpath,
  plotpath,
  longlat,
  plot.width = 10,
  plot.height = 10,
  out.png = FALSE,
  res = 600,
  add.grid = TRUE,
  col.grid = "gray80",
  lwd.grid = 1,
  add.demes = FALSE,
  col.demes = "black",
  pch.demes = 19,
  min.cex.demes = 1,
  max.cex.demes = 3,
  add.outline = TRUE,
  col.outline = "gray90",
  lwd.outline = 2,
  add.coord = FALSE,
  col.coord = "red",
  pch.coord = 3,
  datapath = NULL
)
```

Arguments

`mcmcpath`	A vector of EEMS output directories, for the same dataset. Warning: There is minimal checking that the given directories are for the same dataset.
`plotpath`	The full path and the file name for the graphics to be generated.

`longlat`	A logical value indicating whether the coordinates are given as pairs (longitude, latitude) or (latitude, longitude).
`plot.width`	The width of the graphics region for the two rate contour plots, in inches. The default value is 10.
`plot.height`	The height of the graphics region, in inches. The default value is 10.
`out.png`	A logical value which, if set, forces output graphics to be generated as PNGs (if `TRUE`) or PDFs (if `FALSE`). Defaults to `FALSE`.
`res`	Resolution, in dots per inch; used only for PNG images. The default is 600.
`add.grid`	A logical value indicating whether to add the population grid or not.
`col.grid`	The color of the population grid. Defaults to `gray80`.
`lwd.grid`	The line width of the population grid. Defaults to 1.
`add.demes`	A logical value indicating whether to add the observed demes or not.
`col.demes`	The color of the demes. Defaults to `black`.
`pch.demes`	The symbol, specified as an integer, or the character to be used for plotting the demes. Defaults to 19.
`min.cex.demes`	The minimum size of the deme symbol/character.
`max.cex.demes`	The maximum size of the deme symbol/character. Defaults to 1 and 3, respectively. If `max.cex.demes` > `min.cex.demes`, then demes with more samples also have bigger size: the deme with the fewest samples has size `min.cex.demes` and the deme with the most samples has size `max.cex.demes`.
`add.outline`	A logical value indicating whether to add the habitat outline or not.
`col.outline`	The color of the habitat outline. Defaults to `white`.
`lwd.outline`	The line width of the habitat outline. Defaults to 2.
`add.coord`	A logical value indicating whether to add the original sampling locations to the plot or not.
`col.coord`	The color of the sampling locations. Defaults to `red`.
`pch.coord`	The symbol, specified as an integer, or the character to be used for plotting the sampling locations. Defaults to 3.
`datapath`	The full path and the file name of the input dataset (the three files datapath.coord, datapath.diffs, datapath.outer). Must be specified if `add_coord = TRUE`.

Value

Passes on the return value of `dev.off()` indicating the graphics device.

See Also

`eems.plots`, `eems.voronoi.samples`, `eems.posterior.draws`

Examples

```
# Use the provided example or supply the path to your own EEMS run.
extdata_path <- system.file("extdata", package = "reems")
eems_results <- file.path(extdata_path, "EEMS-example")
# Create a temporary output directory for this example
outdir <- file.path(tempdir(), "path_out")
dir.create(outdir, showWarnings = FALSE)
name_figures <- file.path(outdir, "EEMS-grid_connected")

eems.population.grid(eems_results,
  name_figures,
  longlat = TRUE,
  add.outline = TRUE,
  col.outline = "purple",
  lwd.outline = 3,
  add.grid = TRUE,
  col.grid = "green",
  lwd.grid = 2,
  out.png = FALSE
)

# It is more interesting to see an example where the grid is unconnected
# due to the unusual shape of the habitat.
eems_results <- file.path(extdata_path, "EEMS-popgrid")

name_figures <- file.path(outdir, "EEMS-grid_not_connected")

eems.population.grid(
  mcmcpath = eems_results,
  plotpath = name_figures,
  longlat = FALSE,
  add.outline = TRUE, col.outline = "purple", lwd.outline = 3,
  add.grid = TRUE, col.grid = "green", lwd.grid = 2
)
# Delete the output file to tidy up.
unlink(outdir, recursive = TRUE, force = TRUE)
```

`eems.posterior.draws` *Plotting smoothed Voronoi diagrams of effective migration and diversity rates*

Description

Given a set of EEMS output directories, this function takes random draws from the posterior distribution of the migration and diversity rate parameters. Each draw is visualized as two smoothed Voronoi diagrams; the migration diagram is saved to a file ending in `mvoronoiXX`, the diversity diagram is saved to a file ending in `qvoronoiXX` where `XX` is a numeric id. Specify the number of times to draw from the posterior with the argument `post.draws`. If `post.draws = 10`, then `eems.posterior.draws` will generate plots with id `XX = 1` to `XX = 10`. This function differs from `eems.voronoi.samples()` by plotting smoothed contour diagrams rather than raw Voronoi plots.

Usage

```
eems.posterior.draws(
  mcmcpath,
  plotpath,
  longlat,
  post.draws = 1,
  plot.width = 10,
  plot.height = 10,
  out.png = TRUE,
  res = 600,
  xpd = TRUE,
  add.grid = FALSE,
  col.grid = "gray80",
  lwd.grid = 1,
  add.demes = FALSE,
  col.demes = "black",
  pch.demes = 19,
  min.cex.demes = 1,
  max.cex.demes = 3,
  add.outline = FALSE,
  col.outline = "gray90",
  lwd.outline = 2,
  projection.in = NULL,
  projection.out = NULL,
  add.map = FALSE,
  col.map = "gray60",
  lwd.map = 2,
  eems.colors = NULL,
  add.colbar = FALSE,
  m.colscale = NULL,
  q.colscale = NULL,
  add.title = FALSE,
  m.plot.xy = NULL,
  q.plot.xy = NULL
)
```

Arguments

`mcmcpath`	A vector of EEMS output directories, for the same dataset. Warning: There is minimal checking that the given directories are for the same dataset.
`plotpath`	The full path and the file name for the graphics to be generated.
`longlat`	A logical value indicating whether the coordinates are given as pairs (longitude, latitude) or (latitude, longitude).
`post.draws`	Number of times to sample from the posterior. The default is 1.
`plot.width`	The width of the graphics region for the two rate contour plots, in inches. The default value is 10.
`plot.height`	The height of the graphics region, in inches. The default value is 10.

`out.png`	A logical value which, if set, forces output graphics to be generated as PNGs (if `TRUE`) or PDFs (if `FALSE`). Defaults to `TRUE`.
`res`	Resolution, in dots per inch; used only for PNG images. The default is 600.
`xpd`	A logical value indicating whether to clip plotting to the figure region (`xpd` = TRUE, which is the default) or clip plotting to the plot region (`xpd` = FALSE).
`add.grid`	A logical value indicating whether to add the population grid or not.
`col.grid`	The color of the population grid. Defaults to `gray80`.
`lwd.grid`	The line width of the population grid. Defaults to 1.
`add.demes`	A logical value indicating whether to add the observed demes or not.
`col.demes`	The color of the demes. Defaults to `black`.
`pch.demes`	The symbol, specified as an integer, or the character to be used for plotting the demes. Defaults to 19.
`min.cex.demes`	The minimum size of the deme symbol/character.
`max.cex.demes`	The maximum size of the deme symbol/character. Defaults to 1 and 3, respectively. If `max.cex.demes` > `min.cex.demes`, then demes with more samples also have bigger size: the deme with the fewest samples has size `min.cex.demes` and the deme with the most samples has size `max.cex.demes`.
`add.outline`	A logical value indicating whether to add the habitat outline or not.
`col.outline`	The color of the habitat outline. Defaults to `white`.
`lwd.outline`	The line width of the habitat outline. Defaults to 2.
`projection.in`	The input cartographic projection, specified as a PROJ.4 string.
`projection.out`	The output cartographic projection, specified as a PROJ.4 string.
`add.map`	A logical value indicating whether to add a high-resolution geographic map. Requires the `rworldmap` and `rworldxtra` packages. It also requires that `projection.in` is specified.
`col.map`	The color of the geographic map. Default is `gray60`.
`lwd.map`	The line width of the geographic map. Defaults to 2.
`eems.colors`	The EEMS color scheme as a vector of colors, ordered from low to high. Defaults to a DarkOrange to Blue divergent palette with six orange shades, white in the middle, six blue shades. Acknowledgement: The default color scheme is adapted from the `dichromat` package.
`add.colbar`	A logical value indicating whether to add the color bar (the key that shows how colors map to rates) to the right of the plot. Defaults to TRUE.
`m.colscale`	A fixed range for log10-transformed migration rates. If the estimated rates fall outside the specified range, then the color scale is ignored. By default, no range is specified for either type of rates.
`q.colscale`	A fixed range for log10-transformed diversity rates.
`add.title`	A logical value indicating whether to add the main title in the contour plots. Defaults to TRUE.
`m.plot.xy`	Statements which add graphical elements (e.g. points) on top of the migration sufrace.
`q.plot.xy`	Statements which add graphical elements (e.g. points) on top of the diversity surface.

Details

Note about the implementation: `eems.voronoi.samples` samples randomly from the posterior draws saved during the execution of EEMS, after burn-in and thinning.

Value

None

References

Light A and Bartlein PJ (2004). The End of the Rainbow? Color Schemes for Improved Data Graphics. EOS Transactions of the American Geophysical Union, 85(40), 385.

See Also

`eems.voronoi.samples`

Examples

```
# Use the provided example or supply the path to your own EEMS run.
extdata_path <- system.file("extdata", package = "reems")
eems_results <- file.path(extdata_path, "EEMS-example")
# Create a temporary output directory for this example
outdir <- file.path(tempdir(), "path_out")
dir.create(outdir, showWarnings = FALSE)
name_figures <- file.path(outdir, "EEMS-example")

# Plot a series of Voronoi diagrams for the EEMS model parameters:
# the effective migration rates (m) and the effective diversity rates (q).
eems.posterior.draws(
  mcmcpath = eems_results,
  plotpath = paste0(name_figures, "-posterior-draws"),
  longlat = TRUE,
  post.draws = 2,
  out.png = FALSE
)
# Delete the output directory to tidy up.
unlink(outdir, recursive = TRUE, force = TRUE)
```

`eems.voronoi.samples` *A function to plot raw Voronoi diagrams of effective migration and diversity rates*

Description

Given a set of EEMS output directories, this function takes random draws from the posterior distribution of the migration and diversity rate parameters. Each draw is visualized as two raw Voronoi diagrams; the migration diagram is saved to a file ending in `mvoronoiXX`, the diversity diagram is saved to a file ending in `qvoronoiXX` where `XX` is a numeric id. Specify the number of times to draw from the posterior with the argument `post.draws`. If `post.draws = 10`, then `eems.voronoi.samples` will generate plots with id `XX = 1` to `XX = 10`. This function differs from `eems.posterior.draws()` by displaying raw, unsmoothed Voronoi diagrams.

Usage

```
eems.voronoi.samples(
  mcmcpath,
  plotpath,
  longlat,
  post.draws = 1,
  plot.width = 10,
  plot.height = 10,
  out.png = FALSE,
  res = 600,
  add.grid = FALSE,
  col.grid = "gray80",
  lwd.grid = 1,
  add.outline = TRUE,
  col.outline = "gray80",
  lwd.outline = 2,
  add.demes = FALSE,
  col.demes = "gray80",
  pch.demes = 19,
  cex.demes = 1,
  add.seeds = TRUE,
  col.seeds = "#8AE234",
  pch.seeds = 4,
  cex.seeds = 1,
  eems.colors = NULL,
  m.colscale = NULL,
  q.colscale = NULL,
  add.title = FALSE
)
```

Arguments

`mcmcpath`	A vector of EEMS output directories, for the same dataset. Warning: There is minimal checking that the given directories are for the same dataset.
`plotpath`	The full path and the file name for the graphics to be generated.
`longlat`	A logical value indicating whether the coordinates are given as pairs (longitude, latitude) or (latitude, longitude).
`post.draws`	Number of times to sample from the posterior. The default is 1.

`plot.width`	The width of the graphics region for the two rate contour plots, in inches. The default value is 10.
`plot.height`	The height of the graphics region, in inches. The default value is 10.
`out.png`	A logical value which, if set, forces output graphics to be generated as PNGs (if `TRUE`) or PDFs (if `FALSE`). Defaults to `FALSE`.
`res`	Resolution, in dots per inch; used only for PNG images. The default is 600.
`add.grid`	A logical value indicating whether to add the population grid or not.
`col.grid`	The color of the population grid. Defaults to `gray80`.
`lwd.grid`	The line width of the population grid. Defaults to 1.
`add.outline`	A logical value indicating whether to add the habitat outline or not.
`col.outline`	The color of the habitat outline. Defaults to `white`.
`lwd.outline`	The line width of the habitat outline. Defaults to 2.
`add.demes`	A logical value indicating whether to add the observed demes or not.
`col.demes`	The color of the demes. Defaults to `black`.
`pch.demes`	The symbol, specified as an integer, or the character to be used for plotting the demes. Defaults to 19.
`cex.demes`	The size of the symbol/character used for plotting observed demes. Defaults to 1.
`add.seeds`	A logical value indicating whether to add the Voronoi seeds or not.
`col.seeds`	The color of the Voronoi seeds. Defaults to `green`.
`pch.seeds`	The symbol, specified as an integer, or the character to be used for plotting the Voronoi seeds. Defaults to 4.
`cex.seeds`	The size of the symbol/character used for plotting the Voronoi seeds. Defaults to 1.
`eems.colors`	The EEMS color scheme as a vector of colors, ordered from low to high. Defaults to a DarkOrange to Blue divergent palette with six orange shades, white in the middle, six blue shades. Acknowledgement: The default color scheme is adapted from the `dichromat` package.
`m.colscale`	A fixed range for log10-transformed migration rates. If the estimated rates fall outside the specified range, then the color scale is ignored. By default, no range is specified for either type of rates.
`q.colscale`	A fixed range for log10-transformed diversity rates.
`add.title`	A logical value indicating whether to add the main title in the contour plots. Defaults to TRUE.

Details

Note about the implementation: `eems.voronoi.samples` samples randomly from the posterior draws saved during the execution of EEMS, after burn-in and thinning.

Value

None

References

Light A and Bartlein PJ (2004). The End of the Rainbow? Color Schemes for Improved Data Graphics. EOS Transactions of the American Geophysical Union, 85(40), 385.

See Also

`eems.posterior.draws`

Examples

```
# Use the provided example or supply the path to your own EEMS run.
extdata_path <- system.file("extdata", package = "reems")
eems_results <- file.path(extdata_path, "EEMS-example")
# Create a temporary output directory for this example
outdir <- file.path(tempdir(), "path_out")
dir.create(outdir, showWarnings = FALSE)
name_figures <- file.path(outdir, "eemsplot_out")

# Plot a series of Voronoi diagrams for the EEMS model parameters:
# the effective migration rates (m) and the effective diversity rates (q).
eems.voronoi.samples(
  mcmcpath = eems_results,
  plotpath = paste0(name_figures, "-voronoi-diagrams"),
  longlat = TRUE,
  post.draws = 2,
  out.png = FALSE
)
# Delete the output directory to tidy up.
unlink(outdir, recursive = TRUE, force = TRUE)
```

`ex.coords` *Example coordinate data from ConStruct*

Description

Example coordinate data from ConStruct

Usage

```
ex.coords
```

Format

`ex.coords`**:**
A matrix with 16 rows and 2 columns. The rows designate samples and the two columns store the X and Y coordinate respectively. .

Source

https://github.com/gbradburd/conStruct/tree/master/data

`ex.freqs` *Example allele frequency data from ConStruct*

Description

Example allele frequency data from ConStruct

Usage

```
ex.freqs
```

Format

`ex.freqs`:
A matrix with 16 rows and 10000 columns. The rows designate samples and the columns loci.

Source

https://github.com/gbradburd/conStruct/tree/master/data

`grid.make` *Create a habitat with holes*

Description

`grid.make()` constructs a regular triangular grid with circa nDemes vertices. This function creates three files:

- The pair gridpath.demes and gridpath.edges which specify a custom population grid with holes
- The plot gridpath.png which visualizes the custom grid with demes in red and edges in green

Usage

```
grid.make(outer, holes = NULL, plotpath = NULL, nDemes)
```

Arguments

`outer`	A two-column matrix of coordinates of boundary points (longitude, latitude).
`holes`	List of holes. Each hole is a two-column matrix of coordinates of boundary points (longitude, latitude). This is optional, and defaults to no holes.
`plotpath`	Output filename for the visualisation PNG file. Optional.
`nDemes`	Number of demes, roughly, in the grid without accounting for possible holes.

Value

A two-entry list of `demes` and `edges`, both two-column matrices.

Examples

```
# We use example input from Petkova et al. (2016), found in the '/extdata' directory
data_path <- system.file("extdata", package = "reems")
input <- file.path(data_path, "barrier-schemeX-nIndiv300-nSites3000")
# Load the population habitat
outer <- read.table(paste0(input, ".outer"))
# Each hole is a ring (simple closed polygon) and the holes don't overlap
hole1 <- data.frame(V1 = c(2., 5., 5., 2., 2.), V2 = c(2., 2., 5., 5., 2.))
hole2 <- data.frame(V1 = c(6.5, 10., 8., 6.5), V2 = c(2.5, 5., 5., 2.5))

# Create the new grid  with holes
grid.make(outer = outer, holes = list(hole1, hole2), nDemes = 300)
```

`outer.buffered` *Create a buffered habitat around a set of points.*

Description

Creates a polygon a certain distance from each of a set of points. It is used for creating a default habitat outline for `eems()`.

Usage

```
outer.buffered(coords, d = NULL)
```

Arguments

`coords`	A two-column matrix of point coordinates (longitude, latitude).
`d`	Rough buffer distance. Not necessarily kept completely to keep the polygon simple. Defaults to 0.2 of the length of the hull of the `coords`.

Value

A two-column matrix of coordinates with the outer boundary points of the containing polygon.

Examples

```
#  Create a buffer around the example habitat
outer <- outer.buffered(ex.coords)
```

`reems` *Estimating Effective Migration Surfaces (EEMS)*

Description

Provides several functions to run EEMS analyses and to visualise the results of EEMS. For an exmplanation of and introduction to the EEMS method, see Petkova, D., Novembre, J. & Stephens, M. (2016) <doi:10.1038/ng.3464>.

`eems` is the main entrypoint, running EEMS analyses on single nucleotide polymorphism data allele frequeny available as R matrices.

`eems.from.files` runs an EEMS analysis from input data available as tabular files, and correesponds precisely to the original EEMS utility available at <https://github.com/dipetkov/eems>.

`eems.plots` takes the output of one or more EEMS runs and produces contour plots of the effective migration and diversity rates, as well as scatterplots of observed vs fitted genetic dissimilarities and trace plots to assess convergence.

`eems.population.grid` plots the population grid, with all edges in the same color, to visualize the grid before estimating migration and diversity rates.

`eems.voronoi.samples` and `eems.posterior.draws` both take random samples from the posterior distribution of the migration and diversity rates and plot them to visualize the posterior variance (in a slightly different way).

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