PSCF demo

Contents

1 Preliminaries

From this point it will be assumed that you have generated trajectory files with HYSPLIT (following the instructions in Readme.pdf) and combine them into a `coords.rda` file. The example `coords.rda` file used here was generated for the VOCALS-REx campaign.

First, load libraries and functions. Be sure that you have the R packges `chron`, `fields`, `maps`, `mapproj`, and `akima` installed - this can be done very easily. For example, while connected to the internet, type at the R prompt:

```
> install.packages("chron", repos = "http://cran.r-project.org")
```

After all libraries have been installed, Begin the program:

```
> invisible(capture.output({
+     library(chron)
+     library(fields)
```

```
+     library(maps)
+     library(mapproj)
+     library(akima)
+ }))
> mapf.env <- (if (all(regexpr("mapfunctions", search()) < 0)) attach(NULL,
+     2, name = "mapfunctions") else pos.to.env(grep("mapfunctions",
+     search())))
> sys.source("functions/pscf_functions.r", mapf.env)
> source("functions/classdef.r")
> options(stringsAsFactors = FALSE)
```

Functions are located in a folder called `functions/`, in `functions.r`. Also located in the same folder is a file called `classdef.r`, which contains definitions for object classes used here.

User inputs – tell us where your files are (`Coords_file` should be the same as the one defined in `userinputs/runHYSPLIT_parm`

```
> Coords_file <- "outputs/coords_vocals.rda"
> Group_file <- "userinputs/groupfile-example_alcf.txt"
```

Your group file should look like this:

```
> head(read.delim(Group_file, row.names = 1))
```

```
                  Start               End Group
VX0021 10/21/08 12:03:00 10/21/08 17:32:00   low
VX0022 10/21/08 23:33:00 10/22/08 10:30:00   low
VX0024 10/22/08 11:40:00 10/22/08 21:54:00  high
VX0025 10/22/08 23:51:00 10/23/08 11:16:00  high
VX0026 10/23/08 12:28:00 10/24/08 11:09:00  high
VX0030 10/24/08 12:17:00 10/24/08 23:30:00  high
```

2 Three main objects: trajectories, map, and grid

2.1 Trajectories

Read trajectories; shorten to 3 days (optional):

```
> trajectories <- readtrajectories(Coords_file)
> trajectories <- shorten(trajectories, ndays = 3)
```

Randomly sample 1/2 of trajectories for this example (remove this line for production run).

```
> trajectories <- random(trajectories, fraction = 0.5)
```

2.2 Map

Define map [longitude (xlim) and latitude (ylim) arguments are optional).

```
> mp <- definemap("world", xlim = c(-110, -50), ylim = c(-60, 5))
```

If map database is `"world2"`, the longitudes have to be "unwrapped" (otherwise, leave unchanged, which is determined within `unwrap`).

```
> trajectories <- unwrap(trajectories, mp)
```

2.3 Grid

Define grid. The following line will divide the box containing trajectory endpoints (both latittude and longitude) into 40 even-sized boxes.

```
> xygrid <- definegrid(traj = trajectories, len = 40)
```

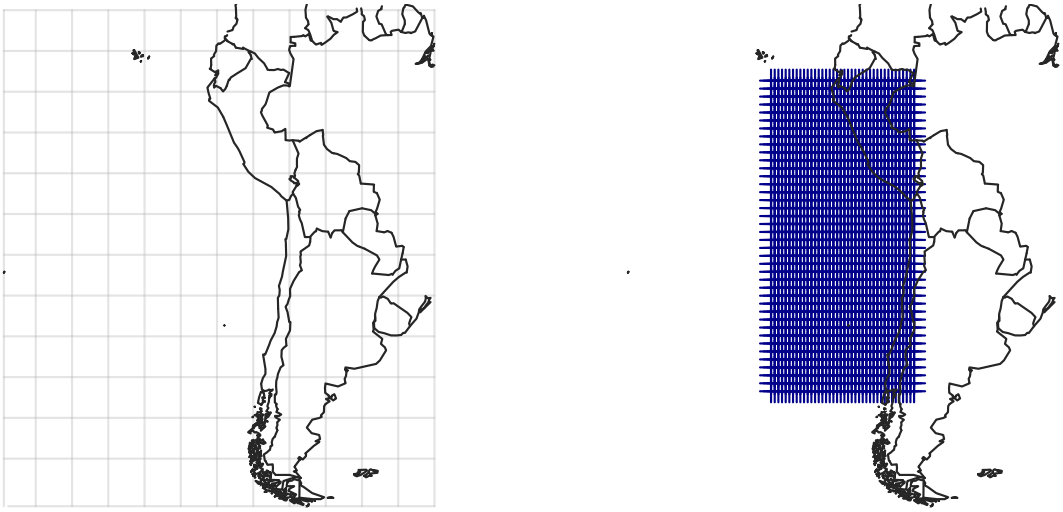
Alternatively, you can specify the grid coordinates directly (not run in this example).

```
> xygrid <- definegrid(longrid = seq(-95, 50, 5), latgrid = seq(35,
+     93, 3))
```

3 Evaluate map and grid

Look at the map boundaries and spacing of grid points overlayed on map; redefine if necessary.

```
> par(mfrow = c(1, 2), mar = rep(1, 4))
> showmap(mp, gridlines = TRUE)
> showmap(mp, xygrid)
```



4 Prepare the trajectories

Overlay trajectories on the grid [the last argument can be either `identity` to count number of trajectory points (default), or `unique` to count unique trajectories over each grid cell]:

```
> trajectories <- overlay(trajectories, xygrid, identity)
```

(See `reports/identity-unique/summary.pdf` for comparison between the two options.)

Read in group file and prepare trajectory object for visualization (intermediate step, call to `addfirst`, will add first diagnostic function to `trajectories`); also attach data to `trajectories` object. If new groups are desired, rerun from this point on (do not have to reload trajectories).

```
> groups(trajectories) <- readgroups(Group_file)
> trajectories <- addfirst(trajectories)
> trajectories <- prepareforvis(trajectories, xygrid)
```

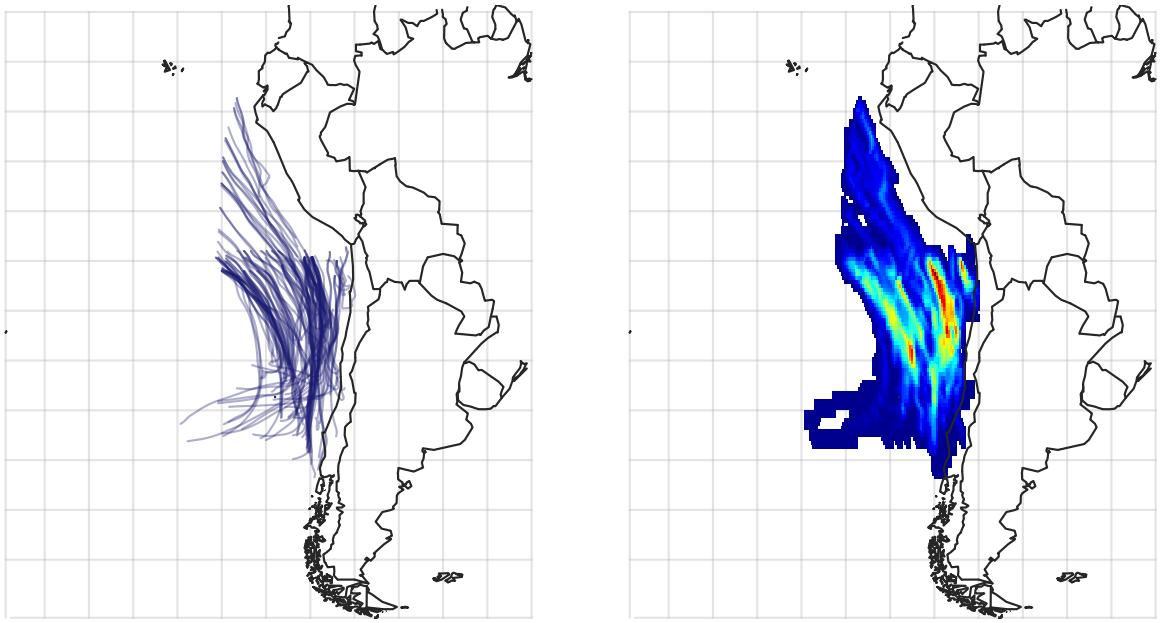
an additional argument, `colorvar`, can be passed to `add_diagnosefn`, which will color the trajectories. For instance, `sub(``.+_([0-9]+)$'',''\\1'',rownames(coords(trajectories)))` will color by altitude.

5 Plotting trajectories

5.1 Examples - VOCALS

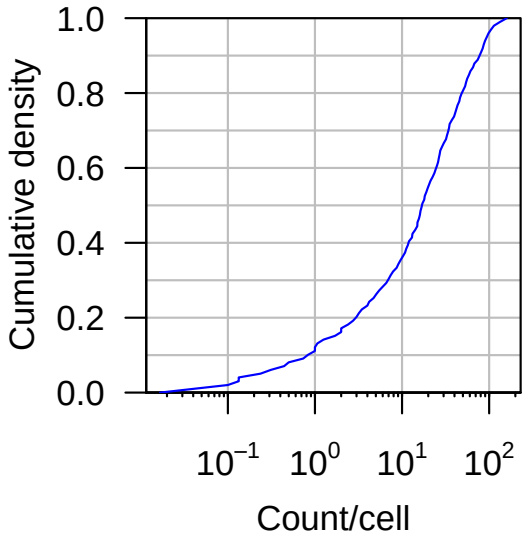
Show all trajectories (as 'spaghetti' and 'density'):

```
> par(mfrow = c(1, 2), mar = rep(1, 4))
> showmap(mp, trajectories, type = "spaghetti", groupindex = 0,
+     gridlines = TRUE)
> showmap(mp, trajectories, type = "density", groupindex = 0, gridlines = TRUE)
```



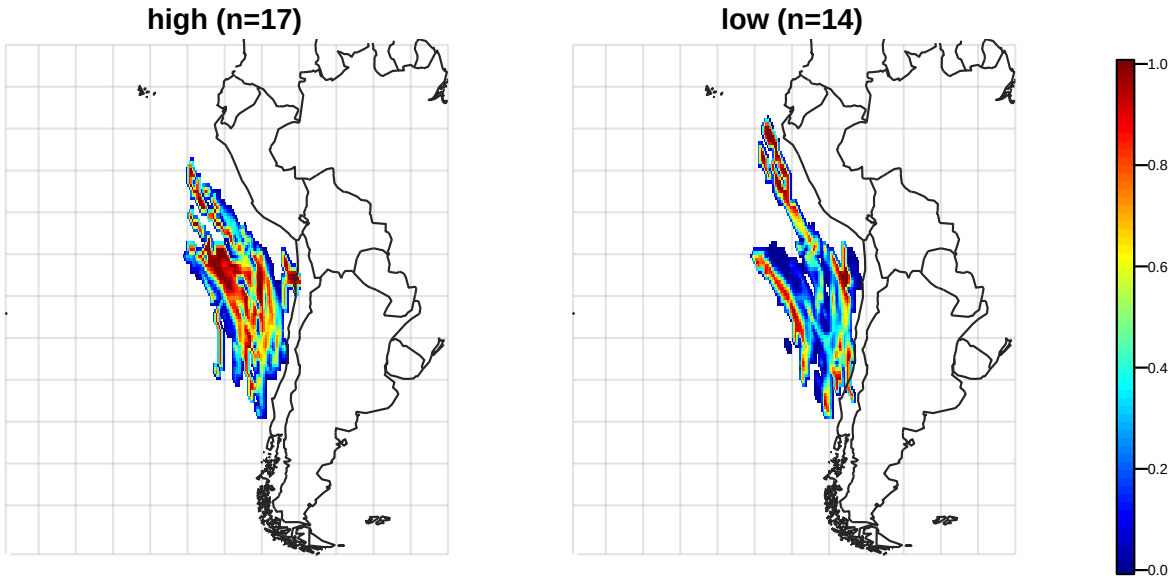
Next, visualize number of trajectories/ points per cell.

```
> par(mfrow = c(1, 1), mar = c(4.5, 4.5, 1.5, 1.5), mgp = c(2.5,
+     1, 0), pty = "s")
> cumuldensp(trajectories)
```



We will only include grid cells for which the number of trajectories/points (count/cell) are above 10, approximately (values <1 indicate cells in which weights (→ fraction of hour) were <1), so we pass the argument `threshold=0.4` to the `showmap()` function. The PSCF plot is created with the following code. Export with graphics desired device (e.g., `pdf()`, `png()`).

```
> ngr <- length(groups(trajectories))
> layout(matrix(1:(ngr + 1), nrow = 1), width = c(rep(5, ngr),
+     1))
> par(mar = c(1, 1, 1.5, 1), mgp = c(1, 1, 0), lend = 3, pty = "s")
> for (i in 1:ngr) {
+     showmap(mp, trajectories, threshold = 0.4, type = "pscf",
+         groupindex = i, gridlines = TRUE)
+     title(main = grpname(trajectories, i), cex.main = 1.2)
+ }
> addlegend(m1 = 2, m2 = 1.5, m3 = 2, m4 = 2, mgp = c(2, 0.5, 0),
+     cex.axis = 0.6)
```



5.2 Additional examples: shiptracks, other projections (not run)

We can also add ship tracks. Calculate it from the originating point for each of the back trajectories:

```
> shiptrack <- lapply(colnames(coords(trajectories))[2:1], function(x,
+     y) sapply(y[, x], `[`, 1), coords(trajectories))
```

Plot ship tracks. For an orthographic projection, we don't need x- and y-limits. To get rid of them, redefine the map without passing values to `xlim` and `ylim` parameters.

```
> mp <- definemap("world")
```

Make the plot:

```
> showmap(mp, shiptrack = shiptrack, projection = "orthographic",
+     orientation = c(90, 0, -12.5))
```

Map in stereographic projection:

```
> par(mfrow = c(1, 2), mar = rep(1, 4))
> showmap(mp, gridlines = TRUE)
> showmap(mp, xygrid)
```

PSCF map with shiptracks in stereographic projection:

```
> ngr <- length(groups(trajectories))
> layout(matrix(1:(ngr + 1), , nrow = 1), width = c(rep(5, ngr),
+     1))
> par(mar = c(1, 1, 1.5, 1), mgp = c(1, 1, 0), lend = 3, pty = "s")
> for (i in 1:ngr) {
+     showmap(mp, trajectories, shiptrack = shiptrack, type = "pscf",
```

```
+         gridlines = TRUE, groupindex = i, projection = "stereographic")
+     title(main = grpname(trajectories, i), cex.main = 1.2)
+ }
> addlegend(m1 = 2, m2 = 1.5, m3 = 2, m4 = 2, mgp = c(2, 0.5, 0),
+     cex.axis = 0.6)
```

5.3 The showmap() function

Summary of arguments to `showmap`:

Argument	Possible values
`mobj`	'Map' object (*required*)
`obj1`	'XYGrid' or 'Traj' object
`type`	'diagnose', 'spaghetti', 'density', or 'pscf' (character)
`gridlines`	TRUE or FALSE (logical)
`groupindex`	1,2,...n or 0 for 'spaghetti' or 'density' (integer)
`shiptrack`	list with longitude and latitude components (list)
`threshold`	exclude grid cells containing less than `threshold` quantile (percentile /100) of trajectory counts.
`...`	projection and parameters to be pased to `mapproject`

The 'Map' object is the only required argument. Not specifying a value for `projection` will give you a rectangular projection.

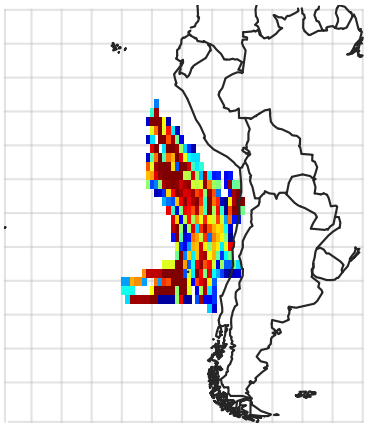
`showmap()` is intended to be an exploratory tool. Edit function `mpj()` in `functions/classdefs.r` if further customizations are desired.

6 Misc.

6.1 Image resolution

Increasing/decreasing image resolution using the `ninterp` argument to `showmap()` - compare with left PSCF figure - 'high' case. In this case I decreased the resolution to constrast the visual difference in appearance.

```
> showmap(mp, trajectories, type = "pscf", gridlines = TRUE, groupindex = 1,
+     ninterp = 30)
> title(main = grpname(trajectories, 1), cex.main = 1.2)
```



6.2 Data extraction for export/ customization

Use `extract()` on object `trajectories`. (You can also pass a `threshold` argument to `extract()`). Note: matrix resolution is defined by `xygrid` using `definegrid()`; `ninterp` is only used for controlling resolution for visualization using `showmap()`.

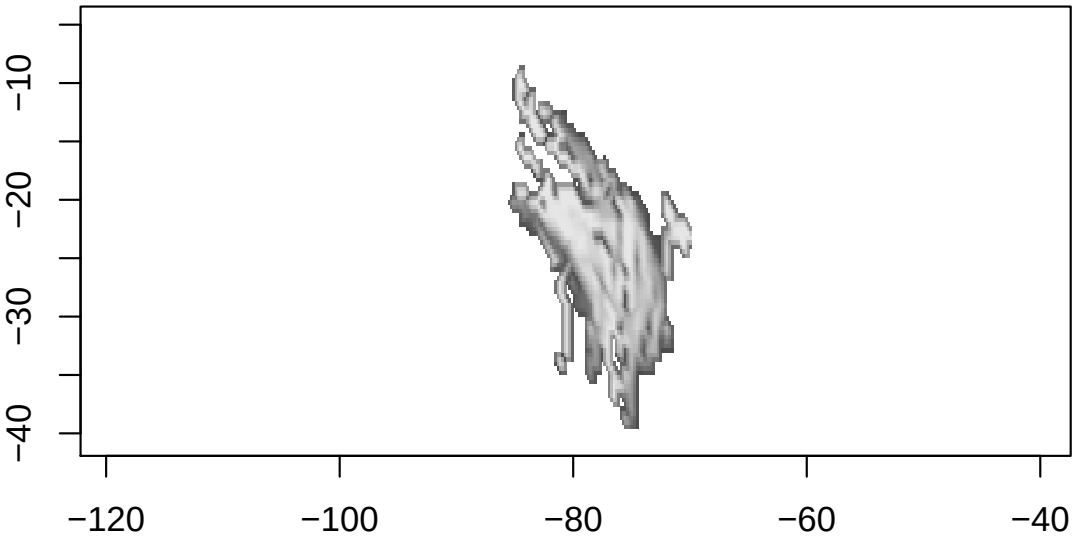
```
> output <- extract(trajectories, type = "pscf", groupindex = 1,
+     threshold = 0.4)
```

You can export the data using `write()`:

```
> write(output$x, file = "xvalues.txt", ncol = 1)
> write(output$y, file = "yvalues.txt", ncol = 1)
> write(t(output$z), file = "zvalues.txt", ncol = ncol(output$z))
```

Or plot it in R using `image()` (which is called internally by `showmap()`).

```
> image(output, col = grey.colors(64), asp = 1)
```


−10
−20
−30
−40
−120
−100
−80
−60
−40