

aermod: an R interface to AERMOD

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1 Working with AERMOD output

1.1 Importing binary files

With the `aermod` package, we can directly read “unformatted” (binary) output created by AERMOD. This is convenient and efficient, avoiding the need to parse “printer-friendly” AERMOD output, and retains the full 64-bit precision of the results. To illustrate, we’ll load a sample file that comes with the `aermod` package:

```
> library(aermod)
> filename <- system.file("extdata", "AERMOD", "output",
  "aertest-1h.bin", package = "aermod")
> records <- read.unformatted(filename, n.receptors = 144)
> length(records)
[1] 96
```

This file contains 1-hour averages computed over four days, so there are 96 records in total. The file was generated by running AERMOD 11103, using the “aertest.inp” scenario packaged with the AERMOD source code; one additional line was added to the control file to generate so-called “POSTFILE” output (see the AERMOD User’s Guide for details). Each record contains the following:

```
> options(max.print = 25, digits = 2)
> records[[1]]
$date
[1] "1988-03-01"

$hour
[1] 1

$avg.period
[1] 1

$group.id
[1] "ALL"

$concentrations
[1] 0.00025 0.00259 0.00448 0.01366 0.00025 0.00259 0.00448
```

```
[8] 0.01366 0.00025 0.00259 0.00448 0.01366 0.00025 0.00259
[15] 0.00448 0.01366 0.00025 0.00259 0.00448 0.01366 0.00025
[22] 0.00259 0.00448 0.01366 0.00025
[ reached getOption("max.print") -- omitted 119 entries ]]
```

We can reformat the predicted receptor concentrations as a matrix with just a few lines of code:

```
> conc.list <- lapply(records, function(x) x$concentrations)
> conc.mat <- do.call(cbind, conc.list)
> conc.mat[, 1:6]
      [,1] [,2] [,3] [,4] [,5] [,6]
[1,] 0.00025 0.0041 0.014 0.20 0.036 0.024
[2,] 0.00259 0.0124 0.043 0.38 0.098 0.054
[3,] 0.00448 0.0151 0.060 0.58 0.132 0.077
[4,] 0.01366 0.0314 0.150 1.18 0.340 0.199
[ reached getOption("max.print") -- omitted 140 rows ]]
> dim(conc.mat)
[1] 144 96
```

Here there are 144 rows, one for each receptor; and 96 columns, one for each averaging period. Above, we show only the first few columns.

1.2 Plotting receptor concentrations

We can compute and plot summary statistics quite easily. First we compute summary statistics for the data, including running averages:

```
> avg <- function(x, n) filter(x, rep(1/n, n), sides = 1)
> runmax.8 <- function(x) max(avg(x, 8), na.rm = TRUE)
> runmax.24 <- function(x) max(avg(x, 24), na.rm = TRUE)
> COL <- 1
> results <- data.frame(mean = apply(conc.mat, COL,
  mean), max.1h = apply(conc.mat, COL, max),
  runmax.8h = apply(conc.mat, COL, runmax.8),
  runmax.24h = apply(conc.mat, COL, runmax.24),
  sd = apply(conc.mat, COL, sd))
> quantile(results$mean, seq(0, 1, by = 0.1))
 0%   10%   20%   30%   40%   50%   60%   70%
0.085 0.132 0.276 0.363 0.425 0.524 0.631 0.903
 80%   90%  100%
1.779 6.354 25.968
```

Next we recreate the polar grid to which these receptors correspond.

```
> grd <- grid.polar(c(175, 350, 500, 1000), 36,
  10, 10)
> grd <- as.data.frame(grd)
```

Finally we bind them together and plot the results:

```
> library(ggplot2)
> p <- ggplot(data.frame(grd, results), aes(x, y)) +
  coord_equal()
> p.mean <- p + geom_point(aes(color = mean, size = mean,
  alpha = mean))
> print(p.mean)
```

