

LaF

A package for processing large ASCII files

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1 Introduction

LaF is a R package for reading large ASCII files. It offers some functionality that is missing from the regular R routines for processing ASCII files. First of all, it is optimised for speed. Especially reading fixed width files is very slow with the regular R routine `read.fwf`. However, since it is optimised for speed some of the flexibility of the regular routines is lost. Secondly, it offers random access: only those rows and columns are read that are needed. With the regular routines one always has to read all columns.

The problem with big files is that they do not fit into memory. One could consider this even to be the definition of ‘big’. To comfortably work with data in R the data set needs to fit multiple (~ 3) times into memory. There are roughly two methods for working with data that doesn’t fit into memory. The first is to read the data in blocks that do fit into memory process each of these block and merge the results. More on this can be found in section 3. The second is to read only that part of the data into memory which is needed for the calculation at hand hoping that that subset does fit into memory. For example to crosstabulate two variables one only needs these two variables. As most datasets contain dozens of variables this can easily reduce the memory needed for the operation by a factor of ten. More on this in section 4.

Why ASCII? Why not use a binary format like `ff` and similar packages do? True, binary storage allows for much faster access since the conversion from ASCII to binary format is not needed and data can often be stored much more compact. The main reason is portability. Almost every program designed for data processing can read ASCII files. And even if one wants to use a package like `ff`, the source files are often ASCII files and first need to be converted to `ff` format. **LaF** can also speed up this last process.

2 Opening a file

2.1 Column types

LaF currently supports the following column types

double Fields containing floating point numbers. Scientific notation (e.g. 1.9E-16) is not supported. The character used for the decimal mark can be specified using the **dec** option of the functions used to open files.

integer Fields containing positive or negative integer numbers (e.g. 42, -100)

categorical Categorical fields are treated as character fields except that a table is built mapping all observed values to integers. A factor vector is returned in R when this type is used. The levels can be read and set using the **levels** method.

string Character fields such as postcodes, identification numbers.

2.2 Fixed width files

In fixed width files columns are defined by character positions in the files. For example, the first seven characters of each line belong to the first column, the next two characters belong to the second, etc. Each line therefore has the same number of characters. This is also a disadvantage of the format. If there is a column with variable string lengths, the column has to be wide enough to accomodate the widest field. The main advantage of the format is that reading in large files (and especially random access) can be very efficient as the positions of rows and columns can be calculated.

Fixed width files can be openen using the function **laf_open_fwf**. In order to open a file the following options can be specified:

filename name of the file to be opened.

column_types Character vector containing the types of data in each of the columns. Valid types are: double, integer, categorical and string.

column_widths Numeric vector containing the width in number of character of each of the columns.

column_names (optional) Optional character vector containing the names of the columns. The default names are 'V1', 'V2', etc.

dec (optional) Optional character specifying the decimal mark. The default value is '.'.

Suppose the following data is stored in the file ‘file.fwf’ in the current working directory (showing only the first five lines):

```
192382F7030VZ 14 195.67
712067F8375UP 38 776.95
 61791F4364IB107 12.24
263536M2925YP 15 139.50
100905M7196H0 27 364.40
```

Then this file can be opened using the following command:

```
> dat <- laf_open_fwf(filename = "file.fwf",
+   column_types = c("integer", "categorical",
+   "string", "integer", "double"), column_names = c("id",
+   "gender", "postcode", "age", "income"),
+   column_widths = c(6, 1, 6, 3, 8))
```

`dat` is now a `laf` object. Data can be extracted from this object using the commands described in sections~3 and~4. For example, to read all data in the file one can use the following command:

```
> alldata <- dat[, ]
```

2.3 Comma separated files

In comma separated files each line contains a row of data, the columns are separated using a separator character which is usually a comma although other separator characters are also used (e.g. the ‘;’ is often used in Europe where the comma is often used as the decimal separator). It is often used format. The disadvantage compared to the fixed width format is that the positions of columns and rows in the file can not be calculated. Therefore, a program reading a comma separated file has to scan through the entire file to find a certain row or column making random access much slower than with fixed width files.

A comma separated file for the `LaF` package has to observe the following rules some of which slightly deviate from the ‘official’ rules of comma separated files:

- The first row can not contain the column names. These should be specified using the option `column_names` of the function `laf_open_csv`. The first line in the file is treated as the first data row and the columns in this line should be of the correct type.
- Quotes are treated slightly different from the way they are normally treated in csv files. Only double quotes are accepted. Everything inside double quotes is considered part of the field except newline characters and double quotes. Double quotes in text fields are therefore not possible. Below are a few examples of how quotes are interpreted:

- 12345 = 12345
- "12345" = 12345
- "123"45 = 12345
- "123""45" = 123"45"
- "123\n45" = ERROR
- 12"345" = 12"345"

- Each line in the file should contain exactly one row of data. Normally line breaks should be possible inside quoted columns. In order to keep the code as fast as possible, this is not the case in the **LaF** package.

Comma separated files can be opened using the function `laf_open_csv`. This function accepts the following arguments:

filename name of the file to be opened.

column_types Character vector containing the types of data in each of the columns. Valid types are: double, integer, categorical and string.

column_names (optional) Optional character vector containing the names of the columns. The default names are 'V1', 'V2', etc.

sep (optional) Optional character specifying separator mark used between the columns. The default value is ','.

dec (optional) Optional character specifying the decimal mark. The default value is '.'.

Suppose the following data is stored in the file 'file.csv' in the current working directory (showing only the first five lines):

```
192382,F,7030VZ,14,195.670000
712067,F,8375UP,38,776.950000
61791,F,4364IB,107,12.240000
263536,M,2925YP,15,139.500000
100905,M,7196H0,27,364.400000
```

Then this file can be opened using the following command:

```
> dat <- laf_open_csv(filename = "file.csv",
+   column_types = c("integer", "categorical",
+   "string", "integer", "double"), column_names = c("id",
+   "gender", "postcode", "age", "income"))
```

`dat` is now a **laf** object. Data can be extracted from this object using the commands described in sections 3 and 4. For example, to read all data in the file one can use the following command:

```
> alldata <- dat[, ]
```

3 Blockwise processing

Blockwise processing of a file usually has the following structure:

1. Go to the beginning of the file
2. Read a block of data
3. Perform calculations on this block perhaps using results from the previous block.
4. Store results
5. Repeat 2–4 until all data has been processed.
6. If necessary combine the results of all the blocks.

In order to go to a specific position in the file **LaF** offers two methods: **begin** and **goto**. The first method simply goes to the beginning of the file while the second goes to the specified line. Assume, a **laf** object named **dat** has been created (see section~2 for this). The only argument needed by **begin** is the **laf** object:

```
> begin(dat)
```

For **goto** also the line number needs to be specified. The following command sets the filepointer at the beginning of line 1000. The next call to **next_block** (see below) will therefore return as first row the data belonging in line 1000 of the file.

```
> goto(dat, 1000)
```

Blocks of data can be read using **next_block**. The first argument needs to be the reference to the file (the **laf** object); other arguments are optional. By default all columns and 5000 lines are read:

```
> d <- next_block(dat)
> nrow(d)
```

```
[1] 5000
```

The number of lines can be specified using the **nrows** argument and the columns that should be read can be specified using the **columns** argument. The following command reads 100 lines and the first and third column.

```
> d <- next_block(dat, columns = c(1, 3), nrows = 100)
> dim(d)
```

```
[1] 100    2
```

If possible the use of the `columns` argument is advised. This can significantly speed up the processing of the file. First of all, the amount of data that needs to be transferred to R is much smaller. Second, the strings in the unread columns do not need to be converted to numerical values.

When the end of the file is reached `next_block` returns a `data.frame` with zero rows. This can be used to detect the end of file. The following example shows how `begin` and `next_block` can be used to calculate the number of elements equal to 2 in the second column.

```
> n <- 0
> begin(dat)
> while (TRUE) {
+   d <- next_block(dat, 2)
+   n <- n + sum(d$gender == "M")
+   if (nrow(d) == 0)
+     break
+ }
> print(n)
```

```
[1] 4992
```

Since processing a file in this way is such a common task, the method `process_blocks` has been defined that automates this and is faster. This method accepts as its first argument a `laf` object. The second argument should be the function that should be applied to each of the blocks. This function should accept as its first argument the data blocks. The last time the function is called it receives a `data.frame` with zero rows. This can be used to do some end calculations. The second argument of the function is the result of the previous function call. The first time the function is called the second argument had the value `NULL`. This can be used to perform initialisation. Additional arguments to `process_blocks` are passed on to the function. The previous example can be translated into:

```
> count <- function(d, prev) {
+   if (is.null(prev))
+     prev <- 0
+   return(prev + sum(d$gender == "M"))
+ }
> (n <- process_blocks(dat, count))
```

```
[1] 4992
```

Using `process_blocks` is faster than using `next_block` repeatedly since the `data.frame` containing the data that is read in, is destroyed and created every iteration, while in `process_blocks` this `data.frame` is created only once.

Below is an example that calculates the average of the third column of the file and illustrates initialisation and finalisation (note this is not how you will want to calculate the average over a column in a large file). Since only the third column of the file is needed for this calculation, the `columns` option is used which makes the calculation much faster.

```
> ave <- function(d, prev) {
+   if (is.null(prev)) {
+     prev <- c(sum = 0, n = 0)
+   }
+   if (nrow(d) == 0) {
+     return(as.numeric(prev[1]/prev[2]))
+   }
+   result <- prev + c(sum(d$income), nrow(d))
+   return(result)
+ }
> (n <- process_blocks(dat, ave, columns = 5))

[1] 1004.474
```

4 Selecting subsets

An other common way of handling large files is to only read in the data that is needed for the operation at hand. This is feasible when such a subset of the data does fit into memory. For this, selections can be performed on a `laf` object using the same methods one would use for a regular `data.frame`. The code below shows several different examples:

```
> result <- dat[1:10, ]
> result <- dat[, 2]
> result <- dat[1:10, 2]
```

Indexing a `laf` object always results in a `data.frame`. For example, the second and last example would have resulted in a vector when applied to a `data.frame`, while in the examples above a `data.frame` with one column is returned.

Using the `$` and `[[` operators columns can be selected from the `laf` object. The result is an object of type `laf_column` which is a subclass of `laf`. It is a `laf` object with a field containing the column number. To get the data inside these columns indexing can be used as is shown in the following examples. In the first example the records are selected from the file for which the age is higher than 65:

```
> result <- dat[dat$age[] > 65, ]
```

The same can be done using the column number

```
> result <- dat[dat[[4]][ ] > 65, ]  
or  
> result <- dat[dat[, 3] > 65, ]  
or  
> result <- dat[dat[, "age"] > 65, ]
```