

# Reading Data

There are a few principal functions reading data into R.

- `read.table`, `read.csv`, for reading tabular data
- `readLines`, for reading lines of a text file
- `source`, for reading in R code files (inverse of `dump`)
- `dget`, for reading in R code files (inverse of `dput`)
- `load`, for reading in saved workspaces
- `unserialize`, for reading single R objects in binary form

# Writing Data

There are analogous functions for writing data to files

- `write.table`
- `writeln`
- `dump`
- `dput`
- `save`
- `serialize`

# Reading Data Files with `read.table`

The `read.table` function is one of the most commonly used functions for reading data. It has a few important arguments:

- `file`, the name of a file, or a connection
- `header`, logical indicating if the file has a header line
- `sep`, a string indicating how the columns are separated
- `colClasses`, a character vector indicating the class of each column in the dataset
- `nrows`, the number of rows in the dataset
- `comment.char`, a character string indicating the comment character
- `skip`, the number of lines to skip from the beginning
- `stringsAsFactors`, should character variables be coded as factors?

# read.table

For small to moderately sized datasets, you can usually call `read.table` without specifying any other arguments

```
data <- read.table("foo.txt")
```

R will automatically

- skip lines that begin with a `#`
- figure out how many rows there are (and how much memory needs to be allocated)
- figure what type of variable is in each column of the table Telling R all these things directly makes R run faster and more efficiently.
- `read.csv` is identical to `read.table` except that the default separator is a comma.