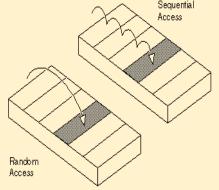
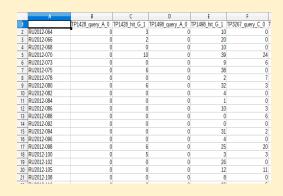
# Lecture 5: Reading and writing data

CPSC 499, Fall 2018

### What is a file?



- Data recorded in a storage medium, such as a hard disk, flash drive, or DVD
  - In contrast to objects in the R environment, which are in the computer's RAM
- Always stored as a linear set of bytes (byte = 8 bits, and a bit is a 0 or 1)
- A file has a beginning and an end, and is usually read or written linearly from beginning to end (sequential access)
- It is also possible for a file to be random access, meaning you can jump to any point in the file. We will do some random access later with Bioconductor.



#### Text files

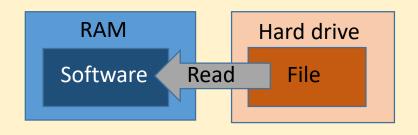
- All the files that we will read and write in R are text files, including spreadsheet-like data such as CSV (comma-separated value) or tab-delimited text
- Text-based formats are generally preferred by scientists
  - Don't require proprietary software to open them
  - Don't require advanced programming skill to process them
  - Good for long-term preservation of data

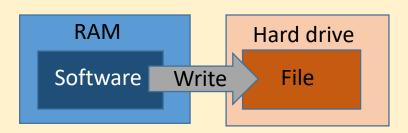
#### Format of text files

- ASCII is the old way of storing text, with one byte per character
- Unicode allows multiple bytes per character
  - UTF-8 is the most common Unicode file encoding on Mac and Linux
  - Windows has its own encodings
- For ordinary letters and numbers, Unicode is identical to ASCII and to the encoding doesn't matter

#### File connections

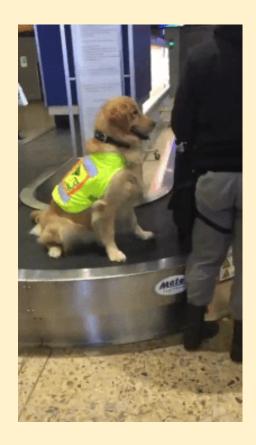
- When a piece of software accesses a file, it first opens a connection to the file
- Every connection has a mode:
  - Read, write, or append
  - Text or binary
- When the software is done with the file, it closes the connection
- You don't have to get to the end of the file to close the connection





# Looping through a file in R

- If we get to the end of a file and run readLines again, it gives a character vector of length zero
- We can use the length of this vector as a test for whether the end of the file has been reached
- Use a while loop to keep reading and processing chunks until we get to the end of the file.



#### Mini exercise

- Use file to open a reading connection to "Illumina\_seq\_example.fastq"
- Use readLines to preview the file a few lines at a time (some multiple of four)
- Use file to open a writing connection to a different text file
- Write just the sequences to the new file (second line out of every four) with writeLines
- Close both connections with close

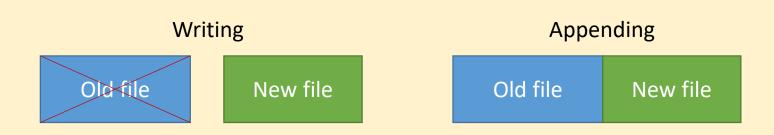


#### File compression

- File is represented in a smaller number of bytes, at the expense of some processing time to compress or uncompress it
- Common compression formats
  - ZIP: mostly just on Windows. Allows multiple files.
  - GZIP: (GNU zip) open-source, very common on Mac and Linux
  - BZIP2: also open-source
  - See ?connections for formats supported in R
- Compressed files can be accessed from beginning to end just like any other file, only with the added step that you compress or uncompress as you go.

### Writing vs. appending

- Do you want to overwrite a file, or write more data to the end of it?
- When you open a connection in mode 'w' (write), if the file exists it will be overwritten
- When you open a connection in mode 'a' (append),
  if the file exists you will add data to the end of it. If
  not you will start a new file.



# Most R functions for reading and writing data will open and close the connections for you

#### From the readlines documentation:

#### **Details**

If the con is a character string, the function calls <u>file</u> to obtain a file connection which is opened for the duration of the function call. This can be a compressed file.

If the connection is open it is read from its current position. If it is not open, it is opened in "rt" mode for the duration of the call and then closed again.

 So basically, instead of passing readLines an open connection, you can pass it the file name if you want to read the file from the beginning.

# So why bother learning to open and close connections?

- Useful if the file is too large to read into memory all at once
  - NGS sequence and alignment files can be many gigabytes
  - Read a piece of the file into RAM, use it for some computations, then discard it
- Useful if the file contains a mix of data types that you may want to read with different functions
  - Alignment and variant files have a header at the top that you might want to import with readLines, followed by tabular data you might want to import with read.table.

### Reading delimited text

 Can follow a call to readLines with a call to strsplit

- For most tabular data, where columns are variables and rows are observations, we want to use the read.table family of functions
  - read.table: space delimiter (can set it to anything though)
  - read.csv: comma delimiter
  - read.delim: tab delimiter

#### Output of read.table

- An object of a class called data frame
- A data frame is a list of vectors where all vectors must be the same length, but not necessarily the same class
- Each vector (column) should usually represent some variable that was measured
- Each row (each element of each vector) should usually represent one observation

#### Subsetting a data frame

- Why did all the spaces get taken out of the column names? It is so they can be used as object names.
  - Any characters that are operators in R are also removed.
- We can use the dollar sign to extract one column
  - mytable\$Marker.name
- We can get one column with double square brackets, like a list (useful if looping through columns)
  - mytable[[1]]
  - mytable[["Marker.name"]]
- We can use single square brackets with a comma to specify row and column
  - mytable[1:10, 1:4]

# stringsAsFactors

- This is an argument to all of the read.table functions that I almost always set to FALSE (default TRUE)
- If I am going to use a column as a categorical variable in linear regression, then it makes sense to have it as a factor
- For most bioinformatics applications, it is much better to keep a string as a string (gene names, DNA sequences, etc.)
- Sometimes it works to treat a factor as a string (e.g. ==
   ), but sometimes results are unexpected (e.g. Sort,
   indexing)

### Other read. table arguments

- header: does the file have column headers? (if not, first row is considered data)
- sep: what character(s) separate entries within a row?
  - Space: "
  - Comma: ","
  - Tab: "\t"
- row.names: 1 if the first column contains row names. Can also be a vector of row names themselves, or name of column with row names

### Other read. table arguments

- col. names: column names, if not taken from the header
- na.strings: how to recognize missing values in character columns
  - Blanks are considered missing data in numeric but not character columns, by default
- colclasses: for specifying what class each column should be, in case R's best guess is incorrect
  - Example: experimental replications may be numbered, but you want to treat them as a factor
- **skip**: number of lines to skip before reading table (e.g. if the file has header lines in addition to col names)

#### Mini-exercise

- Make a call to read.table to correctly import "lecture5\_germplasm\_example.txt"
- Give colclasses a vector with the strings "character", "integer", and "Date" as appropriate
- Have it import "no data" as NA

#### write.table

- Take a data frame and export it to a file (or open connection)
- Many arguments similar to read.table
- write.csv ensures that the file can be opened in MS Excel

# Differences between read.table and write.table

- First argument is data frame, second is file name
- To include column names in the file, use
   col.names = TRUE (not header)
- row.names = TRUE to include row names in output (always first column)
- Use na argument to indicate the string to print for missing data (not na.strings)
- quote: TRUE or FALSE to indicate whether strings should be in quotes

#### Mini-exercise

- Use write.csv to write the germplasm data frame that you imported out to a CSV
- Open it first with Notepad to see what it looks like
- Then open it in MS Excel
- Did Excel change anything?

# Other functions for working with files

- For lots of detailed information, see "R Data Import/Export" on CRAN.
- read. fwf: if file is fixed-width rather than delimited
- scan: faster than read.table if you need to read lots of data that are all one class (less user-friendly)
- cat, write: For writing delimited text straight to file without column and row names
- tempfile: for making temporary files, automatically deleted when computer is shut down

# Saving objects in your R environment

- save.image can write your whole R environment to an .RData file so you can reload it quickly later
- RStudio saves a file called ".RData" by default, but you can give files names like "germplasmWorkOct31.RData" etc.
- save is like save image except you can specify which objects are saved (handy for large datasets)
- These files can't be opened by software other than R
- load is used to import these files into the R environment. Faster than reading data from text files.

(Extra material depending on time)

#### More on Unicode

- Includes
  - Characters from many languages worldwide
  - Characters from ancient languages
  - Symbols
  - Emojis
- More characters are being added every year
  - Codes for existing characters stay the same
- The first 128 characters are the same as ASCII
- If a character doesn't display, it means you are using a font that doesn't include that character

## Codepoints in Unicode

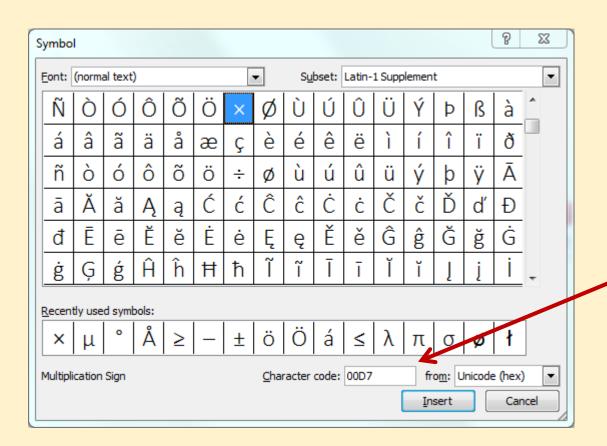
Codepoint	Rune	Name							
16A0	۳	FEHU FEOH FE F							
16A1	۳	V							
16A2	n	URUZ UR U							
16A3	A	YR							
16A4	A	Υ							
16A5	n	W							
16A6	Þ	THURISAZ THURS THORN							
16A7	Þ	ETH							
16A8	F	ANSUZ A							
16A9	۴	OS O							
16AA	F	AC A							
16AB	F	AESC							
16AC	*	LONG-BRANCH-OSS O							
16AD	ŧ	SHORT-TWIG-OSS O							
16AE	4	0							
16AF	*	OE							
16B0	<b>‡</b>	ON							
16B1	R	RAIDO RAD REID R							
16B2	¢	KAUNA							
16B3	k	CEN							

 If you look up Unicode characters, you'll often see four digits for the codepoint

- These are in hexadecimal
  - 0123456789ABCDEF
  - Decimal is 0123456789
- Two hex digits = one byte
  - $16^2 = 2^8$

## Looking up codepoints

"Insert symbol" dialogue in MS Office



## Looking up codepoints

- Wikipedia has lots of Unicode tables
- www.unicode.org/charts has everything

Block [edit]																
Mathematical Operators <sup>[1]</sup> Official Unicode Consortium code chart   (PDF)																
	0	1	2	3	4	5	6	7	8	9	A	В	С	D	Е	F
U+220x	A	С	а	3	∄	Ø	Δ	▽	€	∉	€	∍	∌	э	•	П
U+221x	Ш	Σ	-	Ŧ	÷	/	\	*	٥		√	∛	∜	α	00	L
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U+223x	∰	f	∳	∳	:	::	:	::	-	-:	H	÷	~	~	2	~
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U+227x	≰	≱	\$	≳	\$	≵	<b>≶</b>	≷	*	≹	<	>	<b>«</b>	>	≾	≿
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3	<b>T</b>		<b>Г</b>	∑ 03A3	γ 03B3	<b>σ</b>	Υ 03D3	<b>a</b>	<b>j</b>	
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5	0375	0385	E 0395	Y 03A5	<b>E</b>	<b>U</b>	ф 03D5	q	€ 03F5	
6	<b>1</b>	A 0386	Z 0396	Ф 03A6	<u>د</u>	φ 03C6	<b>W</b>	<b>b</b>	<b>Э</b>	

### Using Unicode in R

- If you are importing a file with special characters, you need to check the encoding to make sure they are read properly
- To manually put a character into a text string, type
   \u and then the four digits
- "jalape\u00F1o" = jalapeño
- Some characters have five digits and can't be used with the R base installation