CATECATECATECATECA	
ATGCATGCATGCATGCATGCA'	
TGCATGCATGCATGGCATGCA	
"GCATGCATGCATGCATGC∤	
CATGCATGCATGCATGCA	
<b>FGCATGCACTGCATGCAT</b> 6	wh
TICATGCCATGCAATGCAT. LA	TGCATELAT
<b>TGCATGCATGCATGCATG</b>	CATGCATC
SCATGCAGGTTGCATGC	ATGCATG
<b>`GCATGCATGC</b> ATGCAT	GCATGCALGLATGCATGCATGC
ATGCATGCATGCATGC	GCATGCATGCATCGCATGCATCGCA
<b>FGCATGCA</b> TGCATGCAT	GCATGCATGCATGCATGCATGCATG
(GCATGCAATGCATGCAT	GCATGCATGCATGCATGCATGCATG
.TGCATGCATGCATGCATGCAT	GCATGCATGCATGCATGCATGCATG
ST SCATGCATGCATGCA	TGCATGCATGCATGCATGCATGCAT
AGTTGCATGCATGCAT	CONTROCATECCATECATECATECATECAT
IGC * TO COTGCA	ATECATECATECATECATECAT
ADE STADE.	CATGCATGCA"
LATCE	[ATGCATAA/
a161	GCATGCAT"
67	GC/
	Т



# Genetic Biversity: Analysis WEEEPEREZED ## 2 Friday 25. June 2021

CC CAR CONTRACTOR

Eidgenössische Technische Hochschule Zürich Swiss Federal Institute of Technology Zurich

### **GDA** > Warm Up > **RepRes**







25.06.21 | GDA21 | JCW





"Application with a GUI are convenient to use but difficult to document and reproduce".

Do you agree or diagree with this statement and can you explain why?



GUI based applications are often balckboxes and it is often not clear what (default) parameters or settings have been used.

# DNA barcoding and metabarcoding of standardized samples reveal patterns of marine benthic diversity

Matthieu Leray and Nancy Knowlton<sup>1</sup>

#### VI. Data Analysis

**A. DNA Barcoding.** Forward and reverse sequences were assembled, checked for stop codons or frame shifts, and edited in Geneious (Biomatters). Our dataset comprised a diversity of taxonomic

The vertebrate mtDNA code differs from the "Universal" code.

- AUA and AUG are both Met codons
- UGA codes for Trp and not a Stop codon
- AGA and AGG codons are read as Stops instead of Arg

Slightly different mtDNA codes are found in Drosophila and other invertebrate groups.

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#### **Material and Methods**

In a first step, all paired-end raw reads were successfully merged using FLASh (version 1.2.9, Magoc and Salzberg 2011) with minimum overlap of 5nt and maximal mismatch ration of 0.8.

#### **Supplementary Data**

```
## (a) Merging overlapping paired-end reads
# -v Version (1.2.9)
# -m minimum overlap (default 10bp)
# -x max mismatch ration (default 0.25)
flash -m 5 -x 0.8 random_1000_R1.fq random_1000_R2.fq -o
merged | tee flash.log
```

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You are part of the Covid broadcast team and you are responsible for the **daily statistics**. All laboratories conducting Covid testing have to send daily reports. It is your duty to collect these reports. The labs are using standardised CSV files. At the end of a day you have hundreds of CSV files and you need to add them to your existing table. Your team-leader recommends to use the spreadsheet editor (e.g. Microsoft Excel) to store the data because he already has create a summary report template. What do you think about it?



#### The Guardian

# CovidNews: how Excel may have caused loss of 16,000 test results in England

Public Health England data error blamed on limitations of Microsoft spreadsheet

One lab had sent its daily test report to PHE (Public Health England) in the form of a **CSV file** – the simplest possible database format, just a list of values separated by commas. That report was then **loaded into Microsoft Excel**, and the new tests at the bottom were added to the main database.

But while CSV files can be any size, Microsoft Excel files can only be 1,048,576 rows long – or, in older versions which PHE may have still been using, a mere 65,536. When a CSV file longer than that is opened, the bottom rows get cut off and are no longer displayed. That means that, once the lab had performed more than a million tests, it was only a matter of time before its reports failed to be read by PHE.

Alex Hern UK technology editor

@alexhern
Tue 6 Oct 2020 08.21 BST

Microsoft's spreadsheet software is one of the world's most popular business tools, but it is regularly implicated in errors which can be costly, or even dangerous, because of the ease with which it can be used in situations it was not designed for.

In 2013, an Excel error at JPMorgan masked the loss of almost \$6bn (£4.6bn), after a cell mistakenly divided by the sum of two interest rates, rather than the average. The news led James Kwak, a professor of law at the University of Connecticut, to warn that Excel is "incredibly fragile".

"There is no way to trace where your data comes from, there's no audit trail (so you can overtype numbers and not know it), and there's no easy way to test spreadsheets, for starters. The biggest problem is that anyone can create Excel spreadsheets – badly. Because it's so easy to use, the creation of even important spreadsheets is not restricted to people who understand programming and do it in a methodical, well-documented way," Kwak wrote.

Errors from the spreadsheet software have even changed the very foundations of human genetics. The names of 27 genes have been changed over the past year by the Human Gene Nomenclature Committee, after Microsoft's program continually misformatted them. The genes SEPT1 and MARCH1, for instance, have been changed to SEPTIN1 and MARCHF1 after they were repeatedly turned into dates, while symbols that were common words have been altered so that grammar tools didn't autocorrect them: WARS is now WARS1, for instance.



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Alex Hern UK technology editor

♥ @alexhern Tue 6 Oct 2020 08.21 BST





# What can you do to increase reproducibility of your R script(s)?

### **GDA** > Warm Up > **RepRes**

### Built-in Help: Example for RStudio

- 1 MV<-get\_manifests(Data,blocks)¬
- 2 check\_MV<-test\_manifest\_scaling(MV,specs\$scaling)¬</pre>
- 3 gens<-get\_generals(MV,path\_matrix)-</pre>
- 4 names(blocks)<-gens\$lvs\_names¬</pre>
- 5 block\_sizes<-lengths(blocks)-</pre>
- 6 blockinds<-indexify(blocks)-</pre>

Show syntax highlighting in console input

- 1 MV<-get\_manifests(Data,blocks)
- 2 check\_MV<-test\_manifest\_scaling(MV,specs\$scaling)</pre>
- 3 gens<-get\_generals(MV,path\_matrix)</pre>
- 4 names(blocks)<-gens\$lvs\_names</pre>
- 5 block\_sizes<-lengths(blocks)</pre>
- 6 blockinds<-indexify(blocks)</pre>

Reformat Code 企業A

1 MV <- get\_manifests(Data, blocks)
2 check\_MV <- test\_manifest\_scaling(MV, specs\$scaling)</pre>

- 3 gens <- get\_generals(MV, path\_matrix)</pre>
- 4 names(blocks) <- gens\$lvs\_names
- 5 block\_sizes <- lengths(blocks)</pre>
- 6 blockinds <- indexify(blocks)</pre>

#### Structure and comment your script



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Is it possible to make "random" processes reproducible? In other words, what can I do to make random objects reproducible for example in R?

> sample(1:100, 3, replace = TRUE)
# 55 28 33



```
# Generate random number(s)
> sample(1:100, 3, replace = TRUE)
# 55 28 33
> sample(1:100, 3, replace = TRUE)
# 34 92 26
```

```
# Repeatable Random Numbers
> set.seed(210625)
> sample(1:100, 3, replace = TRUE)
[1] 71 51 88
```

### Non-Parametric Resampling

```
bootstrap(data, mean)
```

Call: bootstrap(data = CLEC, statistic = mean, seed = 19) Replications: 10000

```
Summary Statistics:

Observed SE Mean Bias

mean 16.50913 3.96866 16.54073 0.03160109
```

```
bootstrap(data, mean)
```

Call: bootstrap(data = CLEC, statistic = mean) Replications: 10000

```
Summary Statistics:

Observed SE Mean Bias

mean 16.50913 3.985572 16.47043 -0.03869548
```

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### Non-Parametric Resampling

```
bootstrap(data, mean, seed = 210625)
```

Call: bootstrap(data = CLEC, statistic = mean, seed = 191029) Replications: 10000

Summary Statistics: Observed SE Mean Bias mean 16.50913 3.957816 16.47054 -0.03859261

#### bootstrap(data, mean, seed = 210625)

Call: bootstrap(data = CLEC, statistic = mean, seed = 191029) Replications: 10000

```
Summary Statistics:

Observed SE Mean Bias

mean 16.50913 3.957816 16.47054 -0.03859261
```

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#### TeachingDemos::dice(4, 2, plot.it = TRUE)



### **GDA** > Warm Up > **RepRes**



set.seed(123)
dice(4, 2, plot.it = TRUE)



set.seed(123)
dice(4, 2, plot.it = TRUE)

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Why would you need comments in your code and what is the connection to reproducibility?



# Good developers write good code; great ones also write good comments.

Everything that increases the readability of your code increases reproducibility!

**GDA** > Warm Up > **RepRes** 



# A Quick Recap

### What can you do to make your research reproducible?

Write Reports

Get Organised

Develop a simple style and cultivate

organisational habits. Ask questions!

Precise description of the workflow including versions and parameters.



### **Avoid applications with GUIs**

and use terminal command instead.

### Publish Your Script / Code

You can publish your polished script together with your other files.

**GDA** > Warm Up > **RepRes** 



# A Quick Recap

# What can you do to make your research reproducible?

**Code Style** Learn and use a common style.



Comment your code and do it generously.

### Code Editor

Make use of the different features like syntax highlighting, code folding or auto-completion.



### **Version Control**

For bigger or collaborative projects use version control and /or cloud based solutions.

### **GDA** > Warm Up > Markdown









Why would you write a markdown report if you can use a word processor like Microsoft Word?





Don't get me started ...





Why would a markdown report help to improve reproducibility?





In a markdown report, you can easily combine text, figures, tables and code. It helps to divide "code junk" into better readable "code chunks" with context.

### **GDA** > Warm Up > **RegEx**











What are Regular Expressions and for what purpose would you use it?





A regular expression (regex or regexp for short) is a special text string for describing a search pattern. You can think of regular expressions as wildcards on steroids.

A regular expression "**engine**" is a piece of software that can process regular expressions, trying to match the pattern to the given string. Usually, the engine is part of a larger application and you do not access the engine directly.

**GD** Genetic Diversity Centre Zurich

Mus musclus Agalma elegans Frillagalma vitiazi Cordagalma tottoni Shortia galacifolia



M. musclus
A. elegans
F. vitiazi
C. tottoni
S. galacifolia

Find: (\w)\w+ (\w+)

Replace: **\$1. \$2** 

### GDA > Warm Up > RegEx

GDC Genetic Diversity Centre Zurich

Sample» Date» Tmp»pH» Collector-A1-P-S» 17.07.12» 28» 7.2»DG¬ A2-P-S» 17.07.12» 28» 7.3»DG-A3-P-S» 17.07.12» 28» 7.7»DG¬ A1-F-S» 17.07.12» 25» 6.3»DG-A2-F-S» 17.07.12» 25» 6.5»DG-A3-F-S» 17.07.12» 25» 6.6»DG¬ A1-F-W» 16.11.26» 7»7.4»MC-A2-F-W» 16.11.26» 7»7.1»MC-A3-F-W» 16.11.26» 7»6.9»MC-B1-P-S» 17.07.18» 29» 7.1»DG¬ B2-P-S» 17.07.18» 29» 7.2»DG-B3-P-S» 17.07.18» 29» 7.2»DG-B1-F-S» 17.07.20» 27» 6.6»MC-B2-F-S» 17.07.20» 27» 6.7»MC-B3-F-S» 17.07.20» 27» 6.5»MC-



Sample» Date» Tmp»pH» Collector¬ Sample\_PS\_A-1»12.07.17» 28» 7.2»DG-Sample\_PS\_A-2»12.07.17» 28» 7.3»DG-Sample\_PS\_A-3»12.07.17» 28» 7.7»DG-Sample\_FS\_A-1»12.07.17» 25» 6.3»DG-Sample\_FS\_A-2»12.07.17» 25» 6.5»DG-Sample\_FS\_A-3»12.07.17» 25» 6.6»DG-Sample\_FW\_A-1»26.11.16» 7»7.4»MC-Sample\_FW\_A-2»26.11.16» 7»7.1»MC-Sample\_FW\_A-3»26.11.16» 7»6.9»MC-Sample\_PS\_B-1»18.07.17» 29» 7.1»DG-Sample\_PS\_B-2»18.07.17» 29» 7.2»DG-Sample\_PS\_B-3»18.07.17» 29» 7.2»DG-Sample\_FS\_B-1»20.07.17» 27» 6.6»MC-Sample\_FS\_B-2»20.07.17» 27» 6.7»MC-Sample\_FS\_B-3»20.07.17» 27» 6.5»MC-

find:	$(\w)(\d)-(\w)-(\w)\t(\d{2}).(\d{2}).(\d{+})\t(\d{-})\t(\d{+})\t($
replace:	Sample_\$3\$4_\$1-\$2\t\$7.\$6.\$5\t\$8\t\$9\t\$10





### $b[A-Z0-9._{8+-}]+@[A-Z0-9.-]+\.[A-Z]{2,4}b$

25.06.21 | GDA21 | JCW



# What is the meaning of this RegEx term

# **[a-Z0-9.\_%+-]+@[**a-Z0-9.-**]+\.[**a-Z**]**{2,4}

# A.Test@test.com