

# Help! My code is broken

Sarah Watkins

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- Build on the broken code session of part 1
- Firstly, we will look at the most common errors in R
- Secondly, we have an analysis that we will walk through together
  - Some of the code will break!
  - We will look at how we can work out what to fix
  - We hope this will give you practical experience and more confidence in how to fix your code

# Common errors in R and how to interpret them

<https://github.com/noamross/zero-dependency-problems/blob/master/misc/stack-overflow-common-r-errors.md>

R error messages are notoriously hard to interpret

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- ...and answers on forums can be equally difficult



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- Noam Ross has looked at the most common error messages in R and given a brief simple description of what they mean

# R error messages are notoriously hard to interpret

- ...and answers on forums can be equally difficult
- Noam Ross has looked at the most common error messages in R and given a brief simple description of what they mean
- The descriptions are not specific but will let you know what aspect of your data or code you need to check

“tl; dr: Most errors in R are due to looking for something that isn't there”

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- Used R to derive errors posted to Stack Overflow

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- >10,000 errors

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<b>##</b>	<b>trigram</b>	<b>freq</b>
## 1	not find function	311
## 2	Error in if	308
## 3	could not find	300
## 4	in eval(expr, envir,	298
## 5	eval(expr, envir, enclos)	291
## 6	envir, enclos) :	287
## 7	Error in eval(expr,	286
## 8	= TRUE) :	249
## 9	value where TRUE/FALSE	239
## 10	missing value where	230
## 11	: cannot open	216
## 12	: missing value	214
## 13	enclos) : object	211
## 14	where TRUE/FALSE needed	201
## 15	: unable to	194

# "could not find function"

- Usually either the package is not loaded, or the function has been misspelled

# "Error in if"

- generally means the logical statement in "if (XXX) { ...}" is not yielding a logical value
- Most of these have missing value where TRUE/FALSE needed, **meaning that the variable in XXX has NA in it.**



# "Error in eval"

- caused by references to objects that don't exist

# "object not found errors"

- the user has written a statement that's looking for an object not in memory
- Have you misspelled the object?
- Have you created the necessary object?
- Have you loaded the object?

# “subscript out of bounds”

- These errors occur when you try to access an element of a vector or list, or a dimension, that isn't there
- I most often get this error if I've missed a comma (specifying rows or columns) or erroneously included a comma

# “replacement has”

- attempt to assign a vector of values to a subset of an existing object when the lengths do not match up
- Check vector length + object dimensions – do they match?

But sometimes, it's not clear what the problem is

But sometimes, it's not clear what the problem is

```
134 or_output$phenotype <- as.character(rownames(or_output))
135 or_output$phenotype <- as.factor(or_output$phenotype)
136 # remove exposures with silly confidence intervals
137 #or_output <- or_output[or_output$upper < 50,]
138 or_output_list[[i]][[j]] <- or_output
139
140 # make the plot
141 fp <- ggplot(data=or_output, aes(x=phenotype, y=estimate, ymin=lower, ymax=upper)) +
142   geom_pointrange() +
143   geom_pointrange(data=or_output[or_output$fisher.exact<0.05,], aes(x=phenotype, y=esti
144   geom_hline(yintercept=1, lty=2) + # add a dotted line at x=1 after flip
145   coord_flip() + # flip coordinates (puts labels on y axis)
146   labs(title=paste0("MESA, ",i,", ",j), x = "EWAS catalog category", y = "Odds of enric
147   theme_bw() # use a white background_
148
149 plot_list[[i]][[j]] <- fp
150 }
151 }
152
```

ggplot code written in a loop in one version of R and printed to jpeg  
in different version – worked fine until a package was updated

# But sometimes, it's not clear what the problem is

```
> jpeg(filename = paste0(output.dir,"/ewascat_enrichment_composite.jpg"),width =  
      13, height = 9, units = "in", res = 600)  
> plot.out <- ggarrange(plotlist=plot_list[[1]][2:12],height = 16, units = "in",  
      labels = c("A","B","C","D","E","F","G","H","I","J","K"),  
      ncol = 3, nrow = 4)
```

```
Error in self$geom$rename_size && "size" %in% names(plot$mapping) :  
  invalid 'x' type in 'x && y'
```

```
> print(plot.out)  
Error in print(plot.out) : object 'plot.out' not found  
> dev.off()  
null device
```

# Google the error?



invalid 'x' type in 'x && y'



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About 2,000,000 results (0.45 seconds)



Stack Overflow

<https://stackoverflow.com> › questions › error-in-drop-...

## Error in drop && !has.j : invalid 'x' type in 'x && y' when ...

18 Aug 2015 — When I run my function as is, I get this error, “**Error in drop && !has.j : invalid 'x' type in 'x && y'.** I am not sure what is throwing me that ...

3 answers · Top answer: `complete <- function(directory, id = 1:332) { files_list <- list.files(direct...`

Trying to subset data and then drop levels of all but 5 specific ... 7 Oct 2017

R : Error in Axis && box : **invalid 'y' type in 'x && y'** 4 Dec 2016

R Shiny error using switch for histogram: Error in &&: **invalid 'x'** ... 18 Feb 2018

R: Error: **invalid 'y' type in 'x || y'** - Stack Overflow 23 Feb 2016

[More results from stackoverflow.com](#)

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Posit

<https://community.rstudio.com> › tmaps-error-invalid-x...

## tmaps error invalid 'x' type in 'x && y' - General - Posit Forum

9 May 2022 — Hi, I am trying to use tmap to create a map using a raster which we've been given as part of a uni assignment (sorry, I don't think I can share ...



GitHub

<https://github.com> › paulgovan › eAnalytics › issues

## Warning: Error in &&: invalid 'x' type in 'x && y' #2

I am new to R and was trying out the eAnalytics demo by doing the following; Installed R v3.4.2  
Go to the R console and installed eAnalytics ...

<https://github.com> › rstudio › shiny › issues

## invalid 'x' type in 'x && y' error · Issue #1606 · rstudio/shiny

13 Mar 2017 — With a particular development version of shiny package on 3/9/2017, we were seeing an issue on RStudioConnect.



Seems like a  
generic message –  
make it more  
specific to ggplot



invalid 'x' type in 'x && y' ggplot size



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Stack Overflow

<https://stackoverflow.com/questions/r-error-in-axis...>

**R : Error in Axis && box : invalid 'y' type in 'x && y'**

4 Dec 2016 — I get the error : Error in axis && box : **invalid 'y' type in 'x && y'** can someone help me please? R Language Collective. r · Share.

2 answers · 0 votes: Change your code on line 4 to `colnames(data) <- c("performance","croiss...`

Error when exporting **ggplot** graphs to pdf: **invalid font type** 20 Sept 2018

Error message "Error in paired || !is.null(y) : **invalid 'x' type in 'x** 25 Oct 2020

Getting an Error in **ggplot**: **Invalid** argument to unary operator 28 Feb 2018

r - Getting "**invalid 'type'** (character) of argument" error with ... 31 Jan 2016

[More results from stackoverflow.com](#)

You visited this page on 12/04/23.



GitHub

<https://github.com/rstudio/shiny/issues>

**invalid 'x' type in 'x && y' error · Issue #1606 · rstudio/shiny**

13 Mar 2017 — With a particular development version of shiny package on 3/9/2017, we were seeing an issue on RSConnect.

Doesn't include: **ggplot** | Must include: **ggplot**



appsloveworld.com

<https://www.appsloveworld.com/r-shiny-error-using-...>

**R Shiny error using switch for histogram: Error in &&: invalid 'x ...**

Coding example for the question R Shiny error using switch for histogram: Error in &&: **invalid 'x' type in 'x && y'-R**.



Statistics Globe

<https://statisticsglobe.com/change-font-size-of-ggplot...>

**Change Font Size of ggplot2 Plot in R | Axis Text, Main Title ...**

In this article, I'll explain how to increase **and** decrease the text font **sizes** of **ggplot2** plots in R.

# Google a different part of the error


Google

self\$geom\$rename\_size


× | 🔊 📷 🔍


🔍 All 🖼 Images 🛒 Shopping 📺 Videos 📍 Maps ⋮ More Tools


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 RDRR.io  
https://rdr.io › CRAN › ggplot2 ⋮  
[ggplot2 source: R/layer.r](#)  
Create a new layer #' #' A layer is a combination of data, stat and geom with ... mapping if (self\$geom\$rename\_size && "size" %in% names(plot\$mapping)) && !  
You've visited this page 2 times. Last visit: 13/04/23

https://rdr.io › GitHub › hadley/ggplot2 ⋮  
[hadley/ggplot2 source: R/geom-.r](#)  
R/geom-.r defines the following functions: check\_linewidth check\_aesthetics. ... aesthetic and param exist if (self\$rename\_size && is.null(data\$linewidth) ...

 Stack Overflow  
https://stackoverflow.com › questions › adding-minor-... ⋮  
[Adding minor tick marks to the x axis in ggplot2 \(with no ...](#)  
23 Jan 2013 — I've seen this request many times and haven't seen a good answer. Options I've seen/used are 1: Use minor grid lines. 2: Manually add tick marks ...  
4 answers · Top answer: This would do it in the precise instance: scale\_x\_continuous(breaks= ...  
Doesn't include: rename\_size | Must include: [rename\\_size](#)

 GitHub  
https://github.com › tidyverse › ggplot2 › blob › master ⋮  
[ggplot2/geom-errorbarh.r at main](#)  
ggplot2/R/geom-errorbarh.r ... draw\_panel = function(self, data, panel\_params, coord, height = NULL, lineend = "butt") { ... **rename\_size** = TRUE.  
https://github.com › tidyverse › ggplot2 › blob › master ⋮  
[ggplot2/geom-path.r at main](#)  
An implementation of the Grammar of Graphics in R. Contribute to tidyverse/ggplot2 development by creating an account on GitHub.

 Tidyverse

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self\$geom\$rename\_size


× | 🔊 📷 🔍


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 Tidyverse

# Is it to do with an update to how ggplot deals with size?

## Make your ggplot2 extension package understand the new linewidth aesthetic



Photo by Ricardo Gomez Angel

📅 2022/08/24

💡 ggplot2

👤 Thomas Lin Pedersen

We are hard at work finishing the next release of ggplot2. While this release is mostly about internal changes, there are a few quite user visible changes as well. One of these upends the idea that the `size` aesthetic is responsible for *both* the sizing of point/text and the width of lines. With the next release we will have a `linewidth` aesthetic to take care of the latter, while `size` will continue handling the former.

There are many excellent reasons for this change, all of which will have to wait until the release post to be discussed. This blog post is for those that maintain an extension package for ggplot2 and are left wondering how they should respond to this — if that is you, please read on!

The way it works [↗](#)

# But none of the layers specify sizing...

```
# make the plot
fp <- ggplot(data=or_output, aes(x=phenotype, y=estimate, ymin=lower, ymax=upper)) +
  geom_pointrange() +
  geom_pointrange(data=or_output[or_output$fisher.exact<0.05,], aes(x=phenotype,
y=estimate, ymin=lower, ymax=upper), colour="#1F968BFF") +
  geom_hline(yintercept=1, lty=2) + # add a dotted line at x=1 after flip
  coord_flip() + # flip coordinates (puts labels on y axis)
  labs(title=paste0("MESA, ", i, ", ", j), x = "EWAS catalog category", y = "Odds of
enrichment (95% CI)")
  theme_bw() # use a white background

plot_list[[i]][[j]] <- fp
```

# Further solutions?

- Run the code with one layer omitted each time to see where the problem is coming from
  - Keep getting the same message

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- Run the code with one layer omitted each time to see where the problem is coming from
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- Save out the data from the loop and create the plot in the version of R used to print the plot
  - Fixed!

# Further solutions?

- Run the code with one layer omitted each time to see where the problem is coming from
  - Keep getting the same message
- Save out the data from the loop and create the plot in the version of R used to print the plot
  - Fixed!

→ Sometimes there are quicker workarounds!



# Summary of part 1

- We often encounter the same errors in our code!
- These will differ for everyone (depends what you are doing/what packages you tend to use)
- Practical tip: make a spreadsheet (or similar) of the errors you encounter and what you did to resolve them; this could help you solve errors quicker in the future
- Sometimes errors are challenging, but there may be other ways to solve your issue

# Part 2: Broken code walkthrough

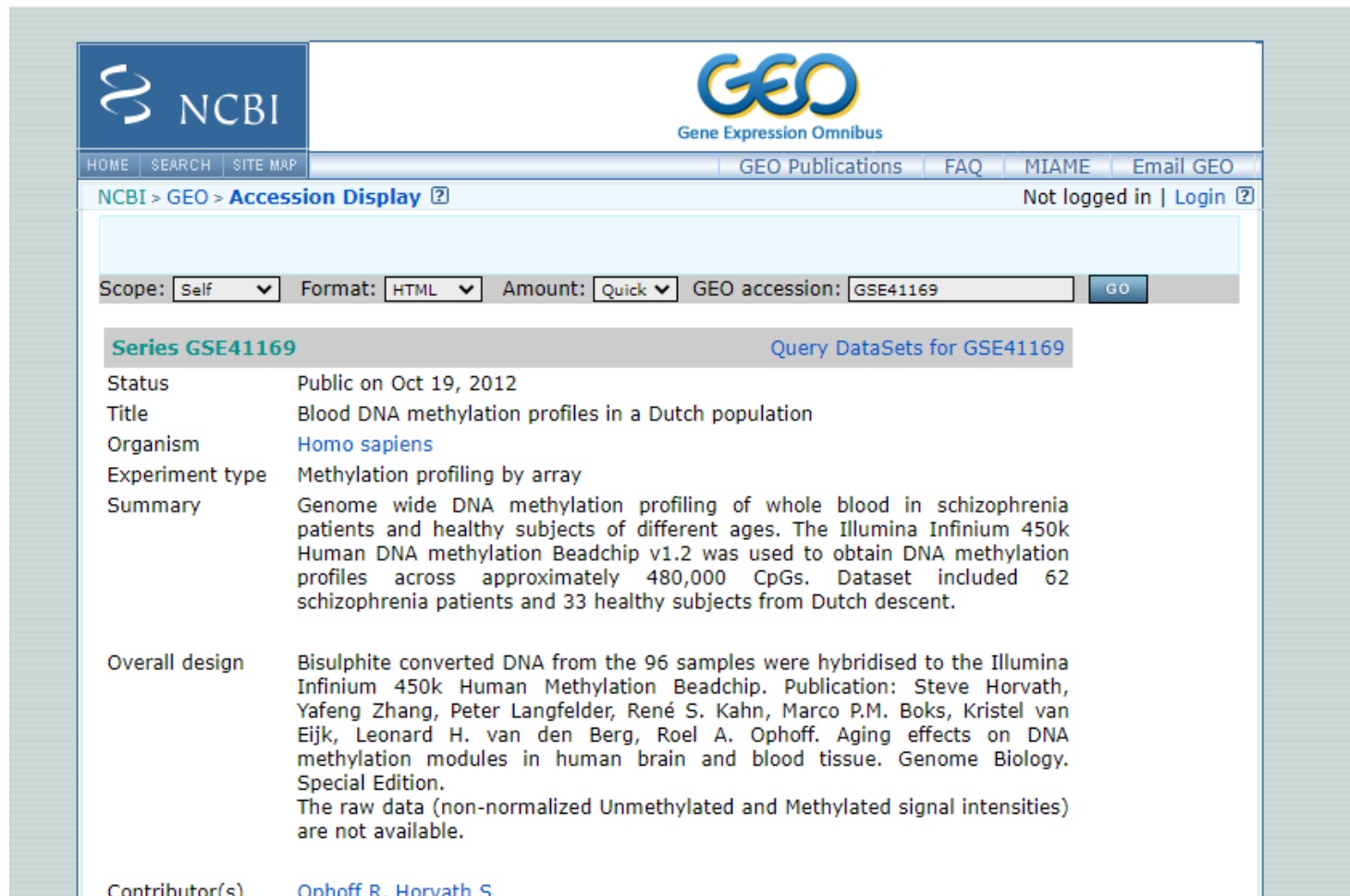
Let's use some of R's functions to help us fix some code

# Introduction to our analysis

- Today we will use a publicly available dataset (GSE41169)

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The screenshot shows the NCBI GEO Accession Display page for GSE41169. The page header includes the NCBI logo and the GEO logo (Gene Expression Omnibus). Navigation links include HOME, SEARCH, SITE MAP, GEO Publications, FAQ, MIAME, and Email GEO. The breadcrumb trail is NCBI > GEO > Accession Display. A login status bar indicates 'Not logged in | Login'. Below the search bar, there are dropdown menus for Scope (Self), Format (HTML), and Amount (Quick), followed by a text input for GEO accession (GSE41169) and a GO button. The main content area displays the series information for GSE41169, including its status, title, organism, experiment type, summary, overall design, and contributor(s).

Series GSE41169	
Status	Public on Oct 19, 2012
Title	Blood DNA methylation profiles in a Dutch population
Organism	<a href="#">Homo sapiens</a>
Experiment type	Methylation profiling by array
Summary	Genome wide DNA methylation profiling of whole blood in schizophrenia patients and healthy subjects of different ages. The Illumina Infinium 450k Human DNA methylation Beadchip v1.2 was used to obtain DNA methylation profiles across approximately 480,000 CpGs. Dataset included 62 schizophrenia patients and 33 healthy subjects from Dutch descent.
Overall design	Bisulphite converted DNA from the 96 samples were hybridised to the Illumina Infinium 450k Human Methylation Beadchip. Publication: Steve Horvath, Yafeng Zhang, Peter Langfelder, René S. Kahn, Marco P.M. Boks, Kristel van Eijk, Leonard H. van den Berg, Roel A. Ophoff. Aging effects on DNA methylation modules in human brain and blood tissue. Genome Biology. Special Edition. The raw data (non-normalized Unmethylated and Methylated signal intensities) are not available.
Contributor(s)	<a href="#">Ophoff R. Horvath S.</a>

# Introduction to our analysis

- Today we will use a publicly available dataset (GSE41169)
- We have phenotype and DNA methylation data for 95 participants

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# Introduction to our analysis

- Today we will use a publicly available dataset (GSE41169)
- We have phenotype and DNA methylation data for 95 participants
- I have edited the dataset slightly (so don't use this version for other projects!)
- We have only kept 10 DNAm sites to keep this simple
- This dataset contains DNAm for controls and individuals with schizophrenia



# 1. Reading in the data

- The datasets are already in R files so you can load by filling in your own file path:

```
load("path/to/samplesheet/GSE41169_samplesheet_intro_to_R.Rdata")
```

```
load("path/to/meth/GSE41169_matrix_intro_to_R.Rdata")
```

# 1. Reading in the data

- The datasets are already in R files so you can load by filling in your own file path:

```
load("path/to/samplesheet/GSE41169_samplesheet_intro_to_R.Rdata")
```

```
load("path/to/meth/GSE41169_matrix_intro_to_R.Rdata")
```

- Let's have a look at our data:

```
colnames(samplesheet)
```

```
dim(samplesheet)
```

```
dim(meth)
```

What's the mean age of our participants?

```
mean(samplesheet$numericage)
```

What's the mean age of our participants?

```
mean(samplesheet$numericage)
```

NA

# What's the mean age of our participants?

```
mean(samplesheet$numericage)
```

NA

Let's use `debug()` to find out what the problem might be

```
debug(mean)
```

```
mean(samplesheet$numericage)
```

We can browse through each line of the `mean()` function, moving to the next by entering `n` and then pressing enter

In each section, we can test our data

# What's the mean age of our participants?

```
Browse[3]> n
debug: if (!is.numeric(x) && !is.complex(x) && !is.logical(x)) {
  warning("argument is not numeric or logical: returning NA")
  return(NA_real_)
}
Browse[3]> is.numeric(samplesheet$numericage)
[1] TRUE
Browse[3]> n
debug: if (na.rm) x <- x[!is.na(x)]
Browse[3]> sum(is.na(samplesheet$numericage))
[1] 1
Browse[3]> c
exiting from: mean.default(samplesheet$numericage)
exiting from: mean(samplesheet$numericage)
[1] NA
> |
```

# What's the mean age of our participants?

Make sure you exit the debugger using `undebug()`

`undebug(mean)`

How do we remove NAs using `mean()`?

`?mean`

So to run `mean` without NAs:

`mean(samplesheet$numericage, na.rm = TRUE)`

## Arithmetic Mean

### Description

Generic function for the (trimmed) arithmetic mean.

### Usage

```
mean(x, ...)
```

```
## Default S3 method:
```

```
mean(x, trim = 0, na.rm = FALSE, ...)
```

### Arguments

- |                   |  |
|-------------------|--|
| <code>x</code>    | An R object. Currently there are methods for numeric/logical vectors and <a href="#">date</a> , <a href="#">date-time</a> and <a href="#">time interval</a> objects. Complex vectors are allowed for <code>trim = 0</code> , only. |
| <code>trim</code> | the fraction (0 to 0.5) of observations to be trimmed from each end of <code>x</code> before the mean is computed. Values of <code>trim</code> outside that range are taken as the nearest endpoint.                               |

## Example 2: Let's do a regression

- We want to test a regression between disease status and DNA methylation using the first 3 DNAm sites
- Let's test one DNAm site to begin with

```
temp<-summary(lm(meth[,1]~samplesheet$diseasestatus2))
```



# Let's do a regression

- We want to test a regression between disease status and DNA methylation using the first 3 DNAm sites
- Let's test one DNAm site to begin with

```
temp<-summary(lm(meth[,1]~samplesheet$diseasestatus2))
```

```
Error in model.frame.default(formula = meth[, 1] ~  
samplesheet$diseasestatus2, : variable lengths differ (found  
for 'samplesheet$diseasestatus2')
```

# Let's do a regression

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- Let's test one DNAm site to begin with

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```

```
Error in model.frame.default(formula = meth[, 1] ~  
  samplesheet$diseasestatus2, : variable lengths differ (found  
  for 'samplesheet$diseasestatus2')
```

```
dim(meth)
```

```
meth[1:5,1:5]
```

Let's try that again

```
meth <- t(meth)
```

Let's try that again

```
meth <- t(meth)
```

```
dim(meth)
```

Let's try that again

```
meth <- t(meth)
```

```
dim(meth)
```

```
temp <-
```

```
summary(lm(meth[,1]~samplesheet$diseasestatus2))
```

Now let's test whether DNAm is associated with some of our covariates

```
exposures <- c("numericage", "plate", "position")
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results_list <- list()
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exposures <- c("numericage", "plate", "position")
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- Create a list to save our output to

```
results_list <- list()
```

- And run a loop to test the association with DNAm

```
for(i in exposures){  
  temp <- lm(meth~samplesheet[,i])  
  results_list[[i]] <- temp  
}
```



Now let's test whether DNAm is associated with some of our covariates

```
exposures <- c("numericage", "plate", "position")
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Error in `contrasts<-`(`\*tmp\*`, value = contr.funs[1 + isOF[nn]]) :  
contrasts can be applied only to factors with 2 or more levels

# Where is that error happening?

- We can use `traceback()` right after the code that didn't work:

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```
traceback()
```

```
5: stop("contrasts can be applied only to factors with 2 or more levels")
4: `contrasts<-`(`*tmp*`, value = contr.funs[1 + isOF[nn]])
3: model.matrix.default(mt, mf, contrasts)
2: model.matrix(mt, mf, contrasts)
1: lm(meth ~ samplesheet[, i])
```

# Where is that error happening?

- We can use `traceback()` right after the code that didn't work:

```
traceback()
```

```
5: stop("contrasts can be applied only to factors with 2 or more levels")
4: `contrasts<-`(`*tmp*`, value = contr.funs[1 + isOF[nn]])
3: model.matrix.default(mt, mf, contrasts)
2: model.matrix(mt, mf, contrasts)
1: lm(meth ~ samplesheet[, i])
```

- So we know that there's a problem with the `lm()` in the loop

# Finding out which loop variable is causing the problem

- We can use `print()` within the loop to find out which variable it's breaking on:

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}
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```
for(i in exposures){  
  print(i)  
  temp <- lm(meth~samplesheet[,i])  
  results_list[[i]] <- temp  
}
```

```
[1] "numericage"
```

```
[1] "plate"
```

```
Error in `contrasts<-`(`*tmp*`, value = contr.funs[1 + isOF[nn]]) :  
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      95
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- If you get an error, check the data going in to the function
  - Are the objects there, are they spelled correctly, check the length/dimensions, check for NAs, etc
- We hope that you have learned a few tricks to investigate the source of coding errors
- We hope you feel a bit more confident in trying to find the source of errors
- Was this helpful? Let us know!