5. Over and over

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In this session

In Sessions 1–4, we completed tasks by breaking them down, into one line of an R script at a time. In principle, we could do *everything* this way. But;

- Repeating the same job many times (i.e. once for each person/guinea pig in the dataset) the typing gets slow & tedious, and is error prone

- For iterative methods, we don't know how much code will be needed before starting the task

This session, and the next, introduce writing loops, so we can re-use the same code in a script, without re-typing it.

NB This module does *not* cover every R tool for looping.

A very first `for()` loop

Many people's first computer program looks like this;

```
> for(i in 1:5){
+   print("hello world!")
+   print(i^2)
+ }
[1] "hello world!"
[1] 1
[1] "hello world!"
[1] 4
[1] "hello world!"
[1] 9
[1] "hello world!"
[1] 16
[1] "hello world!"
[1] 25
```

Two fundamental ideas;

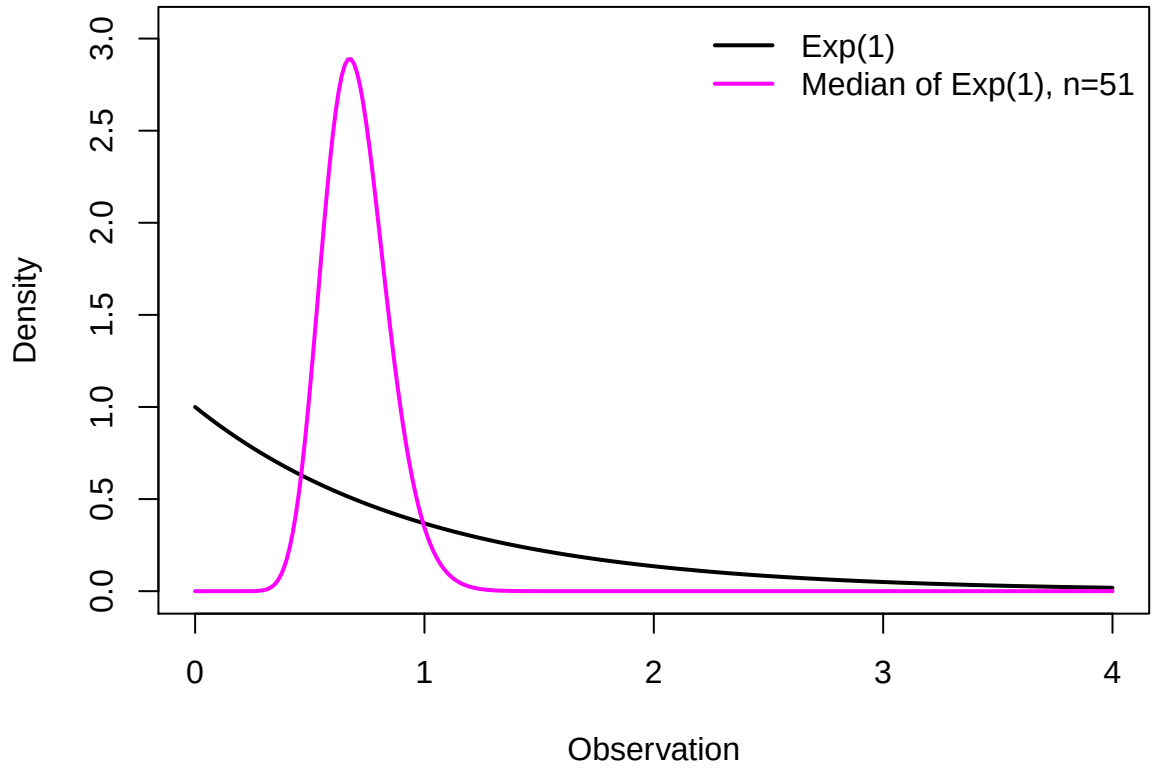
- Go round the loop 5 times
- Each time, do something that may (or may not) depend on which 'go round' it is

Of course, `for()` loops also have more practical uses...

Example: hard math made easy

A question from analysis of survival traits – and its answer!

What is the expected value of the median of a sample, size $n = 51$, of independent data from $Exp(1)$? What is its variance?



Example: hard math made easy

If the picture didn't make it obvious enough (!) here are the *exact* answers;

$$\mathbb{E}[\,\text{Median}_{51}\,] = \frac{2178178936539108674153}{3099044504245996706400}$$

$$\mathbb{E}[\,\text{Median}_{51}^2\,] = \frac{24672823160636679674592332321392579768019 59}{4802038419648657749001278815379823900480000}$$

These are 0.70286 and 0.51380 to 5 d.p. – so the variance is $0.51380 - 0.70286^2 = 0.01978$.

- Yes, there are 'pretty' answers here
- In general there aren't – but the 'expectation' ($\mathbb{E}[\ldots]$) terms just mean averaging over lots of datasets – which is easy, with a computer
- We can get a good-enough answer very quickly

Example: hard math made easy

We'll write code that;

1. Generates a *single* sample of size $n = 51$ from $Exp(1)$
2. Calculates its median and stores this number
3. Repeats steps 1 and 2 many times, then works out the mean and variance of the stored numbers

Here are steps 1 and 2 – run them and see what's created;

```
many.medians <- vector(10000, mode="numeric") # or just rep(NA, 10000)
set.seed(4)
for(i in 1:10000){
   mysample <- rexp(n=51, rate=1)        # take a single sample, size 51
   many.medians[i] <- median(mysample)   # calcuate & store its median
   }
```

The function `set.seed()` tells R where to start its random-number generator – this is important, as it means we can repeat the code and get the same answers. Choose any 'seed' you like.

Example: hard math made easy

How to think of the seed;

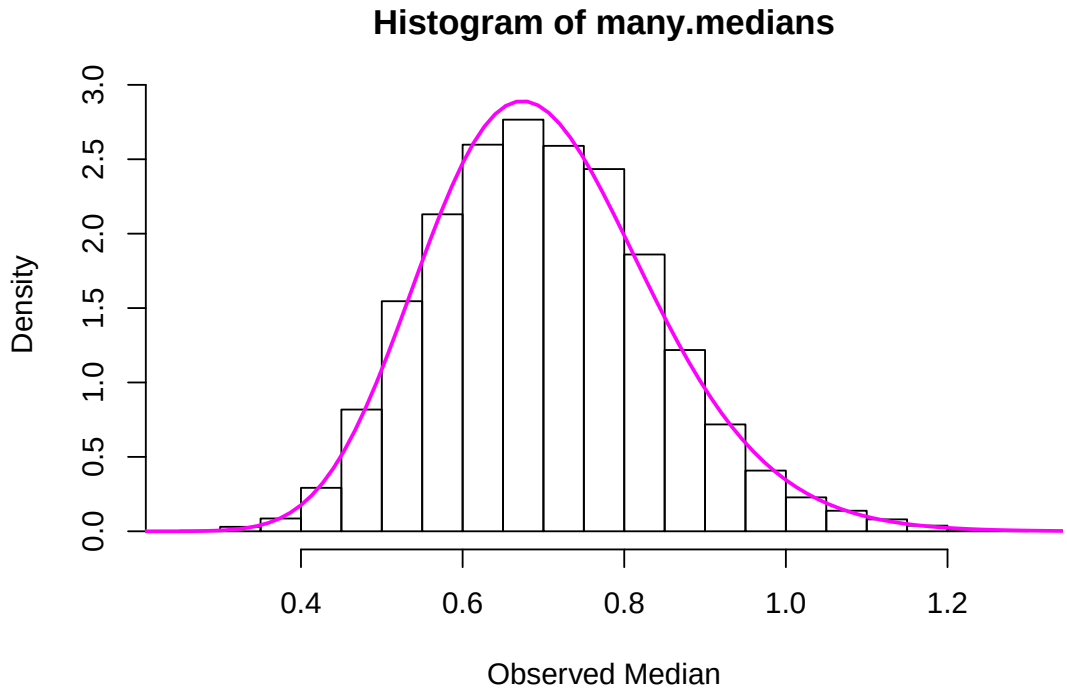
- The seed indicates starting place in the list
- The list closely *resembles* truly random numbers – certainly closely enough for our purposes – but is *actually* fixed

Example: hard math made easy

And the answers, from 10,000 simulations, with that seed?

```
> mean(many.medians)
[1] 0.702171          # exact answer is 0.70286
> var(many.medians)
[1] 0.01955728        # exact answer is 0.01978
```

NB: for large-enough values of 10,000, we could work basically *anything* about the sample median, with little extra work;



Example: hard math made easy

Notes on the coding; (NB see `?Control` for the help page on `for()`, `?for` won't work as `for` is 'restricted')

- `for( [iteration] in [vector of iteration values] )` – the vector of iteration values can be of anything, not just `1:n`
- The expression between the curly brackets { } is evaluated each 'go round' the loop, substituting `i` for 1,2, ... 10,000 in turn
- Very important – create an object to store the output first (but no need to create `i` first). To do this, you'll need to know how big the output is going to be.
- Last-used version of objects used (`i`, `mysample`) are available when the loop terminates – which is very helpful, if (when!) an error occurs
- We used `rexp()`, but there are *many* built-in distributions; `rnorm()`, `rgamma()`, `rbinom()`, `rpois()` etc

Example: data manipulation

Recall the salary example – on faculty measured over several years. Suppose we were interested in the *final* observation for each person – how to construct that dataset?

- Different numbers of observations per person – so can't just look at e.g. rows 1,5,11,15, ... (but see `seq()` if you *do* want to do this)
- Different entry and exit years
- `subset()` won't work, neither will use of square brackets

Instead, we can go through every `id` number, pull out the rows with that `id` and record the one for which `year` is highest. Or, if the data is sorted first (by `id` and `time`) pull out the *last* row for each `id` number.

As before, it's very important that we prepare an object for the results ('pulled out' data, here) *before* running any loops.

Example: data manipulation

First sort the data, and make the empty object ready to take output;

```
salary <- salary[ order(salary$id, salary$year), ]
View(salary) # check we know what we should get from subsetting

n <- length(unique(salary$id)) # how many individual people?
finalsalary <- salary[0,] # take just column names from salary
finalsalary[1:n,] <- NA   # fill in with missing values
str(finalsalary)          # check the structure we made
```

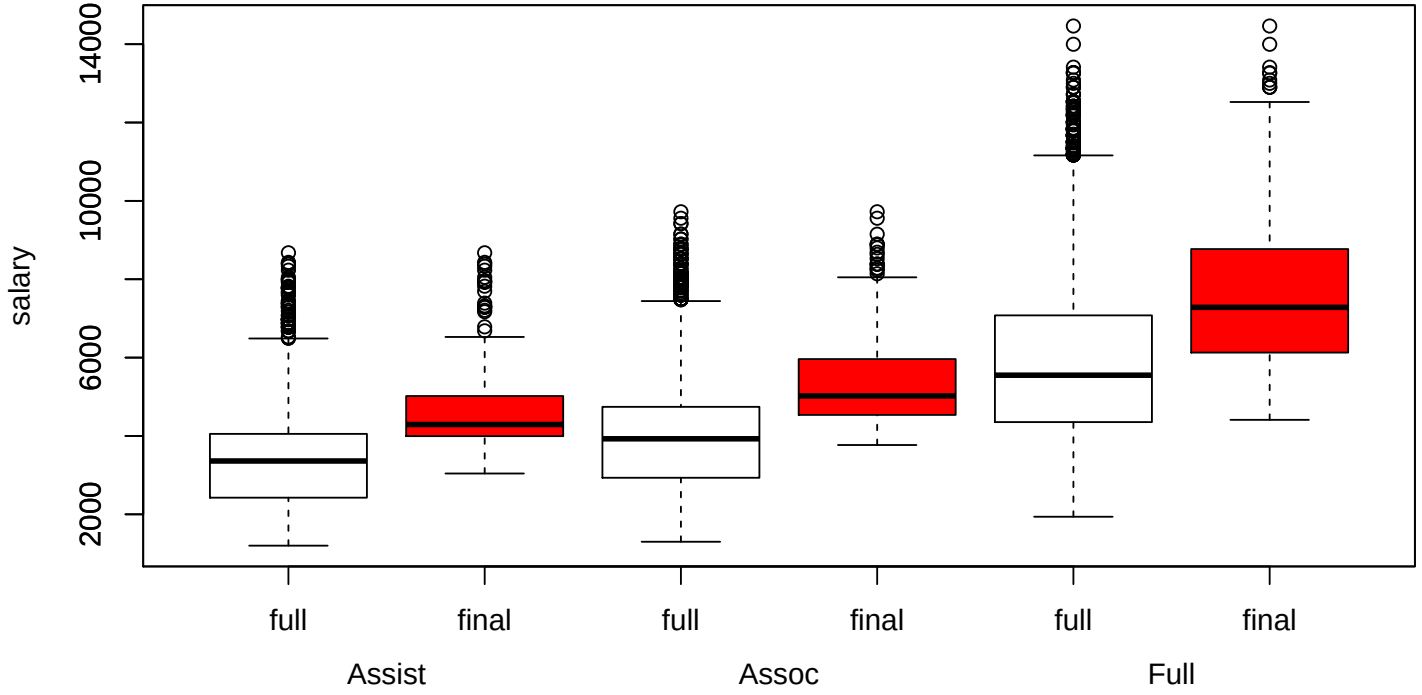
- `order()` returns the vector that puts objects in order. There is a `sort()` function, but it accepts only vectors and not data frames
- A less-sneaky way to make a new empty data frame uses e.g. `data.frame(id=NULL, age=NULL, sex=NULL)`
- In RStudio, `View()` operates in the Source window; in vanilla R it opens up a new window. Neither refreshes automatically

Example: data manipulation

Now for the loop;

```
for(i in 1:n){
   id.i             <- unique(salary$id)[i]
   salary.i         <- subset(salary, id==id.i)
   n.i              <- dim(salary.i)[1]        # dim() for dimension
   finalsalary[i,] <- salary.i[n.i,]           # i.e. just the last row
   } # View(finalsalary) a good idea, to check it worked
```

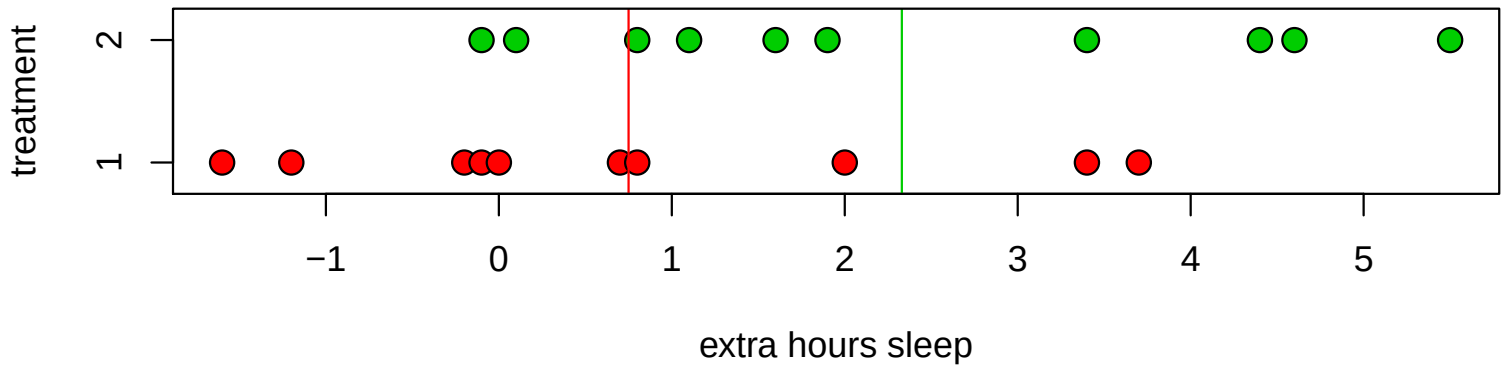
Compare the full dataset (white) and final-only version (red);



Example: permutation test

A classical statistical question: are the data we've observed *unexpected*, if there's nothing going on?

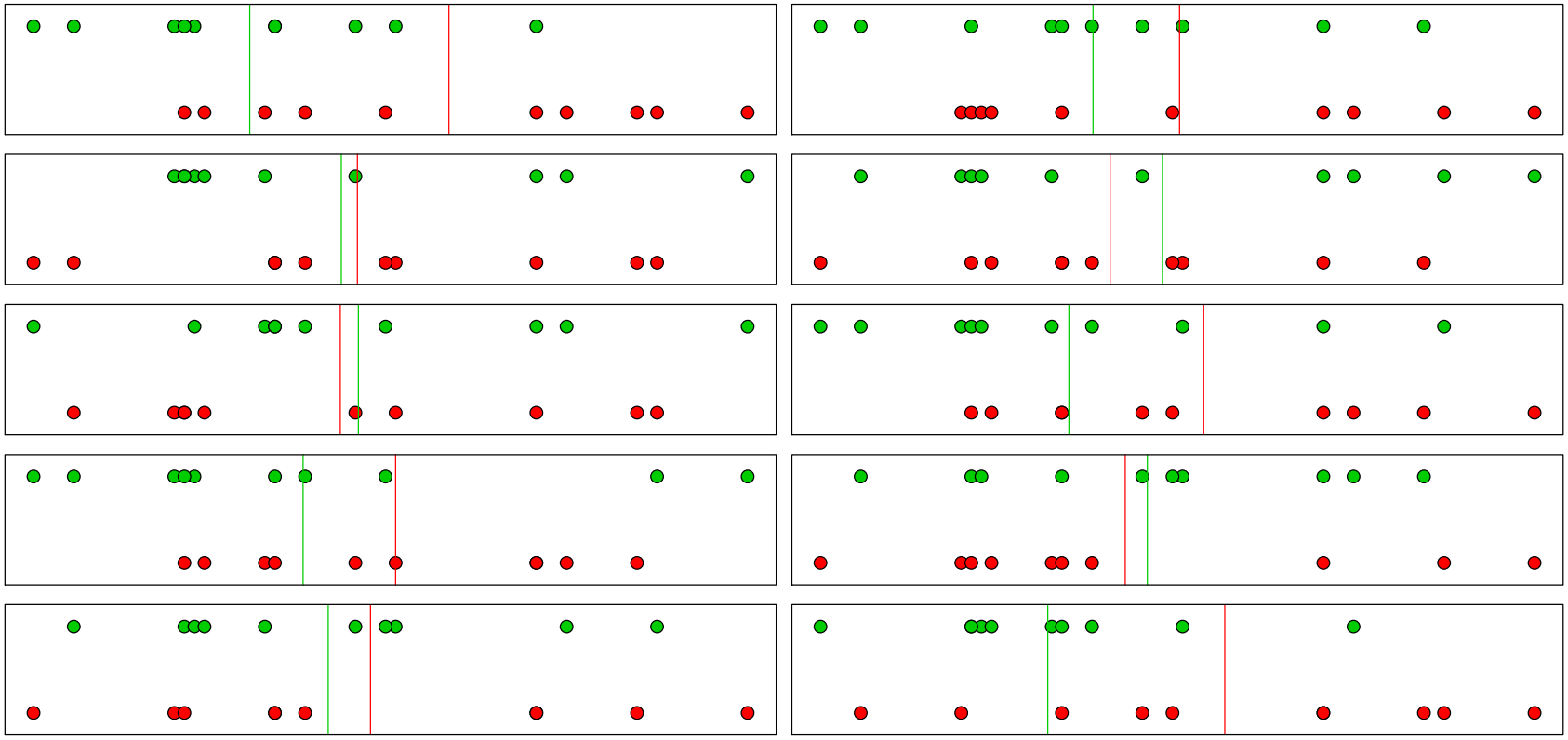
An example where we can answer this is R's `sleep` data;



- 10 subjects per group
- Groups receive different treatments, we record how many hours sleep they get, compared to baseline
- Mean extra hours sleep is higher in group 2 (2.33 hrs vs 0.75 hrs, so difference is 1.58 hrs)

Example: permutation test

What if there were nothing going on*, i.e. what if any differences in mean were just chance? If so, the data we saw would be just as likely as that obtained assigning the group labels *at random*;



* Formally, what if the *null hypothesis* of equal means held, in the population from which this data has been sampled?

Example: permutation test

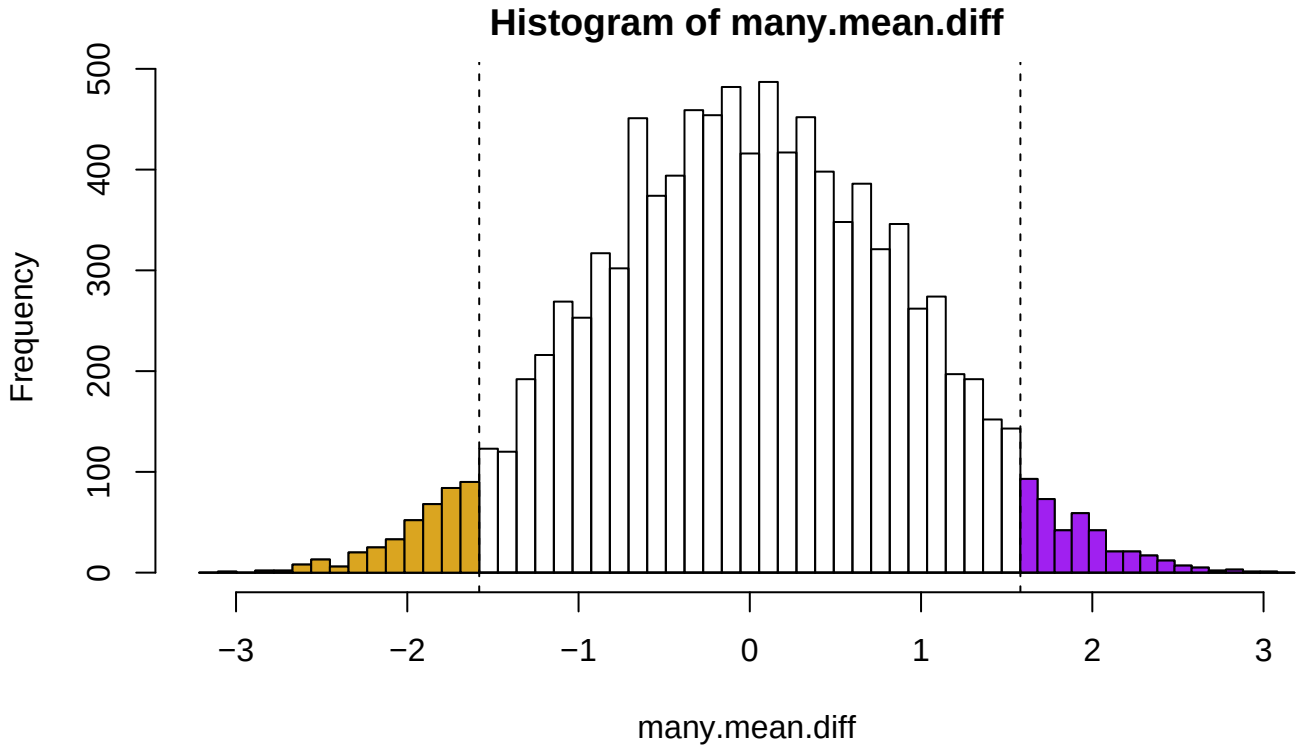
To measure how unexpected our data is, we compute the red/green difference in means for many of these *permutations*, and see how the *observed* data compares.

```
orig.mean.diff <- with(sleep,
      mean(extra[group==2]) - mean(extra[group==1])
      )
orig.mean.diff

many.mean.diff <- vector(10000, mode="numeric") # set up place to put output
set.seed(4)                                     # set the random seed

for(i in 1:10000){                              # do this bit 10,000 times
  group.shuffle <- sample(sleep$group)
  many.mean.diff[i] <- with(sleep,
    mean(extra[group.shuffle==2]) - mean(extra[group.shuffle==1])
    )
}
```

- `sample()` returns a random shuffle of a vector
- The same calculation is made, for the original data and the shuffled version; the difference in means is called the *test statistic*

Example: permutation test

How does original data (w/ mean diff=1.58) compare to these?




```
> table(many.mean.diff>orig.mean.diff)
FALSE  TRUE
 9601   399
> mean(many.mean.diff>orig.mean.diff)
[1] 0.0399
> mean(abs(many.mean.diff)>abs(orig.mean.diff))
[1] 0.0789
```

Example: permutation test

- The proportion of sample in the RH tail is a (valid) p-value for a one-tailed test, where the alternative is that green $>$ red. $p = 0.04$, here
- The proportion in both tails is the p-value for a two-tail test; $p = 0.079$
- There is some 'Monte Carlo' error in these p-values; roughly ± 0.004 here, i.e. 2 decimal places in p. If that's not good enough, use more permutations. (Here, could use all 184,756 – but in larger samples it's not possible)

To get a quicker (but approximate) version of the same thing;

```
> t.test(extra~group, data=sleep) # recall extra 'depends on' group
Welch Two Sample t-test
data:  extra by group
t = -1.8608, df = 17.776, p-value = 0.07939
alternative hypothesis: true difference in means is not equal to 0
```

The t test makes fewer assumptions than most people think!

Notes on timing, and speed

Doing a lot of calculations can take a long time – it's useful to know how long. Try out the `system.time()` command on a smaller version of the problem, i.e.

```
system.time({
  for(i in 1:1000){                        # just 1000, not 10000
    group.shuffle <- sample(sleep$group)
    many.mean.diff[i] <- with(sleep,
      mean(extra[group.shuffle==2]) - mean(extra[group.shuffle==1])
    )
  }
})
```

This returns the time taken to run the outer curly brackets;

```
  user  system elapsed
  0.57    0.00    0.60
```

... so running 100,000 permutations would take `100*0.6/60` = 1 minute, roughly. (NB this is much less time than it took to write the code!)

If RStudio hangs, there is a 'STOP' button on the Console window; in vanilla R hit Escape, or Ctrl-D.

Notes on timing, and speed

Throughout, we have stressed the importance of setting up empty objects for the loop's output. Why? Let's code the permutation test without doing this;

```
many.mean.diff <- NULL          # this will 'grow', in the loop
system.time({
  for(i in 1:100000){
    group.shuffle <- sample(sleep$group)
    mean.diff <- with(sleep,
       mean(extra[group.shuffle==2]) - mean(extra[group.shuffle==1]))
    many.mean.diff <- c(many.mean.diff, mean.diff) # 'grow' the dataset
  }})

   user  system elapsed # CPU/child process/total
 115.53    4.93  122.07
```

- This works, but at half the speed of the other version
- The extra time is *all* spend copying vector `many.mean.diff` – R copies objects slowly
- The slowdown is worse for larger objects, i.e. gets worse with more permutations, i.e. when speed really matters

Notes on timing, and speed

Compared to using a single R command (when available) to do the job, `for()` loops can be inefficient.

- Add two vectors (`x <- y + z`) don't add them element by element (`for(i in 1:n){ x[i] <- y[i] + z[i]}`)
- Recall `ifelse()` earlier, rather than looping over a vector.

```
many.samples <- matrix(data=NA, nrow=100000,ncol=20)

for(i in 1:100000){
    many.samples[i,] <- sample(sleep$extra)
}
many.mean.diff <- rowMeans(many.samples[,1:10]) - rowMeans(many.samples[,11:20])
```

- Shuffling the outcomes is equivalent to shuffling the groups
- A `matrix` has all entries of the same type – less flexible than a `data.frame`, but faster to work with
- This version takes 4.3s, i.e. it's $\times 14$ faster than the loop.
- Not available for every task – also uses more memory

Summary

- Writing loops saves a lot of typing – essential for serious computing jobs, but helpful for data management too
- `for()` loops offer enough flexibility for several jobs – more to come in the next session!
- As with all programming; break the job into lots of small pieces, and do each one in turn
- Never never *never* grow the output except when doing tiny jobs where speed is irrelevant, and then **only** if you promise not to fall into bad habits!
- Other looping methods exist in R – but aren't in this module