5. Over and over

Ken Rice
Tim Thornton

University of Washington

Seattle, July 2013

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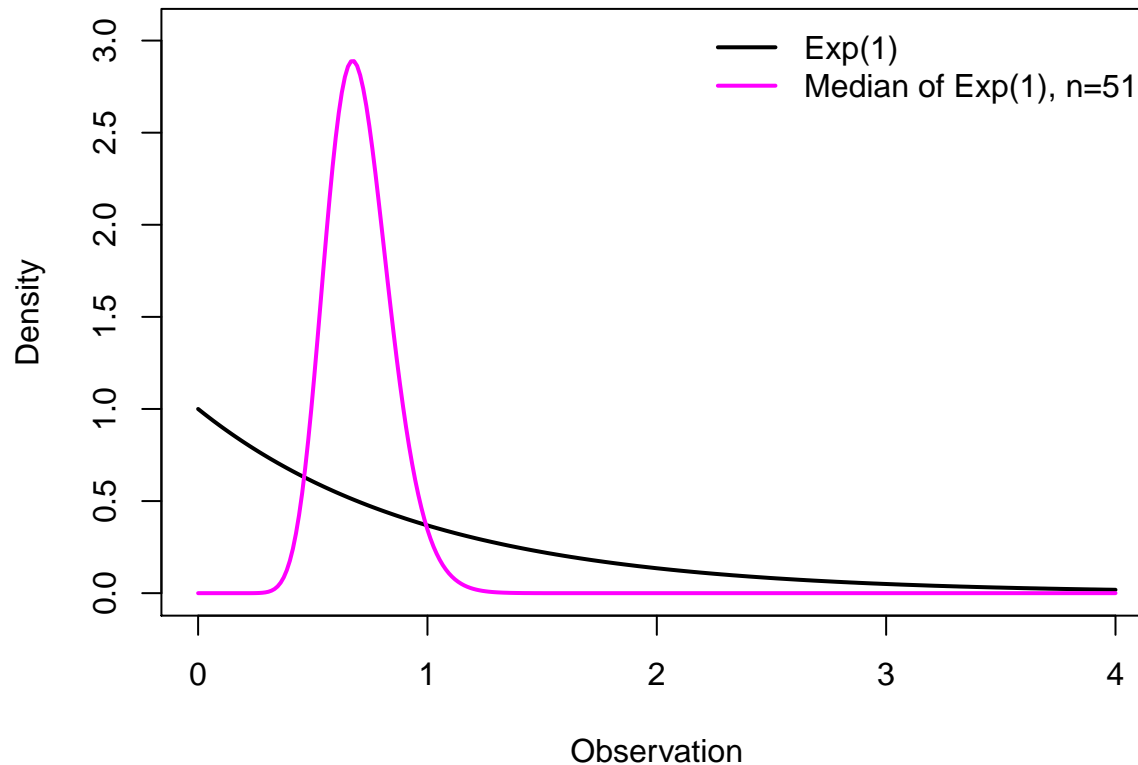
Of course, `for()` loops also have more practical uses...

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;

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

$$\mathbb{E}[\,\text{Median}_{51}^2\,] = \frac{2467282316063667967459233232139257976801959}{4802038419648657749001278815379823900480000}$$

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 samples of size $n = 51$ from $Exp(1)$

2. Calculates their median and stores this number

3. Does 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 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

And the answers, from 10,000 simulations?

```
> 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 10000, we could work basically *anything* about the sample median, with little extra work;

Histogram of many.medians

Observed Median
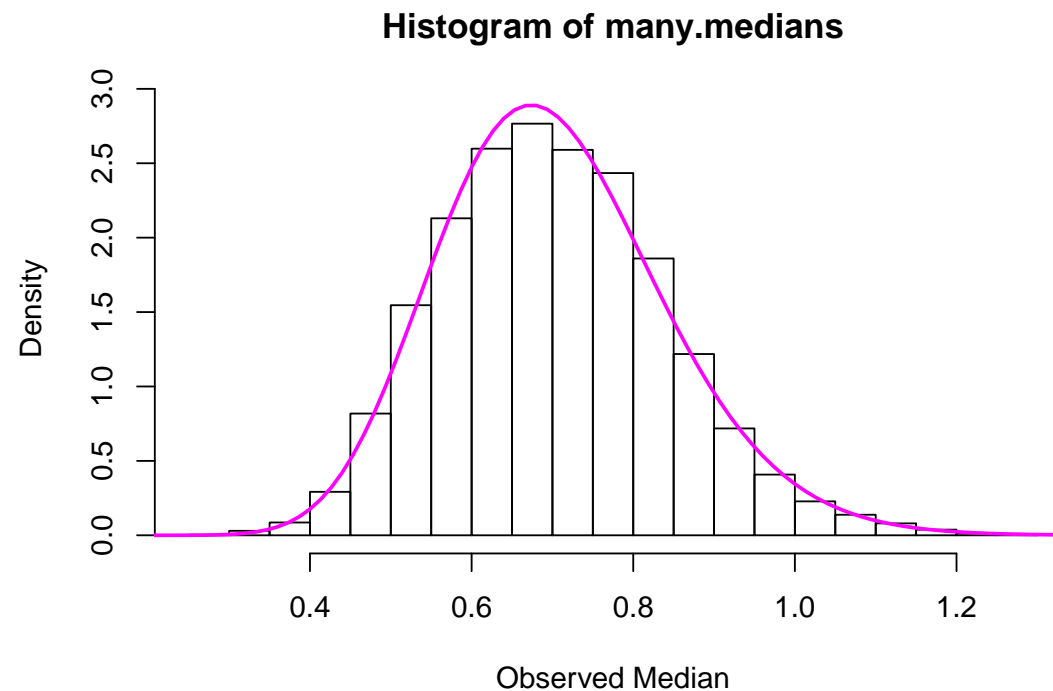
Example: hard math made easy

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))
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
```
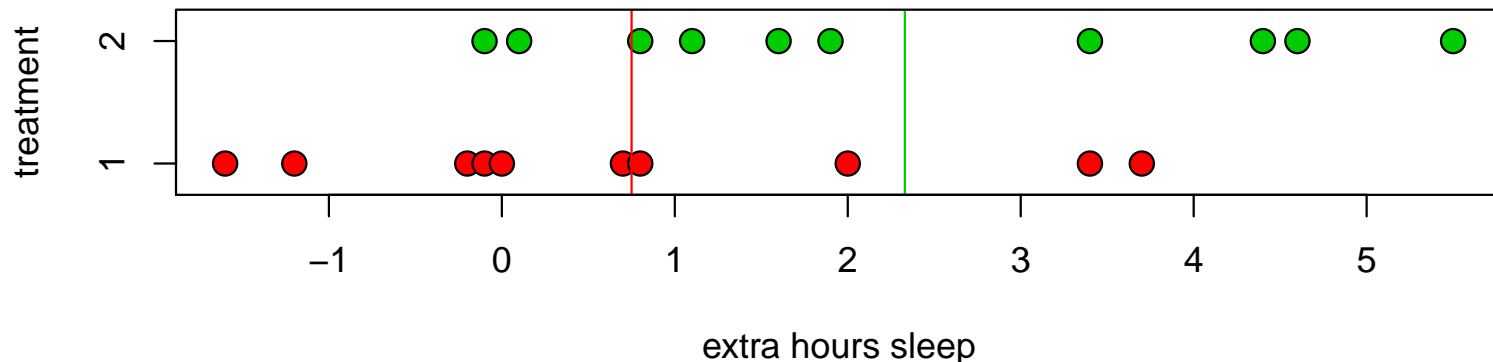
Compare the full dataset (white) and final-only version (red);
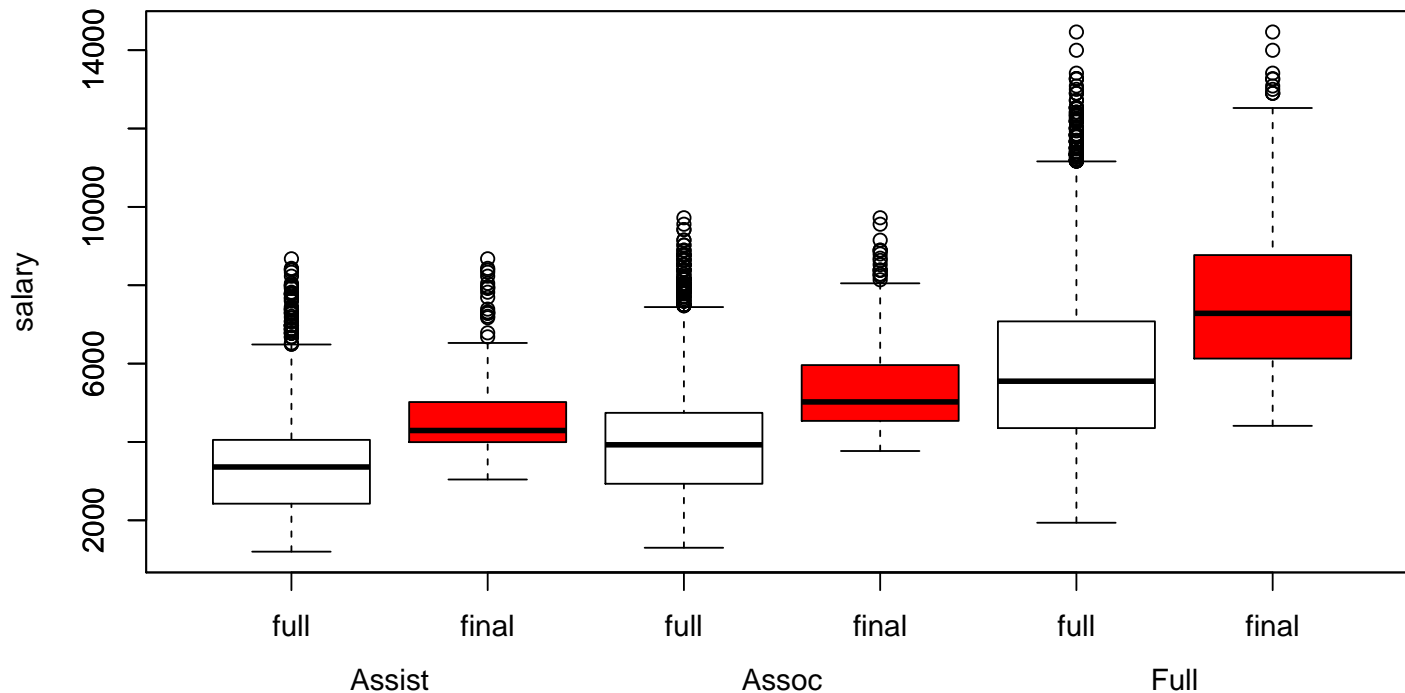
Example: permutation test

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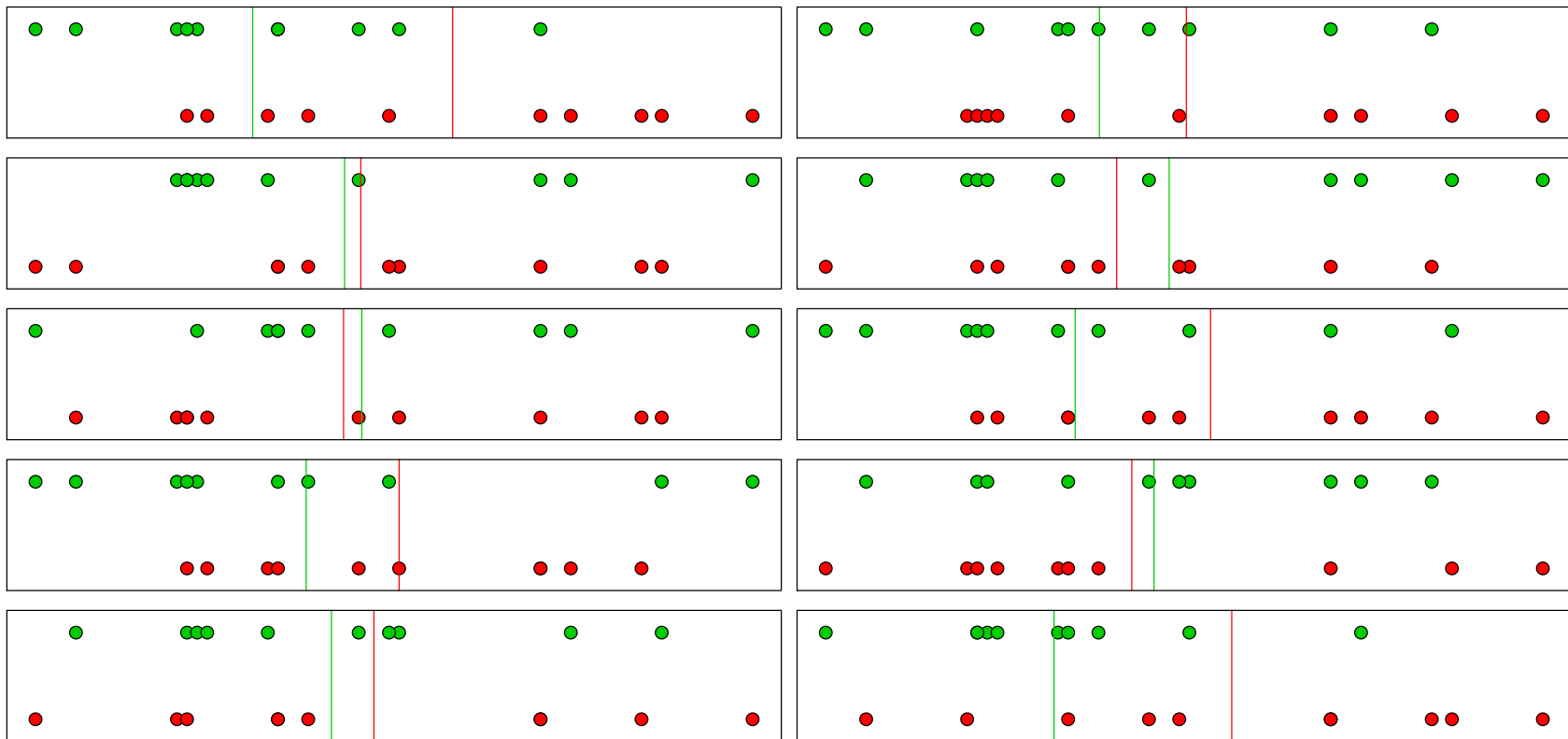
* Formally, what if the *null hypothesis* of equal means held, in the population from which this data has been sampled?

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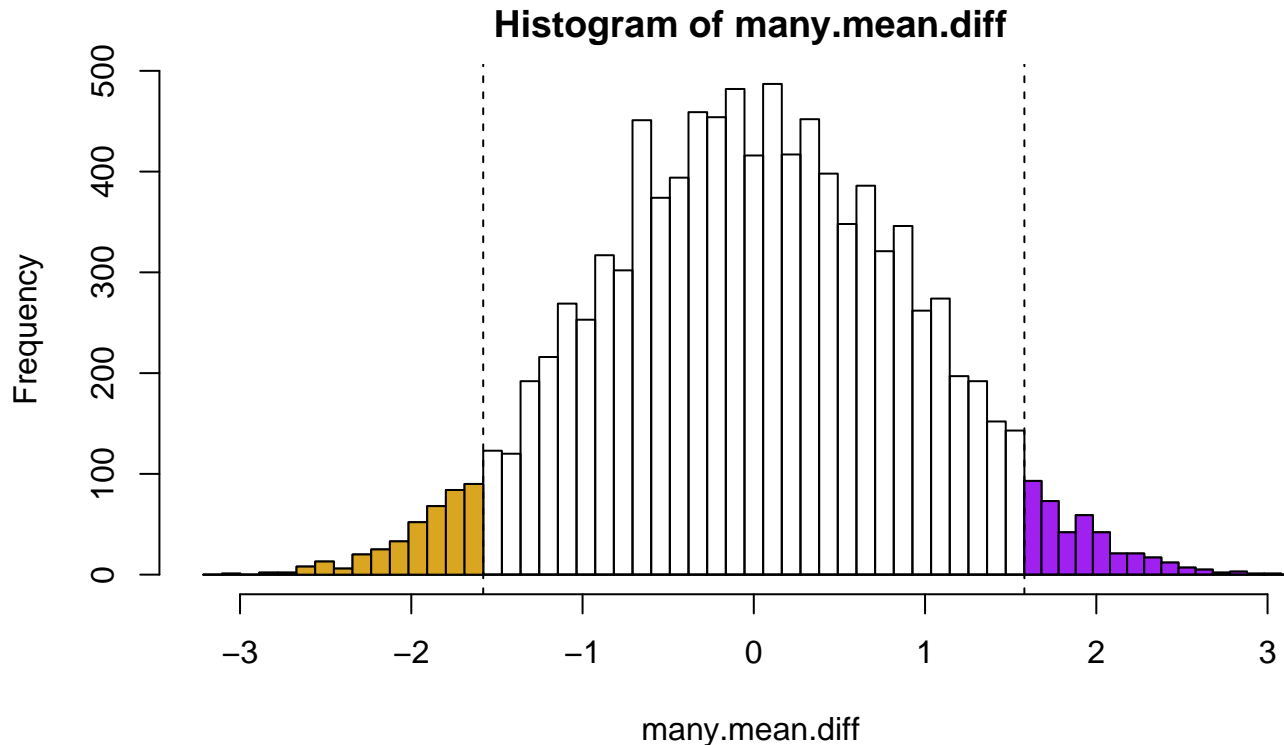
- `sample()` returns a random shuffle of a vector
- The same calculation is made, for the original data and the shuffled version; the difference in means is called the *test statistic*

Example: permutation test

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

Histogram of many.mean.diff


```
> 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 is slow at copying objects
- 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

- Other methods exist in R − but not in this module