CPUs - why do we have more than one?

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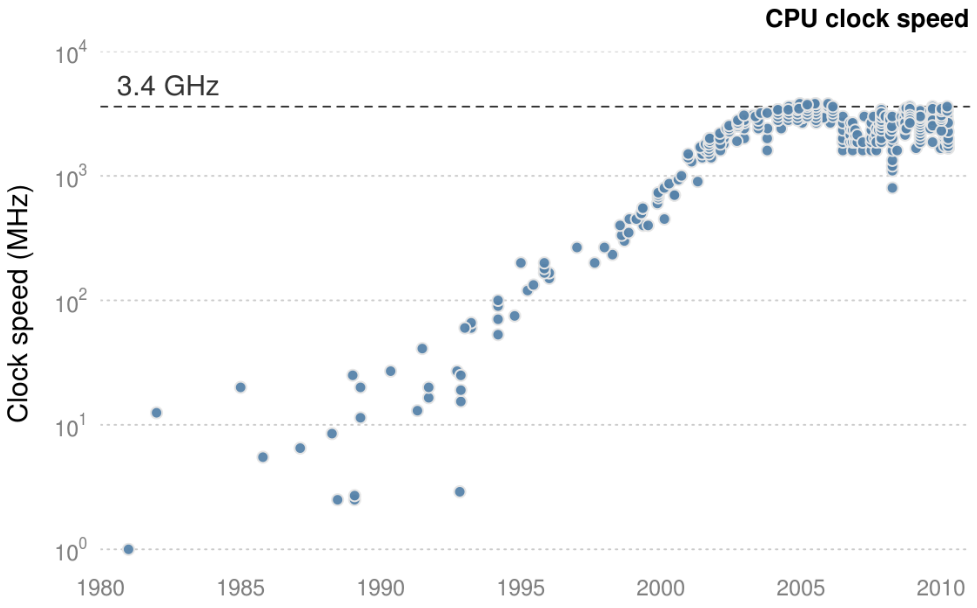
CPUs

- CPU: brains of the computer
  - Speed has slowly stabilized
    - CPUs were getting too hot
  - Multi-core CPUs
  - But R only uses 1 core :(



Your CPU

```r
library("parallel")
detectCores()
```

```
8
```

```r
library("benchmarkme")
get_cpu()
```

```
$vendor_id
"GenuineIntel"

$model_name
"Intel(R) Core(TM) i7-4702HQ CPU

$no_of_cores
8
```

Let's practice!

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What sort of problems benefit from parallel computing

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Cooking

AN EXTRA HAND

TOO MANY COOKS

Running in parallel

- Not every analysis can make use of multiple cores
  - Many statistical algorithms can only use a single core

So where can parallel computing help?

Monte-Carlo simulations

```
for(i in 1:8)
    sims[i] <- monte_carlo()
```

```
# User defined function
combine_simulations(sims)
```

- 8 core machine
  - One simulation per core
  - Combine the results at the end
- *Embarrassingly parallel*

Not everything runs in parallel

```
x <- 1:8
for(i in 2:8)
    x[i] <- x[i-1]
```

```
x[8] = x[7] = ... x[2] = x[1] = 1
```

- Can we run this in parallel?
    - NO
        - But order of evaluation in parallel computing *can't* be predicted
        - We'll get the wrong answer, since `x[3]` may get evaluated before `x[2]`

Rule of thumb

Can the loop be run forward and backwards?

```
for(i in 1:8)
    sim[i] <- monte_carlo_simulation()

for(i in 8:1)
    sim[i] <- monte_carlo_simulation()
```

- Both loops give the same result
- So we can run the loops in parallel

Rule of thumb

Can the loop be run forward and backwards?

```
x <- 1:8
for(i in 2:8)
    x[i] <- x[i-1]
for(i in 8:2)
    x[i] <- x[i-1]
```

- The loops give different answers
  - The first: `x[8] = x[7] = ... = 1`
  - The second: `x[8] = x[7] = 7`
- Can't use parallel computing

Remember: If you can run your loop in reverse, you can *probably* use parallel computing.

Let's practice!

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The parallel package - parApply

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The parallel package

- Part of R since 2011

```
library("parallel")
```

  - Cross platform: Code works under Windows, Linux, Mac
  - Has parallel versions of standard functions

The apply() function

- `apply()` is similar to a for loop
  - We *apply* a function to each row/column of a matrix
- A 10 column, 10,000 row matrix:

```
m <- matrix(rnorm(100000), ncol = 10)
```

- apply is neater than a for loop

```
res <- apply(m, 1, median)
```

Converting to parallel

- Load the package
    - Specify the number of cores
    - Create a cluster object
    - Swap to `parApply()`
    - Stop!

```
library("parallel")
```

```
copies_of_r <- 7
```

```
cl <- makeCluster(copies_of_r)
```

```
parApply(cl, m, 1, median)
```

```
stopCluster(cl)
```

The bad news

As Lewis Caroll said

The hurrier I go, the behinder I get.

- Sometimes running in parallel is slower due to thread communication

```
# Serial version
apply(m, 1, median)
```

```
# Parallel version
parApply(cl, m, 1, median)
```

- Benchmark both solutions

Let's practice!

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The parallel package - parSapply

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The apply family

There are parallel versions of

- `apply()` - `parApply()`
- `sapply()` - `parSapply()`
  - applying a function to a vector, i.e., a for loop
- `lapply()` - `parLapply()`
  - applying a function to a list

The sapply() function

sapply() is just another way of writing a for loop

The loop

```
for(i in 1:10)
    x[i] <- simulate(i)
```

Can be written as

```
sapply(1:10, simulate)
```

We are applying a function to each value of a vector

Switching to parSapply()

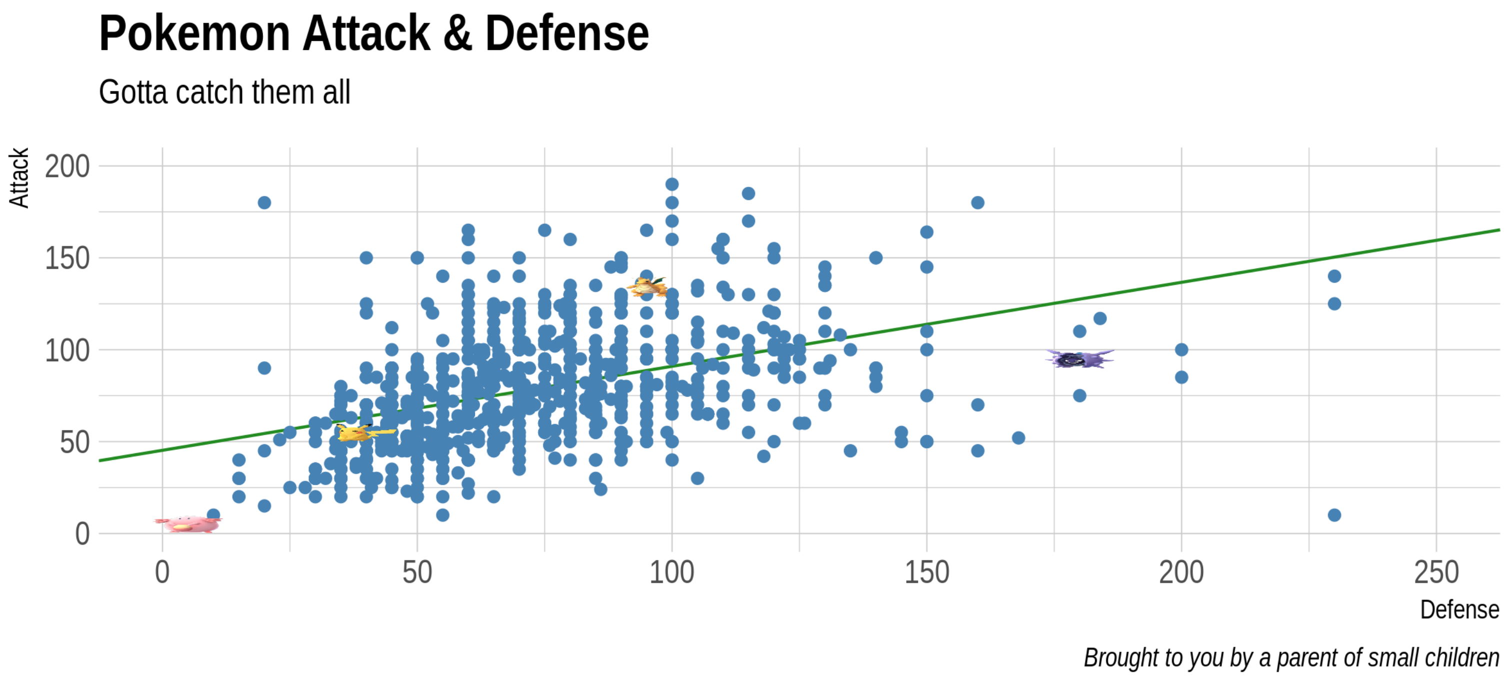
It's the same recipe!

1. Load the package
2. Make a cluster
3. Switch to `parSapply()`
4. Stop!

Example: Pokemon battles

```
plot(pokemon$Defense, pokemon$Attack)
abline(lm(pokemon$Attack ~ pokemon$Defense), col = 2)
cor(pokemon$Attack, pokemon$Defense)
```

```
0.437
```



Bootstrapping

In a perfect world, we would resample from the *population*; but we can't

Instead, we assume the original sample is representative of the population

1. Sample with *replacement* from your data
    - The same point could appear multiple times
2. Calculate the correlation statistics from your new sample
3. Repeat

A single bootstrap

```r
bootstrap <- function(data_set) {
    # Sample with replacement
    s <- sample(1:nrow(data_set), replace = TRUE)
    new_data <- data_set[s,]

    # Calculate the correlation
    cor(new_data$Attack, new_data$Defense)
}
```

```r
# 100 independent bootstrap simulations
sapply(1:100, function(i) bootstrap(pokemon))
```

Converting to parallel

- Load the package
- Specify the number of cores
- Create a cluster object
- Export functions/data
- Swap to `parSapply()`
- Stop!

```
library("parallel")
```

```
no_of_cores <- 7
```

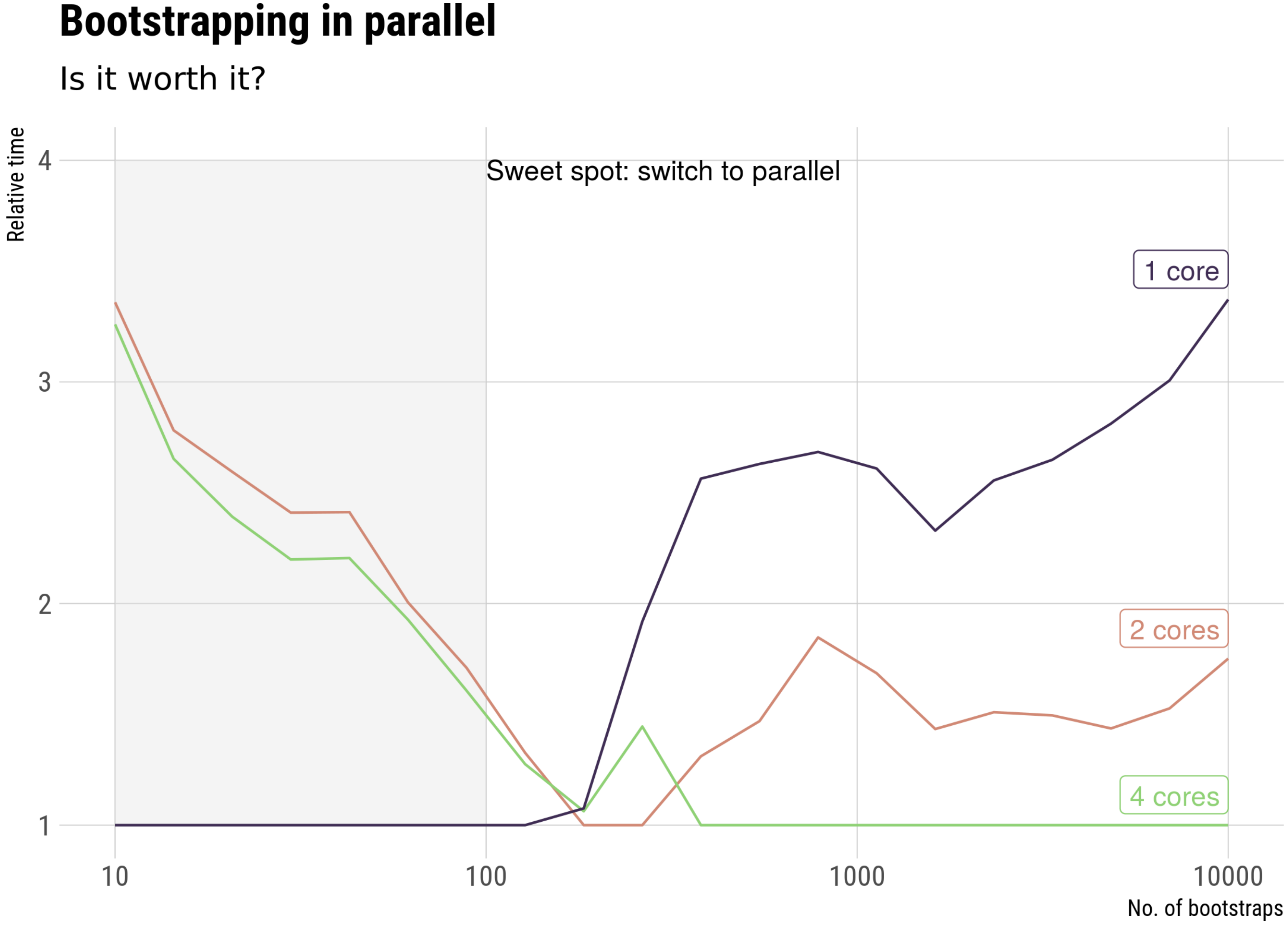
```
cl <- makeCluster(no_of_cores)
```

```
clusterExport(cl,
  c("bootstrap", "pokemon"))
```

```
parSapply(cl, 1:100,
  function(i) bootstrap(pokemon))
```

```
stopCluster(cl)
```

Timings


Bootstrapping in parallel
Is it worth it?
Relative time
4
3
2
1
Sweet spot: switch to parallel
1 core
2 cores
4 cores
10
100
1000
10000
No. of bootstraps

Let's practice!

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Congratulations!

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Final Slide

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