

Performance and Parallel Evaluation

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Performance & Parallel Evaluation

R code

- ▶ Correct, then efficient

Parallel evaluation

- ▶ Computer
- ▶ Cluster
- ▶ Cloud

R code

Priorities

1. Correct!
2. Robust – works for most realistic inputs
3. Simple
4. Fast

R code: deadly sins

1. Unnecessary iteration

```
x <- 1:10000; for (i in seq_along(x)) x[i] = log(x[i])
```

2. Copy-and-append iteration

```
answer <- numeric()  
for (i in 1:10000) answer <- c(answer, 1/i)  
for (i in 1:10000) answer[i] <- 1/i
```

3. Unnecessary evaluation

```
x <- 1:1000000  
for (i in seq_along(x)) x[i] = x[i] * sqrt(2)
```

4. Re-implementation

R code: saving graces I

```
fun1 <- function(n) {  
  ## How many sins?  
  x <- numeric()  
  for (i in 1:n)  
    x <- c(x, log(i) * sqrt(2))  
  x  
}  
  
fun2 <- function(n)  
  log(seq_len(n)) * sqrt(2)
```

R code: saving graces II

1. Validation – `identical()`, `all.equal()`

```
identical(fun1(1000), fun2(1000))  
## [1] TRUE
```

2. Timing – `system.time()`, *microbenchmark()*

```
library(microbenchmark)  
microbenchmark(fun1(1000), fun2(1000))  
  
## Unit: microseconds  
##          expr          min           lq          mean  
## fun1(1000) 1726.480 1746.0545 2518.5444  
## fun2(1000)   36.131   36.8945  41.0648  
##      median           uq          max neval  
## 1771.0925 2556.803 5122.918   100  
##   40.6885   43.264   63.635   100
```

R code: saving graces III

3. 'Experience' – available packages & functions
4. Profiling – `Rprof()`
5. Foreign languages – e.g., C, *Rcpp*

Parallel evaluation

- ▶ Most often: ‘embarassingly parallel’ evaluation of iterative for loops / `lapply()`

Other packages

- ▶ *parallel* – a base package; single computer
- ▶ *foreach* – popular ‘for’ loop paradigm
- ▶ *BatchJobs* – clusters with job schedulers
- ▶ *Rmpi* – classic HPC

BiocParallel

- ▶ Consistent interface
- ▶ Plays well with many *Bioconductor* packages

Parallel evaluation

```
library(BiocParallel)
fun <- function(i) {
  Sys.sleep(1)
  i
}
system.time(res1 <- lapply(1:5, fun))

##      user  system elapsed
##  0.002   0.000   5.007

system.time(res2 <- bplapply(1:5, fun))

##      user  system elapsed
##  0.035   0.024   1.085

identical(res1, res2)

## [1] TRUE
```

Parallel evaluation: *BiocParallel*

- ▶ Different `*Param()` objects for styles of computing, e.g.,
 - ▶ `SerialParam()`: no parallel evaluation
 - ▶ `MulticoreParam()`: separate forked processes on one computer
 - ▶ `BatchJobsParam()`: jobs submitted to a cluster queuing system
- ▶ `register()` a param or provide it as an argument for use in `bplapply()`.
- ▶ Sensible default values.

Parallel evaluation: processing large genomic files

Restrict input to minimum necessary data

- ▶ Select columns or fields of files to import, e.g., `colClasses` argument to `read.table()`; `ScanBamParam()` and `ScanVcfParam()`.
- ▶ Use a data base, hdf5, or other file format that allows queries or slices of the data to be imported.

Iterate through files to manage memory use

- ▶ File connections in base R
- ▶ `BamFile("my.bam", yieldSize=1000000)`

GenomicFiles

- ▶ Functions to help manage collections of genomic files

Parallel evaluation: extended example

Goal: for a vector of paths to bam files, `f1s`, summarize GC content of each aligned read.

```
library(Rsamtools); library(GenomicFiles)
bfls <- BamFileList(f1s, yieldSize=100000)
yield <- function(bfl) # input a chunk of alignments
  readGAlignments(bfl, param=ScanBamParam(what="seq"))
map <- function(aln) { # GC content, bin & cumulate
  gc <- letterFrequency(mcols(aln)$seq, "GC",
    as.prob=TRUE)
  cumsum(tabulate(1 + gc * 50, 51))
}
reduce <- `+`

gc <- bplapply(bfls, reduceByYield, yield, map, reduce)
```

Summary

- ▶ **Correct** first, performance second
- ▶ No need to worry about code that doesn't take very long!
- ▶ 'Embarassingly' parallel (`lapply()`-like) problems easily parallelized, especially on a single computer.
- ▶ Opportunity for very scalable computations, e.g., via AMI & StarCluster.

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