Working with Large Data

Martin Morgan[1]

June 23 – 28, 2013

[1] mtmorgan@fhcrc.org

Write efficient *R* code

1. **Vectorize**
2. Pre-allocate and fill
3. Exploit existing software
4. Use appropriate algorithms
5. Avoid expensive conveniences

Symptom It takes too long to perform a simple mathematical calculation

Solution Vectorize, e.g., `log(x)`, `x %*% y`

Write efficient *R* code

1. Vectorize
2. **Pre-allocate and fill**
3. Exploit existing software
4. Use appropriate algorithms
5. Avoid expensive conveniences

Symptom A loop appends to a result vector; it starts quickly but then gets slower and slower!

Solution Fill a pre-allocated result vector or, better, use `result <- lapply(x, function(...) ...)`.

Write efficient *R* code

1. Vectorize
2. Pre-allocate and fill
3. **Exploit existing software**
4. Use appropriate algorithms
5. Avoid expensive conveniences

Symptom Everyone must be doing this, why do I feel like I'm re-inventing the wheel (and doing it poorly!)?

Solution Use established, performant software, e.g., *limma*, *DESeq2*

Write efficient *R* code

1. Vectorize
2. Pre-allocate and fill
3. Exploit existing software
4. **Use appropriate algorithms**
5. Avoid expensive conveniences

Symptom Execution time increases dramatically as data size increases

Solution Choose algorithms that scale linearly or better with data size.

Write efficient *R* code

1. Vectorize
2. Pre-allocate and fill
3. Exploit existing software
4. Use appropriate algorithms
5. **Avoid expensive conveniences**

Symptom An over-zealous 'feature' hurts performance

Solution Avoid the feature, e.g., `l = list(a=1:3); unlist(l, use.names=FALSE)`

Write efficient *R* code

1. Vectorize
2. Pre-allocate and fill
3. Exploit existing software
4. Use appropriate algorithms
5. Avoid expensive conveniences

> *There are many fast ways to get the wrong answer* – R. Gentleman

Manage data and processors

1. **Restriction**
2. Sampling
3. Iteration
4. Parallel evaluation

```
library(Rsamtools)
gr <- GRanges("chr7",
  IRanges(100000, width=100))
param <- ScanBamParam(
  what = c("rname", "pos", "cigar"),
  which = gr)
scanBam("a.bam", param = param)
```

Manage data and processors

1. Restriction
2. **Sampling**
3. Iteration
4. Parallel evaluation

```
library(ShortRead)
samp <- FastqSampler("end1.fastq")
yield(samp)
set.seed(123); yield(samp)
set.seed(123); yield(samp)
```

Manage data and processors

1. Restriction
2. Sampling
3. **Iteration**
4. Parallel evaluation

```
library(Rsamtools)
bf <-
  BamFile("a.bam", yieldSize=1e6)
open(bf)
repeat {
  gl <- readGAlignments(bf)
  if (length(gl) == 0)
    break;
  ## do work
}
close(bf)
```

Manage data and processors

1. Restriction
2. Sampling
3. Iteration
4. **Parallel evaluation**

```
library(parallel)
options(mc.cores=detectCores)
fls <- c("a.bam", "b.bam")

## sequential
x0 <- lapply(fls, countBam)

## parallel, 1 core per BAM file
x1 <- mclapply(fls, countBam)

identical(x0, x1)  # TRUE
```

Other parallel solutions possible, e.g., clusters, Windows

Acknowledgments

- Vince Carey
- Michael Lawrence
- Hervé Pagès
- Valerie Obenchain
- Marc Carlson
- Paul Shannon
- Dan Tenenbaum