

# Advanced R Programming - Lecture 6

## Parallel programming

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(slides based on Leif Jonsson's and Måns Magnusson's)

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# Today

Parallelism

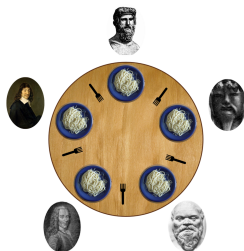
Theoretical limits

Parallelism in R

Balance and subsetting

# Questions since last time?

# Classical introduction: dining philosophers problem



wait until left fork available  
wait until right fork available  
eat  
release left fork  
release right fork

Solutions:  
synchronize: pick lower number (Dijkstra)  
wait for permission (mutex)  
release and random wait

[https://en.wikipedia.org/wiki/Dining\\_philosophers\\_problem](https://en.wikipedia.org/wiki/Dining_philosophers_problem)

Mostly we will not (a.s.) be concerned with such problems.

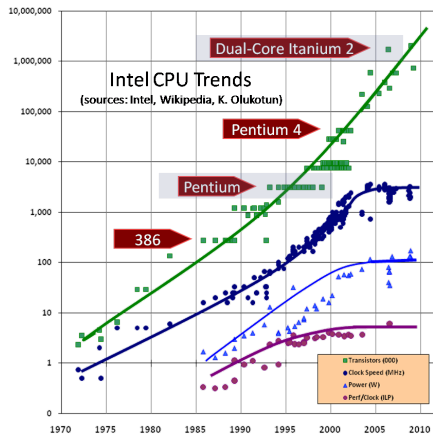
# What is parallelism?

Multiple cores

Each core work with its own part

Cores can exchange information

# Why parallelism?



<http://www.gotw.ca/publications/concurrency-ddj.htm>

Navigation icons: back, forward, search, etc.

# Why parallelism?

Single core limits

Handling larger data

Solving problems faster

More and more important

Is there any **but** ... ?

# Types of parallelism

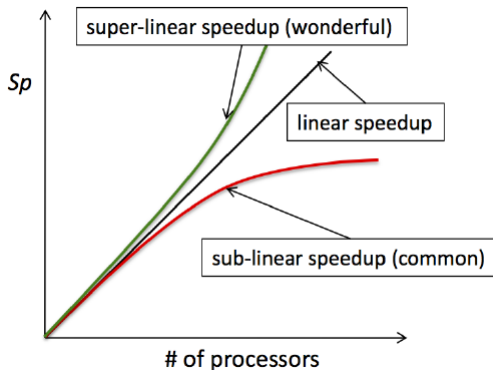
Multicore systems

Distributed systems

Graphical processing units (GPU)



# Speedup



[https://portal.tacc.utexas.edu/c/document\\_library/get\\_file?uuid=e05d457a-0fbf-424b-87ce-c96fc0077099&groupId=13601](https://portal.tacc.utexas.edu/c/document_library/get_file?uuid=e05d457a-0fbf-424b-87ce-c96fc0077099&groupId=13601)

# Theoretical limits

## **Strong scaling: Amdahl's law**

Deals with *fixed problem size, increasing resources*

## **Weak scaling: Gustafsons law**

Deals with *increasing size problem along with increasing resources*

# Amdahl's law

$$\text{Speedup : } S_p = \frac{\text{execution time on 1 processor}}{\text{execution time on } P \text{ processors}}$$

$$S_p \leq \frac{1}{f_s + \frac{f_p}{P}}$$

Where:

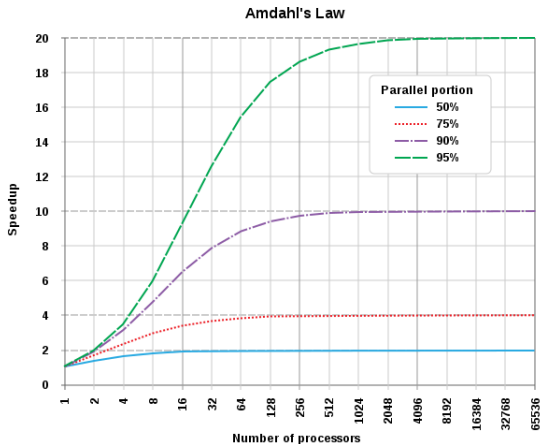
$f_s$  = serial fraction of computations

$f_p$  = parallel fraction of computations

$P$  = number of cores

For a *fixed size problem*, single core computation time is fixed= 1!

# Amdahl's law



[https://en.wikipedia.org/wiki/Amdahl's\\_law](https://en.wikipedia.org/wiki/Amdahl's_law)

## Gustafsons law

$$\text{Speedup : } S_p = \frac{\text{execution time on 1 processor}}{\text{execution time on } P \text{ processors}}$$

$$S_p \leq \frac{\alpha + (1 - \alpha)P}{\alpha + (1 - \alpha)} = P - \alpha * (P - 1)$$

Where:

$\alpha$  = fraction of time dedicated to serial computations

$P$  = number of cores

*Problem size scales with  $P$ , parallel execution time is fixed= 1!*  
if we only had one core, then the  $P$  parallel computations would have to be done on that core with time  $(1 - \alpha)P$

# Practical problems

Costs of parallelism  
communication

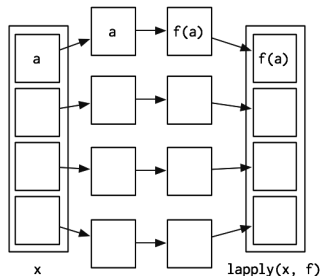
load balancing (NP-hard)  
scheduling (NP-hard) but  $4/3 = k$ -approximate algorithm

fine-grained vs embarrassingly parallel (EP)

## Parallelism in R (embarassingly parallel)

Based on `lapply()`

iterations inside a loop are independent of each other



(H. Wickham, Advanced R, p. 201)

What about: `fctl<-1;for(i in 1:n){fctl<-i*fctl}` ?

# parallel package

Two approaches:

1. `mclapply()`
2. `parLapply()`



# mclapply()

## Pros

Simple to use  
Low overhead (startup)

## Cons

Does not work on Windows  
Only multi core

```
parLapply(type="psock")
```

### Pros

Works everywhere  
Good for testing/developing

### Cons

Slow on multiple nodes

```
parLapply(type="mpi")
```

### Pros

Good for multiple computers Good for production

### Cons

Can be used interactively Needs Rmpi package

## Load balance

`lapply(list,...)` does in order of `list`

load balancing is NP-hard

often we do not know running time for `list[[i]]`

submit to cores in order?

split into consecutive equal chunks?

Example:

all  $2^p$  regression models on  $p$  predictors

generate all combinations:  $\emptyset, \{1\}, \dots, \{p\}, \{1, 2\}, \dots$

**randomize** order in `list`

R's `par` family has load balancing capabilities

## Subset methods (non-EP)

`glm()`: large number of observations

### **Chunk averaging** (estimation)

- break data into chunks of rows

- to each chunk (in parallel) apply `glm()`

- average the results to obtain single estimate

Observations i.i.d. and model is *decent*

Asymptotic equivalence for large samples

Chunks are not identically distributed: first cases then controls

**randomly** permute observations

(will not harm an initial random arrangement)

## Subset methods (non-EP)

`glm()`: large number of predictors

### **Subsetting variables** (prediction, *decent* model)

- create random subsets of predictors

- to each subset apply `glm()`

- do prediction for each subset

- combine predictions e.g. average, majority rule

prediction difficult in high dimensions—*curse of dimensionality*

# Example

[https://github.com/STIMALiU/AdvRCourse/blob/master/Code/parallel\\_example.R](https://github.com/STIMALiU/AdvRCourse/blob/master/Code/parallel_example.R)

Parallel code example

The End... for today.  
Questions?  
See you next time!