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

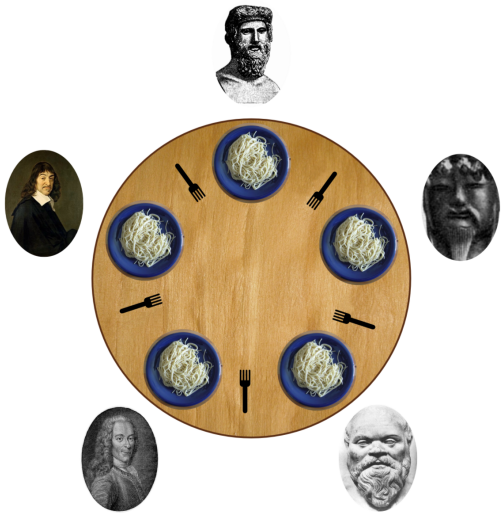
Theoretical limits

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`

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

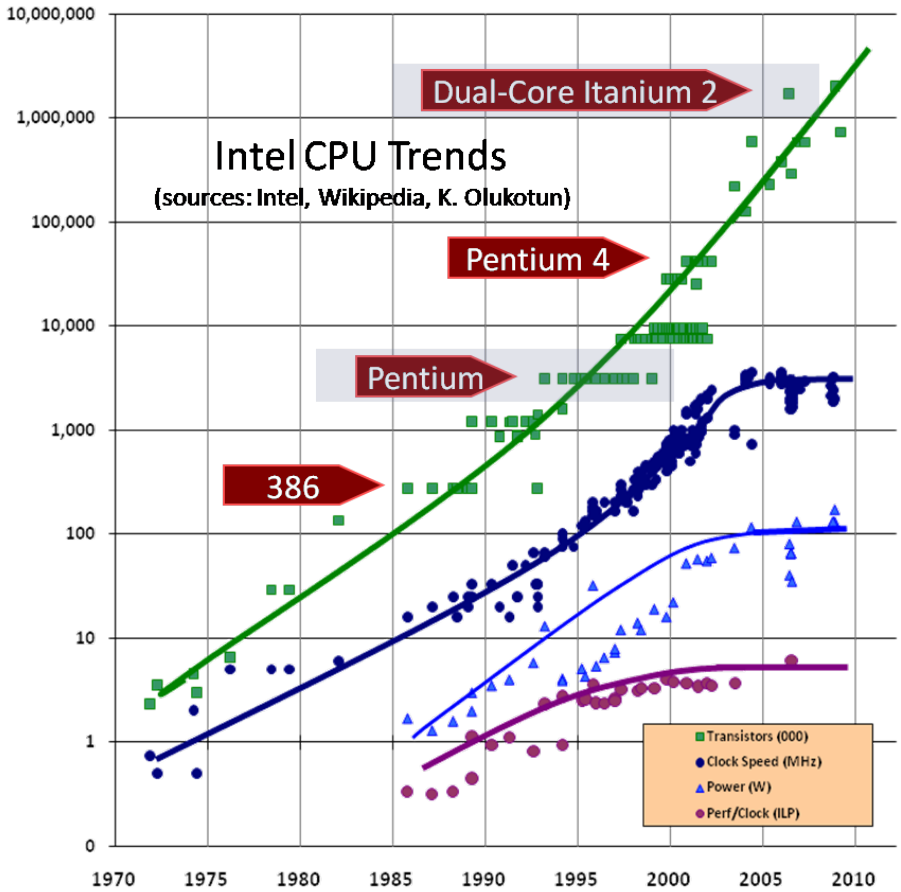
What is parallelism?

Multiple cores

Each core work with its own part

Cores can exchange information

Why parallelism?



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

Why parallelism?

Single core limits

Handling larger data

Solving problems faster

More and more important

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

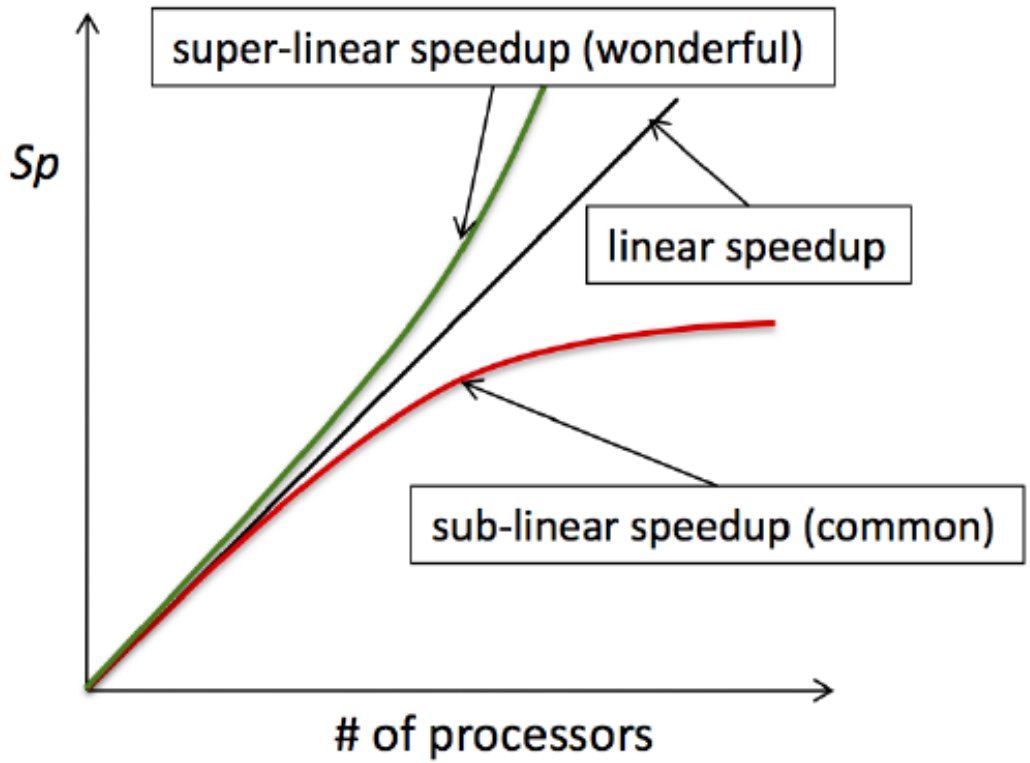
Types of parallelism

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

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

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

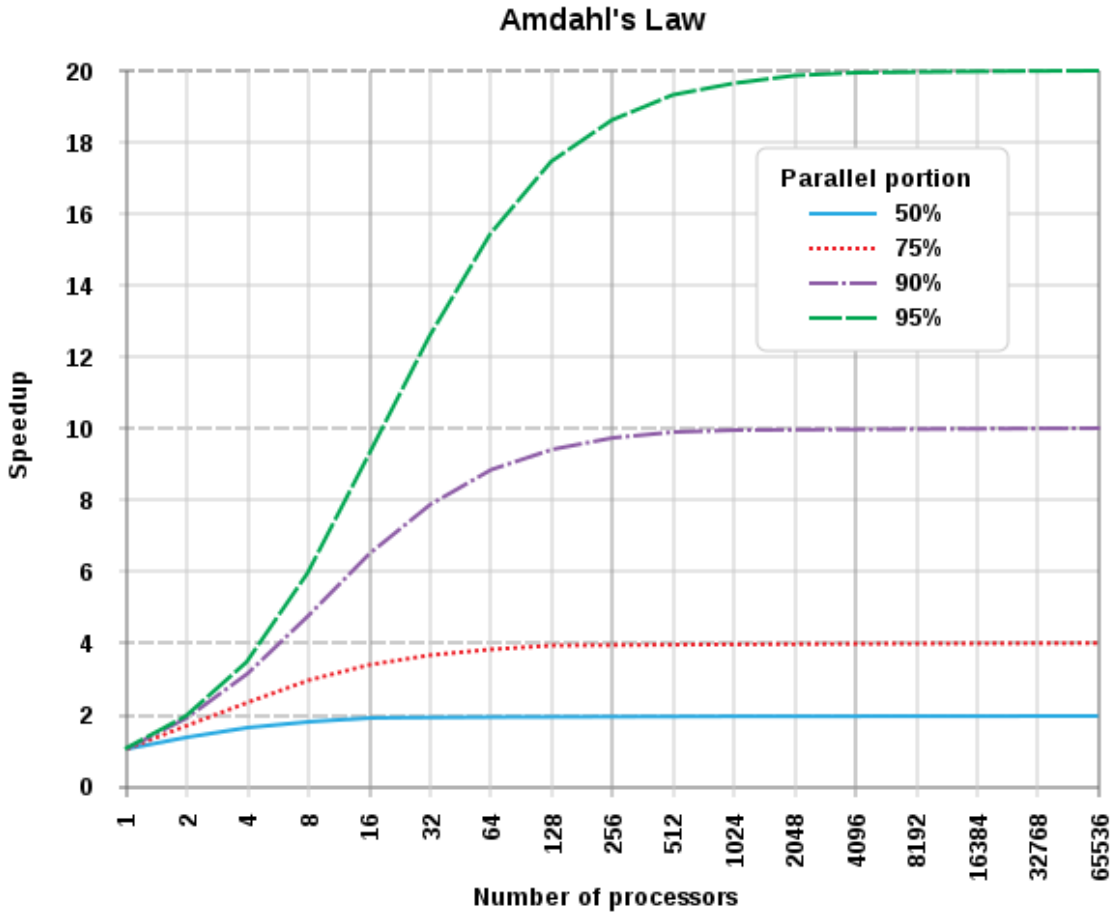
$$S_p \leq \frac{1}{f_s + \frac{f_p}{P}}$$

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

Gustafsons law

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

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

Where:

α = 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

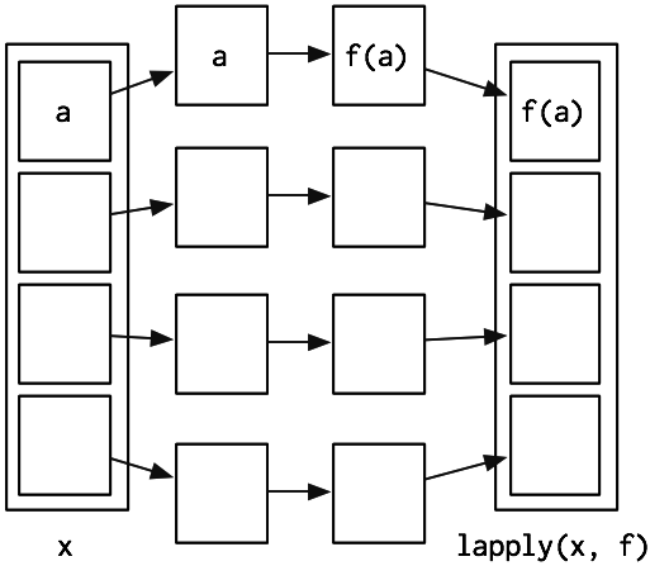
Costs of parallelism
communication

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 indepenendent 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: $\emptyset, \{1\}, \ldots, \{p\}, \{1,2\}, \ldots$

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 equivalance 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`
Parallel code example

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