Weak Models For Distributed Computing

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Gadi: I am not an implementor of tools, programming languages, or platforms!

Annie: ... pls mention where computers can help you except from text editor and a slides editor ...
Part I

Genome-Wide Epigenetic Modifications as a Shared Memory Consensus Problem

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The human genome
The entire DNA of a single human cell

- Two meters long
- 3 billion base pairs
- About 25,000 genes

(Only about 1 percent of DNA is made up of protein-coding genes)
Chromatin

Package DNA into a small volume to fit into the nucleus of a cell

Short region of DNA double helix

Nucleosomes: the basic unit of chromatin

Chromatin fiber of packed nucleosomes

Figure 12-11a
Introduction to Genetic Analysis, Eleventh Edition
© 2015 W. H. Freeman and Company
Q: How can an organism have different cell types yet one genome?

A: Each cell expresses, or turns on, only a fraction of its genes. The rest of the genes are repressed, or turned off.
Regulation of gene expression
Turning genes on and off

Condensed chromatin

Open chromatin

Activate

Deactivate

Off

On
Environmental influences, such as a person’s diet, stress and exposure to pollutants, impact gene expression.
Epigenetics

Modifications that do not change the DNA and affect gene activity
Nucleosome
The epigenetic consensus problem
The epigenetic consensus problem

1-writer
0-eraser
0-writer
1-eraser

\{empty, 0, 1\}
Very weak model

- Randomization
- Anonymous processes (no identifiers)
- Anonymous shared memory
- Memory-less processes (well may 1-2 bits)
- A transition from 0 to 1 cannot occur directly
- No sense of direction
- Self-stabilization

We present an algorithm that matches the biological assumptions, prove it correctness and derive bounds on its expected run time both theoretically and in simulations.
The epigenetic consensus problem

1-writer
0-eraser
0-writer
1-eraser

{empty, 0, 1}
The epigenetic consensus problem

**Corollary 6.2** Assume $W_1/W_0 \geq 3$. The probability that the final decision value is 1 is more than

$$(1 - (1/3)^N) \times \left(1 - e^{-N/12}\right)$$

**Corollary 7.2** Assuming $W_1/W_0 \geq 3$, $E[T] \leq 6.4N^2$
Annie’s question: Where computers can help you except from text editor and a slides editor?
Simulations

Figure 1: Distribution of number of steps to reach consensus. Plots summarize 300 random runs of the algorithm. a) low and b) high level of competitions between 1-writers and 0-writers. $\mu$ denotes the average time to reach consensus.
Figure 2: a) Number of zeros and collisions vs steps in the algorithm. While the initial number of collisions is a linear function of the number of 0’s, we observe that towards the end of the algorithm there are very few collisions while the number of 0’s remains relatively high. b) Comparison between the proposed original model and a revised model that allows writers to attach themselves with the erasers and the erasers wait until a collision is resolved. Here we can see that the waiting version is faster at both competition level compared to the original model.
Conclusion #1

Weak models are interesting!
Part II

Anonymous Shared Memory
Classical view of SM

Objects have names

shared memory
Anonymous shared memory

NO prior agreement on the names of the objects!
Anonymous shared memory

Gadi Taubenfeld

April 15th, 2019

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Anonymous shared memory
Coordination without prior agreement
by Gadi Taubenfeld
## Algorithms & space bounds

<table>
<thead>
<tr>
<th>Algorithms</th>
<th>Can do</th>
<th>Cannot do</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Deadlock-free symmetric mutual exclusion for two processes</strong></td>
<td>✔️</td>
<td>✗</td>
</tr>
<tr>
<td></td>
<td>odd # of registers</td>
<td>even # of registers</td>
</tr>
<tr>
<td><strong>Obstruction-free consensus for n ≥ 2 processes</strong></td>
<td></td>
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<tr>
<td></td>
<td>2n-1 or more</td>
<td>n or less</td>
</tr>
<tr>
<td><strong>Obstruction-free adaptive perfect renaming for n ≥ 2 processes</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>2n-1 or more</td>
<td>n or less</td>
</tr>
</tbody>
</table>

(The # of registers is not 1)
Optimal Memory-Anonymous Symmetric Deadlock-Free Mutual Exclusion

Theorem. For every $n \geq 1$, there is a symmetric deadlock-free mutual exclusion algorithm for $n$ processes using $m \geq 1$ anonymous R/W registers if and only if for every positive integer $1 \leq k \leq n$, $m$ and $k$ are relatively prime.

The same result holds also for RMW registers! *

* It is trivial to do also with one RMW register.
Resolving two open problems

For a universe which includes (also) anonymous objects,

- Are atomic read/write registers the weakest objects?
- Are deterministic (oblivious) objects with the same set-consensus number have the same computational power?

NO
Conclusion #2

Weak models are interesting!
Fractions were studied by Egyptians mathematicians around 1600 B.C. However, fractions, as we use them today, didn't exist in Europe until the 17th century.
Part III
Fractions in Distributed Computing

- We understand what it means to tolerate one process failure.
- But what does it mean to tolerate 0.8 process failure?
**Motivation**

*Something is better than nothing*

- FLP: Impossibility of consensus in the presence of a single failure.

- Is consensus possible in the presence of a single *weak* failure?
Weak Failures: Definitions, Algorithms and Impossibility Results by Gadi Taubenfeld

Is consensus possible in the presence of a single weak failure?

YES !!!
Suppose you can solve a problem in the presence of $f$ traditional failures, but not in the presence of $f+1$ such failures.

Maybe it is possible to solve the problem in the presence of $f$ traditional failures plus several weak failures.
Set agreement and renaming in the presence of contention-related crash failures

Anaïs Durand  Michel Raynal  Gadi Taubenfeld
Conclusion #3

Weak models are interesting!