Single-Pass List Partitioning

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MuCoCos’08
Outline

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2. Problem Definition
3. The SINGLEPass Algorithm
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Motivation

Effectiveness of many parallel algorithms relies on partitioning the input into pieces.
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ALTHOUGH there are common settings where the input cannot be partitioned so easily.
Example: Sequences as input to algorithms in the Standard Template Library (STL), part of the C++ standard library.
Input given using *(forward) iterator*, abstract from the underlying data structure.
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Operations on a **forward iterator** `it`:
Algorithms in the STL

Input given using \textit{(forward) iterator}s, abstract from the underlying data structure.

Operations on a \textit{forward iterator} it:

- \texttt{*it}: Dereference.
Algorithms in the STL

Input given using (forward) iterator, abstract from the underlying data structure.

Operations on a forward iterator it:
  • *it: Dereference.
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Operations on a *forward iterator* `it`:

- `*it`: Dereference.
- `++it`: Advance to next element.
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Operations on a *forward iterator* it:
- *it: Dereference.*
- ++it: Advance to next element.
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Forward sequence
How to partition forward sequences or alike?

In compile-time:

1. The sequence is actually a **random access sequence** (e.g. an array)
   - More operations: \( it + k, it - k, it2 - it1, \ldots \)
   - Sequence length can be known in constant time

2. The sequence is **not** random access
   - Sequence length is **unknown** in constant time
Naïvely:

- **TRAVERSETWICE**
- **POINTERARRAY**
How to partition forward sequences or alike? (2)

Naïvely:

- **TRAVERSE_TWICE**
  1. Determine length (1st traversal)
  2. Partition (2nd traversal)

- **POINTER_ARRAY**
How to partition forward sequences or alike? (2)

Naïvely:

- **TRAVERSETWICE**
- **POINTERARRAY**
  1. Store pointers in a dynamic array (linear auxiliary memory)
  2. Trivial index calculation
How to partition forward sequences or alike? (2)

Naïvely:

- **TRAVERSE_TWICE**
- **POINTER_ARRAY**

Cannot this be done more efficiently?
How to partition forward sequences or alike? (2)

Naïvely:

- TRAVERSE_TWICE
- POINTER_ARRAY

Cannot this be done more efficiently?
Amdahl’s law: speedup limited by the sequential portion.
Our contribution

An efficient sequential algorithm to divide *forward sequences*.

- Only *one traversal*
- *Sub-linear* additional space
List Partitioning problem

Given a *forward sequence*, divide it into *p parts* of almost equal length.
List Partitioning problem

Given a forward sequence, divide it into \( p \) parts of almost equal length.

Quality ratio \( r \): \( 1 \leq \frac{\text{longest part}}{\text{shortest part}} \)

\( r \) correlates to the efficiency of processing the parts in parallel (given that processing time is proportional to parts length)
Given a forward sequence, divide it into $p$ parts of almost equal length.

**Quality ratio $r$:** $1 \leq \frac{|\text{longest part}|}{|\text{shortest part}|} \leq R$

$r$ correlates to the efficiency of processing the parts in parallel (given that processing time is proportional to parts length)

$R$: constant, depends only on a tuning parameter, namely the oversampling factor $\sigma$.

$\sigma \in \mathbb{N} \setminus \{0\}$. 

**List Partitioning problem**
**List Partitioning** as an online problem

Only one element is given at a time, no global information.
**List Partitioning** as an online problem

Only one element is given at a time, no global information.

Optimal offline algorithm: the difference in length between the parts is at most 1.

Quality ratio: \( r_{\text{OPT}} = \left\lfloor n/p \right\rfloor / \left\lceil n/p \right\rceil \xrightarrow{n \to \infty} 1. \)
Let $\sigma = 2$, $p = 3$

**Algorithm**

1. Initialization.
2. Iteratively append to $S$ at most $2\sigma p$ elements from $L$.
3. While $L$ has more elements do:
   1. Merge each two consecutive subsequences into one.
   2. Let $k := 2k$.
4. Iteratively append to $S$ at most $\sigma p$ consecutive subsequences of length $k$ from $L$.
5. Merge the subsequences in $S$ to obtain $p$ subsequences.
Algorithm

Let $\sigma = 2, \ p = 3$

L:

1. Initialization.

$k = 1, \ S = \{}$

$0 \rightarrow 1 \rightarrow 2 \rightarrow 3 \rightarrow 4 \rightarrow 5 \rightarrow 6 \rightarrow 7 \rightarrow 8 \rightarrow 9 \rightarrow 10 \rightarrow 11 \rightarrow 12 \rightarrow 13 \rightarrow 14 \rightarrow 15$
Let $\sigma = 2$, $p = 3$

1. Initialization.
2. Iteratively append to $S$ at most $2\sigma p$ 1-elem subsequences from $L$. 

L: \[0 \rightarrow 1 \rightarrow 2 \rightarrow 3 \rightarrow 4 \rightarrow 5 \rightarrow 6 \rightarrow 7 \rightarrow 8 \rightarrow 9 \rightarrow 10 \rightarrow 11 \rightarrow 12 \rightarrow 13 \rightarrow 14 \rightarrow 15\]

$k = 1, \quad S = \{\}$
Algorithm

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$L:\begin{array}{cccccccccccccc}
0 & 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 & 12 & 13 & 14 & 15
\end{array}$

$k = 1, \quad S = \{0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12\}$

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\end{array}
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$\begin{align*}
0 & \rightarrow 1 & \rightarrow 2 & \rightarrow 3 & \rightarrow 4 & \rightarrow 5 & \rightarrow 6 & \rightarrow 7 & \rightarrow 8 & \rightarrow 9 & \rightarrow 10 & \rightarrow 11 & \rightarrow 12 & \rightarrow 13 & \rightarrow 14 & \rightarrow 15 \\
\text{begin} & & & & & & & & & & & & & & & & & \text{next end}
\end{align*}$

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Getting $p$ subsequences of similar length

$L:$

\[ S = \{0, 2, 4, 6, 8, 10, 12, 14, 15\} \]

At the beginning of step 4:
\[ \sigma p \leq s = |S| - 1 \leq 2\sigma p \] subsequences ($s = 8$)
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\text{begin} & \text{end}
\end{array}$

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$s \mod p$ rightmost subsequences: $\text{merge } \left\lceil s/p \right\rceil$ subsequences
Getting $p$ subsequences of similar length

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- \begin{align*} S &= \{0, 2, [4, 6, 8, [10), 12, 14, 15]\} \\
& \text{At the beginning of step 4:} \\
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Getting \( p \) subsequences of similar length

\[ L : \]

\[ S = \{[0, 2, 4), 6, 8, 10, 12, 14, 15\} \]

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\( p - (s \mod p) \) leftmost subsequences: \textit{merge} \( \lfloor s/p \rfloor \) subsequences

Special care with the \textit{last subsequence} in \( S \), which may be \textit{not} full. The algorithm guarantees that two parts differ in length in at most in \( k \) elements.
Analysis

Auxiliary space (i.e. $|S|$): $\Theta(\sigma p)$

**Time:** $\Theta(n + \sigma p \log n)$.

- L traversal: $\Theta(n)$
- Step 3 visits $\Theta(\sigma p)$ elements of $S$ in $\Theta(\log n)$ iterations.
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Ratio:
- worst-case: $r$ bounded by $\frac{\sigma + 1}{\sigma}$.
- average: $\mathbb{E}r < \frac{1}{\sigma p} \sum_{\ell = \sigma p}^{2\sigma p - 1} \frac{\ell}{p} \approx 1 + \frac{1}{\sigma p} ((p - 1) \ln(2))$
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E.g. if $\sigma = 10$ and $p = 32$, then $r \leq 1.1$ and $\mathbb{E} r < 1.07$
Generalization of the \textsc{SINGLEPass} Algorithm

Performs \textit{merge} steps only every $m$\textsuperscript{th} loop iteration. In the remaining iterations, \textit{S} is doubled in size, so that more subsequences can be added.
Generalization of the **SINGLEPASS** Algorithm

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Generalization of the SINGLEPass Algorithm

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Thus, the total number of iterations is kept the same: $\Theta(\log n)$.

Equivalent to increasing the oversampling factor to $\sigma n^\gamma$ with $\gamma = 1 - 1/m$. 
Analysis

\[ n^\gamma = \frac{n}{\sqrt{m n}} = \sqrt[n]{n^{m-1}} \]

Auxiliary space (i.e. \( |S| \)): \( O(\sigma p n^\gamma) \).

Time: \( \Theta(n + \sigma p(n^\gamma + \log n)) \).
Analysis

\[ n^{\gamma} = \frac{n}{\sqrt[\gamma]{n}} = \sqrt[\gamma]{n^{m-1}} \]

Auxiliary space (i.e. \( |S| \)): \( O(\sigma pn^{\gamma}) \).

Time: \( \Theta(n + \sigma p(n^{\gamma} + \log n)) \).

Ratio:
\[
\frac{|\text{longest}|}{|\text{shortest}|} = \frac{(\sigma n^{\gamma} + 1)k}{\sigma n^{\gamma}k} = 1 + \frac{1}{\sigma n^{\gamma}} = 1 + \frac{m \sqrt{n}}{\sigma n} \xrightarrow{n \to \infty} 1
\]
Choosing $m$

The choice of $m$ trades off time and space versus solution quality (better $r$ as $m$ larger).
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Some interesting cases:

- $m = 1$: $merge$ is performed each iteration $\rightarrow$ simple $\text{SINGLEPass}$ Algorithm
- $m = 2$: $merge$ is performed once each two iterations
  - $n^\gamma = \sqrt{n}$
  - Auxiliary space: $O(\sigma p \sqrt{n})$
  - Time: $\Theta(n + \sigma p(\sqrt{n} + \log n))$.
  - Ratio: $1 + \frac{1}{\sqrt{n}}$
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Some interesting cases:

- $m = 1$: merge is performed each iteration → simple SINGLEPass Algorithm
- $m = 2$: merge is performed once each two iterations
  - $n^\gamma = \sqrt{n}$
  - Auxiliary space: $O(\sigma p \sqrt{n})$
  - Time: $\Theta(n + \sigma p (\sqrt{n} + \log n))$.
  - Ratio: $1 + \frac{1}{\sqrt{n}}$

$m = 2$ appears to be a good compromise.
C++ implementation

Algorithms

- generalized SINGLEPass
  - included in the MCSTL [SSP]
    MCSTL = Multicore STL, parallel implementation of the STL

- TRAVERSETWICE

- POINTERARRAY
Testing

Performance and quality results for $p = 4$. Quality evaluated according the overhead $h = r - 1$.

Setup

- AMD Opteron 270 (2.0 GHz, 1 MB L2 cache).
- GCC 4.2.0 + libstdc++, optimization (-O3).

Parameters for **SINGLEPASS**

- $(o = 1, \ m = 1)$, $\Theta(p)$ space
- $(o = 10, \ m = 1)$, $\Theta(10p)$ space
- $(o = 1, \ m = 2)$, $\Theta(\sqrt{np})$
Time results

- **PointerArray**
- **TraverseTwice**
- **SinglePass o=1,m=1**
- **SinglePass o=10,m=1**
- **SinglePass o=1,m=2**

Running time [ns] / n vs Number of elements (n)
Quality results

![Graph showing quality results](image-url)

- **Overhead r-1 (%)** vs **Number of elements (n)**
- Trivial
- SinglePass $o=1,m=1$
- SinglePass $o=10,m=1$
- SinglePass $o=1,m=2$

**Legend:**
- Trivial
- SinglePass $o=1,m=1$
- SinglePass $o=10,m=1$
- SinglePass $o=1,m=2$
Conclusions

We have solved the list partitioning problem using only one traversal and sub-linear additional space.
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The larger $m$, the better the quality, trading off memory. In the worst-case:

- $m = 1$: $h = 1/\sigma$
- $m > 1$: $h$ decreases exponentially with $n$.

For large input instances and in most practical situations, no difference with optimally partitioned sequences.
[SK08] describes some of the problems and challenges in parallelizing algorithms in the context of the C++ standard library.
References
