Fast parentheses matching on GPU

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Abstract

Parentheses matching is an important fundamental algorithm, with applications including parsing and processing of tree-structured data. Previous literature presents work-efficient parallel algorithms targeting an abstract PRAM machine, but does not address modern GPU hardware. This paper analyzes the parentheses matching problem using two monoids, the bijective semigroup and a novel “stack monoid,” and presents a practical, fast algorithm interleaving these two monoids to map to the thread, workgroup, and dispatch levels of the GPU hierarchy. This algorithm is implemented portably using compute shaders, and performance results show that the algorithm operates at a significant fraction of the raw memory bandwidth of a typical GPU.

1 Introduction

This paper presents an efficient parallel solution to the *parentheses matching problem,* tuned for high throughput on GPU hardware. Parentheses matching is an important subproblem of parsing, and is a general building block for disparate other algorithms, including bin packing[AMW89] and tree pattern matching[PJ20]. The immediate motivation for the present work is calculating clipping rectangles for each node in a tree representing a 2D rendering task.

1.1 Limitations of current state of the art

The literature on the parentheses matching problem goes back decades (at least to [BOV85]), but until now there is no known satisfactory solution running on actual GPU hardware. The literature falls into several categories:

- Theoretical investigations which present work-efficient algorithms analyzed in terms of an abstract Parallel Random Access Machine model but no clear mapping to an efficient GPU implementation ([BOV85], [LP92], [PDC94]).
- Practical algorithms which run on GPU but have a work factor dependent on maximum nesting depth ([Hsu19]).

- More limited GPU-based parsing algorithms which cannot handle arbitrary tree structure ([SJ19]). This category also includes the use of standard generalized prefix sum algorithms with a small fixed bound on nesting depth.

Thus, the prevailing wisdom remains that parsing of arbitrary tree structured data is inherently a serial problem and must be done on CPU rather than GPU.

1.2 Key insights and contributions

There are several key insights in this paper, culminating in presentation and empirical performance measurement of an algorithm that is fast and practical to implement on standard GPU hardware.

The first insight is that the parentheses matching problem can be expressed in terms of two monoids, both of which can be used to compute matches, but with different time/space tradeoffs. The first of these is the well-known bicyclic semigroup which is cheap to compute and can be queried by binary search, and the second is a "stack monoid" which takes more space but can be queried in $O(1)$ time. Either by itself can be used to derive an algorithm which is parallel but has $O(\log n)$ work factor.

The second insight is that *interleaving* these two approaches yields a work-efficient algorithm. Further, the two approaches map well to the hierarchical structure of actual GPU hardware. We present a simple algorithm consisting of reduction of the stack monoid (computing stack snapshots at partition granularity), followed by binary search of the bicyclic semigroup to resolve matches within a partition. The second step can be done within a workgroup, using efficient shared memory. It is reasonably fast but not truly work-efficient.

A faster version of the algorithm adds a third level of hierarchy: a sequence of k elements processed per thread, instead of just one as in the simpler algorithm. This technique is analogous to that used for high performance prefix sum implementations, but requires more sophistication. Stack monoid reduction is used for the smallest granularity, then binary search for the workgroup level, and then stack monoids again for finding matches across workgroup boundaries.

1.3 Experimental methodology and artifact availability

The primary empirical claim is that the proposed algorithm is fast on standard GPU hardware. To demonstrate this claim, we run the code on an AMD 5700 XT as Vulkan compute shaders. The test consists of a random sequence of parenthesis. The GPU time is measured with Vulkan timer queries.

All software is available on GitHub with a permissive Apache 2 open source license[1]. The infrastructure for running and measuring compute shader performance is cross-platform and runs on Metal and Direct3D 12 as well as Vulkan. Such cross-platform infrastructure is unusual for compute-centric tasks, though it is relatively common in game engines.

[1] `https://github.com/linebender/piet-gpu`

1.4 Limitations of the proposed approach

The main limitation of the proposed algorithm is that the presentation and implementation is a 2-dispatch pipeline and is limited to inputs of w^2k^2, where w is workgroup size and k is the number of elements processed per thread. In many cases it is possible to increase k to accommodate the problem size (as is the case for the motivating 2D graphics example), but as inputs scale up the algorithm would need to be extended to 3 or more dispatches.

Parentheses matching in isolation is not an especially useful task. To put this technique into practice will require integration with other subsystems that can utilize parentheses matching as a subtask. For example, parsing of textual tree-structured data formats such as XML and JSON would also require lexical analysis.

2 The parentheses matching problem

The classical version of the parentheses matching problem is, for every index in the source string, find the index of the corresponding matching parenthesis. This paper actually considers a stronger version of the problem: for every closing parenthesis, find the index of the matching open parenthesis. But for every opening parenthesis, find the index of the immediately enclosing opening parenthesis. It is straightforward to reconstruct the traditional version, but the converse is not true.

One statement of the problem is as a simple sequential program which uses a stack.

```
stack = [-1]
for i in range(len(s)):
    out[i] = stack[len(stack) - 1]
    if inp[i] == '(':
        stack.push(i)
    elif inp[i] == ')':
        stack.pop()
```

We will be concerned with *snapshots* of the stack at step i. An appealing quality of this specific formulation of the parentheses-matching problem is that all stacks can be recovered from the output, just by repeatedly following references until the root is reached (here represented by a value of -1).

3 The bicyclic semigroup

The theoretical derivation of the algorithm relies heavily on the *bicyclic semigroup,* actually a monoid, which is well known to model the balancing of parentheses. An element of the bicyclic semigroup Bic can be represented as a pair of nonnegative integers, with $(0, 0)$ as an identity and the following associative operator:

$$(a, b) \oplus (c, d) = (a + c - \min(b, c), b + d - \min(b, c))$$

An open parenthesis maps to $(0, 1)$ and a close parenthesis maps to $(1, 0)$. We will overload the function $\mathrm{Bic}(s)$ over a string to result in the $\oplus$-reduction of this mapping applied to the elements of the string; thus $\mathrm{Bic}($`'))()('`$) = (2, 1)$. We will use slice notation on strings; $s[i..j]$ represents the substring beginning at index i of length $j - i$.

The bicyclic semigroup gives rise to an alternate definition of the parentheses matching problem. In particular, parenmatch(s)[j] is the maximum value of i such that $\mathrm{Bic}(s[i..j]).b = 1$. This is one less than the minimum value such that the b field is 0. Note that $\mathrm{Bic}(s[i..j]).b$ is monotonically increasing as i decreases.

4 The stack monoid

Another related monoid is the *stack monoid,* which is a sort of hybrid of the bicyclic semigroup and the free monoid. Essentially, rather than just counting the number of stack pushes, it contains the actual values pushed on the stack.

$$(a_0, l_0) \oplus (a_1, l_1) = (a_0 + a_1 - \min(|l_0|, a_1), l_0[..\max(0, |l_0| - a_1)] + l_1)$$

Another interpretation of the stack monoid is that the stack monoid reduction of a slice of input represents the unmatched open parentheses in that slice. It is a free monoid, meaning that the sequence can contain values of any type, but in this paper we will (without loss of generality) exclusively store indices.

Like the bicyclic semigroup, the stack monoid lends itself to a straightforward definition of the parenthesis matching problem. A reduction of the stack monoid over a prefix of the input represents a snapshot of the stack, as computed by the sequential algorithm, up to the end of that slice. The result of the parentheses matching algorithm is the top of the stack at each step.

The parenthesis match value at j is the topmost value of stack snapshot taken at position j. Here we use $enum(s)$ to represent the enumeration of the indices of the sequence s, for example, $enum($`'))('`$)$ is the sequence $[(0,$ `')'`$), (1,$ `')'`$), (2,$ `'('`$)]$.

$$parenmatch(s)[j] = last(\mathrm{Stk}(enum(s)[..j]))$$

The k-suffix of the stack monoid is simply the last k values.

The storage required by a single stack monoid value is unbounded, but that does not preclude efficient implementations. In particular, the combination of two values of size k can be done in-place by $2k$ processors in one step. This result generalizes to combination of a vector of values, which can be represented as a stream compaction.

$$rev(\mathrm{Stk}(enum(s)[i_0..i_2])[k] = rev(\mathrm{Stk}(enum(s)[i_0..i_1]))[k{+}j] \text{ where} \mathrm{Bic}(s[i_1..i_2]) = (j, 0)$$

The significance of this relation is that, given the value of the Bic monoid and a materialized stack slice, it is possible to resolve queries in O(1) time. In cases where Bic has a nonzero $.b$, the match is foudn

5 Core parallel algorithm

The core parallel algorithm is a binary search over the bicyclic semigroup. That algorithm by itself is fully parallel and reasonably efficient; it has a work factor of $O(\log n)$ for the binary search.

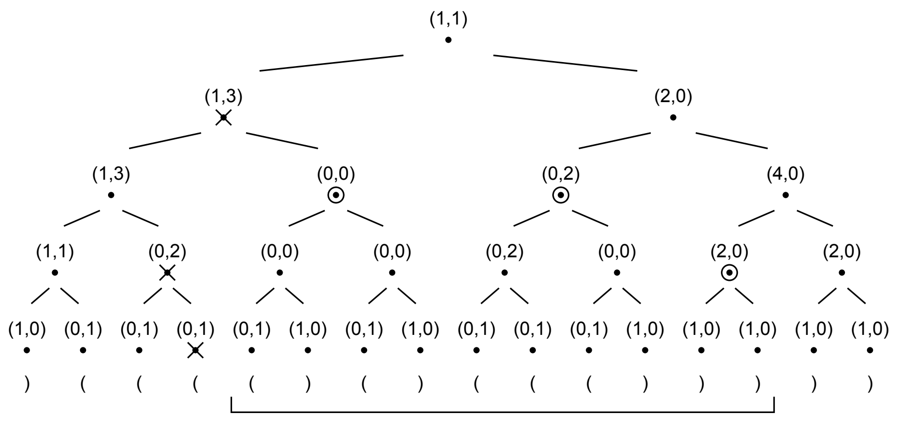
Before running this algorithm, a binary tree of bicyclic semigroup values is constructed; this is the same as the up-sweep phase of a standard parallel prefix sum implementation. Specifically, the leaf nodes of the tree are defined by $tree[0][i] = \mathrm{Bic}(s[i])$, and parent nodes by the relation $tree[j{+}1][i] = tree[j][2i] \oplus tree[j][2i + 1]$. Construction of this tree takes $\lg n$ steps, and the tree itself requires storage of $2n - 2$ bicyclic semigroup elements.

Then, for each index i, the following algorithm searches the tree for a parentheses match.

```
$i \leftarrow i_1$
$b \leftarrow (0, 0)$
$j \leftarrow 0$
while $j < \lg w$ do
    if $i$ bitand $2^j \neq 0$ then
        $q \leftarrow tree[j][\lfloor i/2^j \rfloor - 1] \oplus b$
        if $q.b = 0$ then
            $b \leftarrow q$
            $i \leftarrow i - 2^j$
        else
            break
        end if
    end if
    $j \leftarrow j + 1$
end while
if $i > 0$ then
    while $j > 0$ do
        $j \leftarrow j - 1$
        $q \leftarrow tree[j][\lfloor i/2^j \rfloor - 1] \oplus b$
        if $q.b = 0$ then
            $b \leftarrow q$
            $i \leftarrow i - 2^j$
        end if
    end while
end if
```

On termination, i contains the smallest value such that $\mathrm{Bic}(s[i..i_1]).b = 0$, thus $i - 1$ is the solution to the parentheses matching problem.

Operation of the algorithm is illustrated in the figure below. Here, i_1 is 14 (of a 16 element sequence), and the final value of i is 4, indicating that $\mathrm{Bic}(s[4..14]).b = 0$ but $\mathrm{Bic}(s[3..14]).b = 1$. There is an upward scanning pass followed by a downward scanning pass. At each level, one node from the tree is examined. If combining that node with b would preserve $.b = 0$, it is



incorporated (and i adjusted to point to the beginning of the range covered by the node), otherwise it is rejected. Nodes incorporated are marked with a circle, nodes rejected by an X.

This binary search takes $2 \lg n$ steps in the worst case. Thus, while the algorithm is highly parallel, it cannot be considered work-efficient.

6 Simple algorithm

In this section, we describe a simple algorithm which is not strictly work-efficient, but may be practical, especially if the problem is small or if the costs associated with code complexity are significant. For simplicity, it is presented as two dispatches, effective up to a problem size of w^2, where w is the size of a workgroup.

6.1 Stack slices

The first dispatch computes slices of the stack, with each workgroup computing a partition of w values. More precisely, each workgroup computes $\mathrm{Stk}(enum(s)[p..p+w])$, where p is the start of the partition, in this case $w \cdot i$.

This dispatch is very simple. We do a partition-wide reverse scan of the bicyclic semigroup on the mapping of the input elements, followed by a simple stream compaction step: the index is written if the $.a$ of the scan of all following elements is zero, and the memory location to write is derived from the $.b$ value of that scan.

In more detail, for each index i covering the input, index $p+i$ is written to the output at location $\mathrm{Bic}(s[p..p+w]).b - \mathrm{Bic}(s[p+i..p+w]).b$ if the element is an open parenthesis and $\mathrm{Bic}(s[p+i+1..p+w]).a = 0$. ***Give example.

In this simpler variant, each thread handles one element, and a simple Hillis-Steele scan[HS86].

6.2 Main matching pass

The second dispatch performs the main parentheses-matching task, resolving all matches within the partition, and also using the stack slices generated by the previous dispatch for the rest. Each workgroup handles one partition independently, performing the following steps sequentially (separated by workgroup barriers).

- Materialize the stack for the prefix of the input up to the current partition. This results in the w-suffix of $\mathrm{Stk}(enum(s)[..p])$ in workgroup-shared memory. It consists of a reverse Hillis-Steele scan of the bicyclic semigroups produced in the previous step (up to i), followed by stream compaction which is a per-element binary search of the $.b$ values for the stack value.
- Compute a binary tree of the bicyclic semigroup from the elements in the partition. This is a simple up-sweep as described by [Ble90]. This binary tree requires storage of $2w-1$ bicyclic semigroup elements in shared memory storage, and $\lg w$ steps.
- For each element j, find the least value j such that $\mathrm{Bic}(s[p+i..p+j]).b = 0$, searching the binary tree in an upwards then a downwards pass. The algorithm is very similar to that given in [BOV85].
- If $i > 0$ then the match is found within the partition, and $p + i - 1$ is written to the output. If $i = 0$ then the match is in outside the partition, and the $\mathrm{Bic}(s[p..p+j]).a$ is used to index into the stack as materialized in the first step.

7 Work-efficient algorithm

In a PRAM model, a simple Hillis-Steele scan over n elements consists of n processors running $\lceil \lg n \rceil$ steps. Thus, it has a *work factor* of $\lceil \lg n \rceil$ compared to the sequential algorithm running in $O(n)$ steps on one processor.

There are a number of work-efficient variations. The most straightforward to implement on GPU is for each thread to process k elements sequentially, amortizing the logarithmic cost over these k elements. In a PRAM model, n/k processors each take $O(\lg(n/k))$ steps, which is work-efficient when $k \geq logn$. See [HSO07] for more discussion of efficient GPU implementation of scan.

7.1 Work-efficient stack slices

The work-efficient version of the algorithm for producing stack slices is straightforward, and based on standard techniques. We will present it in a bit of detail, as other parts of the algorithm will use similar techniques.

Recall that production of a stack slice is a stream compaction based on a reverse scan of the bicyclic semigroup. The standard work-efficient algorithm for scan is for each thread to process k elements; this way the cost of the Hillis-Steele scan is amortized over k. On an actual GPU, each workgroup will have w threads, so will end up processing wk elements. An argument for the optimality of that approach on an EREW PRAM is given at the end of section 1.2 of [Ble90].

Applying that technique, the first step is for each thread to do a sequential reduction of the bicyclic semigroup for k elements. Then a standard (reverse) Hillis-Steele reduction over the resulting w elements, which takes $\lg w$ steps. Lastly, each thread does a sequential walk (also in reverse), starting with the exclusive scan value. At each step, the value is written if the $.a$ field of the bicyclic semigroup is 0, and the location is determined from the $.b$ field.

The actual shader code is straightforward, and the speedup significant. (TODO: probably refer to quantitative measurements later)

7.2 Work-efficient matching

This section needs to be expanded to be clearer, but the basic ideas are presented in bullet form:

- Stream compaction of stack. Breaks down into work-efficient reverse scan of bicyclic semigroup; create bitmaps of size k to identify non-empty segments; create linked list data structure (scan of max operation) of non-empty segments; finally generate output, where each step either consumes one element from a segment, steps to the next bit in the bitmap, or follows the linked list (all O(1)). Result is the same stack slice as before.

- Build binary tree of bicyclic semigroup. This is the same as before, except that we start by a sequential reduction of the monoid for k elements. Also build bitmap representing stack monoid reduction (k bits per thread).

- Do *two* searches of tree. One for the first element in the k-chunk, the second for the first unclosed open parenthesis in the k-chunk. The second induces a linked list data structure to reconstruct all stack snapshots at k granularity.

- Sequentially walk input elements. Start with search based on the first element of the chunk. Maintain a local stack. For each element, push and pop local stack as in sequential algorithm. When local stack is empty, use hierarchy to resolve: next bit in bitmap, follow linked list induced by second search, and, when it steps out of the partition, resolve in prefix stack.

8 Portable compute shaders

A goal of this work was to develop an algorithm that could be run efficiently and reliably on a wide range of GPU hardware. To this end, we avoided constructs that would pose problems, such as inter-workgroup communication.

We also implemented the algorithm on the piet-gpu-hal infrastructure, which runs compute shaders on multiple back-ends, currently Vulkan, Metal, and DX12.

9 Performance results

This section will need to be filled in with detailed performance results, especially graphs of throughput over problem size.

Preliminary numbers: For the $k = 1$ case, with $w = 512$ so the problem size is limited to 2^{18}, we see 3.9G elements/s on AMD 5700 XT. For $k = 8$, on same problem size, throughput increases to 8.5G for that problem size, and 12.9G as the problem size reaches the maximum of 2^{24}. This latter number is approximately 40% of the "speed of light" on that hardware, meaning the amount of time it takes to read the input twice and write the output.

10 Related Work

There is an extensive literature of algorithms for parentheses matching described in terms of the PRAM model. We will briefly survey those. Generally, an algorithm that runs on n processors in $O(\log n)$ time is straightforward, but adaptations to make it work-efficient add significant complexity.

The first work-efficient algorithm in the literature is [BOV85]. The core of this algorithm is essentially equivalent to the up-sweep of the bicyclic semigroup followed by efficient binary search; they don't describe it in terms of a single semigroup, but rather do two passes, one a simple prefix sum for nesting depth, the second an up-sweep using a minimum operation. Certainly on modern GPUs the bicyclic semigroup formulation is superior, as a single pass is more efficient than two, and the calculation of the semigroup itself compiles to a small number of inexpensive machine operations. The work-efficient adaptation depends on scans in both directions.

Much of the following literature is concerned with efficient execution on weaker PRAM variants, in particular EREW rather than CREW. These concerns don't map well to actual GPU hardware. Indeed, after a dispatch boundary, having many threads read from the same location is a potentially good for performance, due to caching.

The parentheses matching problem is very similar that of deriving parent and left sibling vectors from a depth vector. The depth vector is a representation of tree structure popular in the APL world, and it can readily be derived as a prefix some from a sequence of parentheses. A highly parallel algorithm is given in Section 3.3 of [Hsu19]. This algorithm, however, is not work-efficient, but rather has an additional work factor proportional to the maximum depth of the tree. The present work has no such limitation, and tree depth is unbounded with no impact on performance.

The parentheses matching is related to prefix sum [Ble90]. The latter has both a solid theoretical foundation and a host of practical implementations on actual GPU. A state of the art implementation is decoupled look-back [MG16].

11 Discussion and future work

The parentheses matching is similar in many ways to prefix sum, for which there is much work on efficient implementations. In particular, both can be represented as monoids, though the monoidal structure of parentheses matching is trickier than pure sums. In particular, for parentheses matching there are two monoids with different time/space tradeoffs, and only through their interleaving is a work-efficient algorithm possible. This algorithm is not merely theoretically work-efficient in a PRAM model, but maps well to efficient implementation on GPU using similar techniques as existing prefix sum implementations.

The decomposition into monoids has the advantage that pure parentheses matching problem can readily be fused with other monoid operations. The main motivating example for this work is computing bounding boxes for clipping, which can be modeled as the intersection of rectangles on all paths from the root of a tree to the leaves. Reduction of the stack monoid generalizes easily as it is free and can be extended to include some other monoid such as rectangle intersection in addition to indices. Other related tasks such as parsing likely can be expressed in terms of monoids as well.

Possible extension of the algorithm presented in this paper includes scaling up to larger problem sizes than can fit in w^2k^2. There are a few different approaches, depending on the exact application. If the nesting depth can be bounded by wk, then the most straightfoward approach is a standard tree reduction applied at the workgroup granularity approach; this is work-efficient and straightforward to implement. If unbounded nesting depth is required, other tradeoffs exist.

This work should help make parsing and other manipulation of tree-structured data practical for implementation on GPU, pushing past the common misconception that this work is inherently serial and must be run on CPU.

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