

Beauty And The Beast

Exploiting GPUs In Haskell

Alex Cole

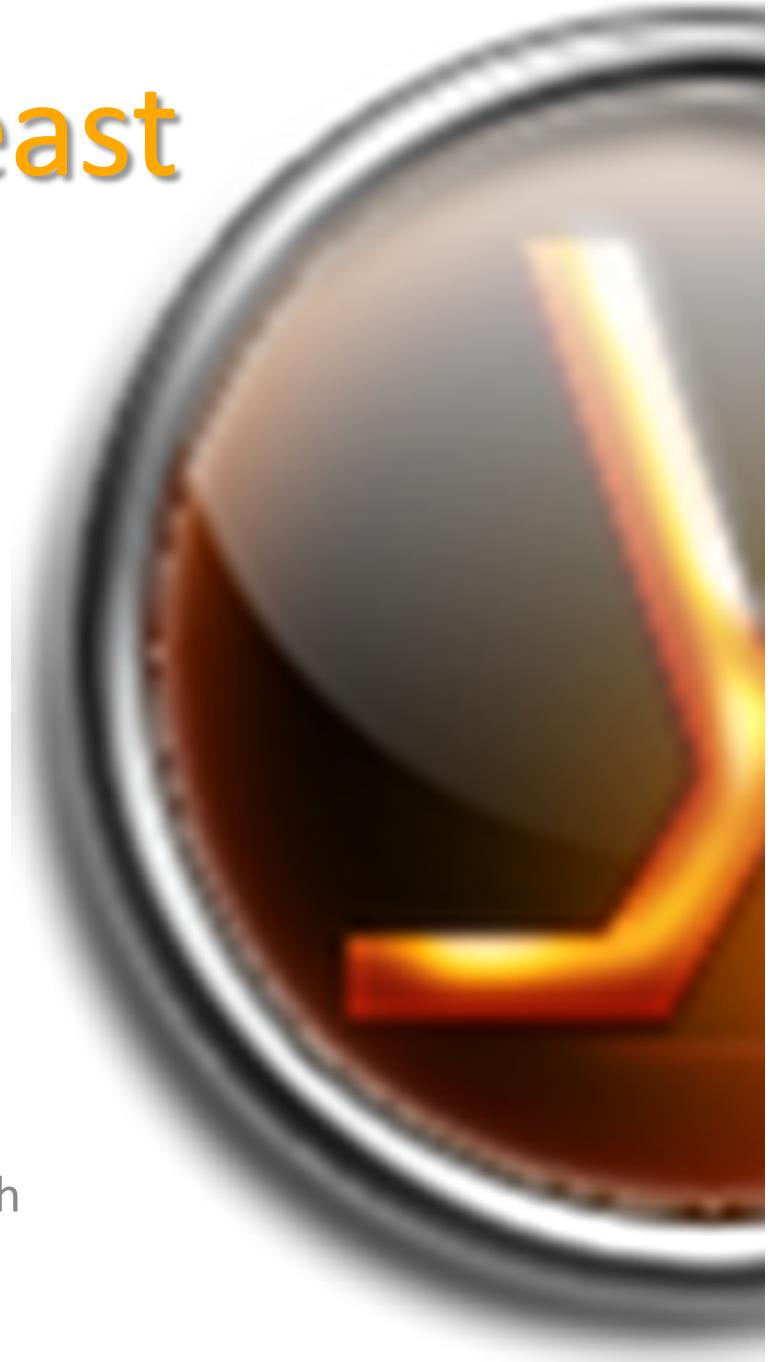
University of Leicester

CPA 2012, Dundee

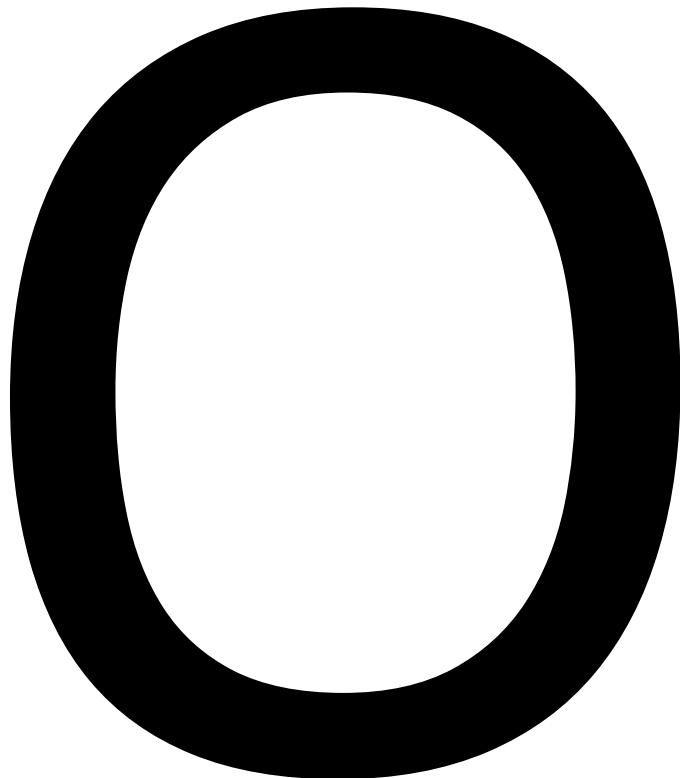
27th August 2012

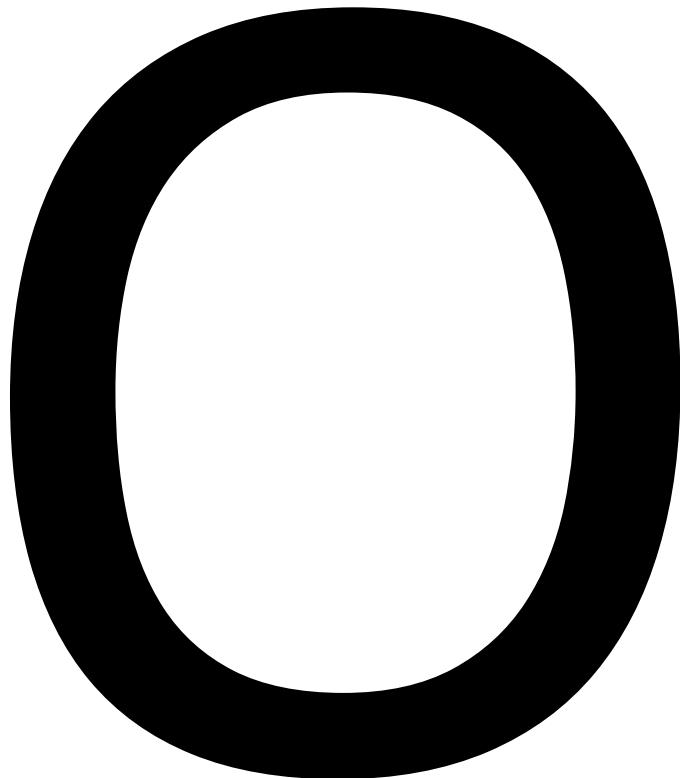
Alistair A McEwan
University of Leicester

Geoff Mainland
Microsoft Research



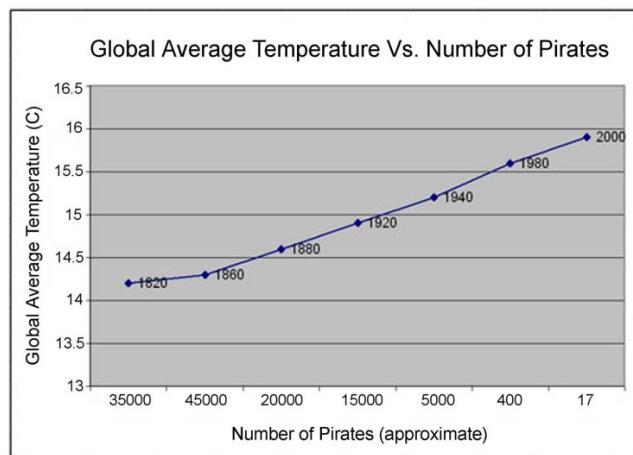
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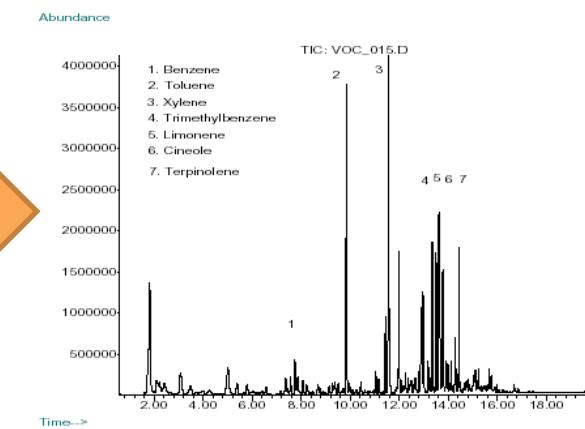
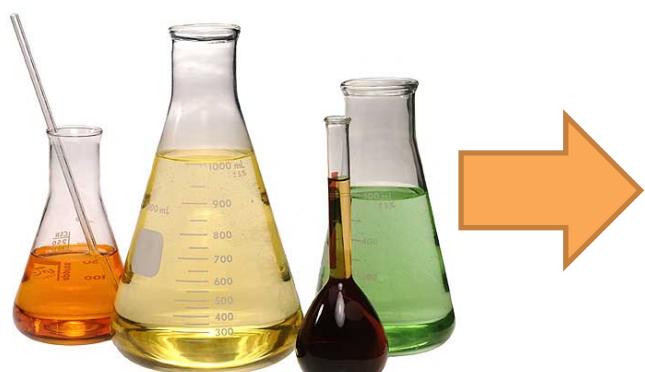


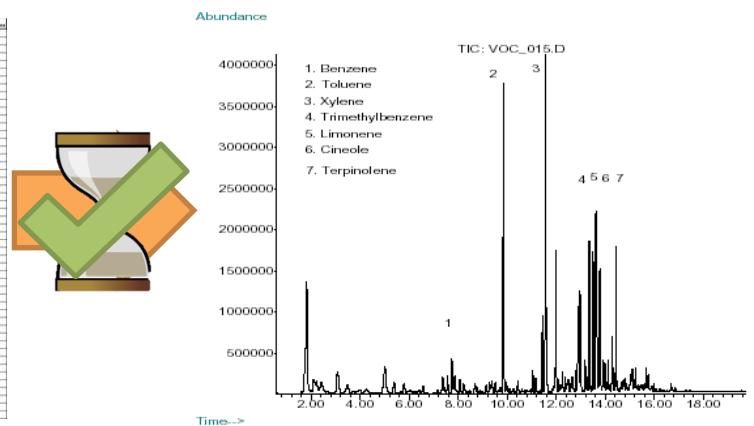
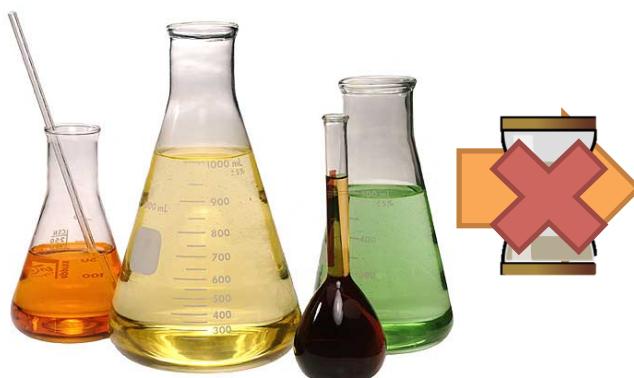
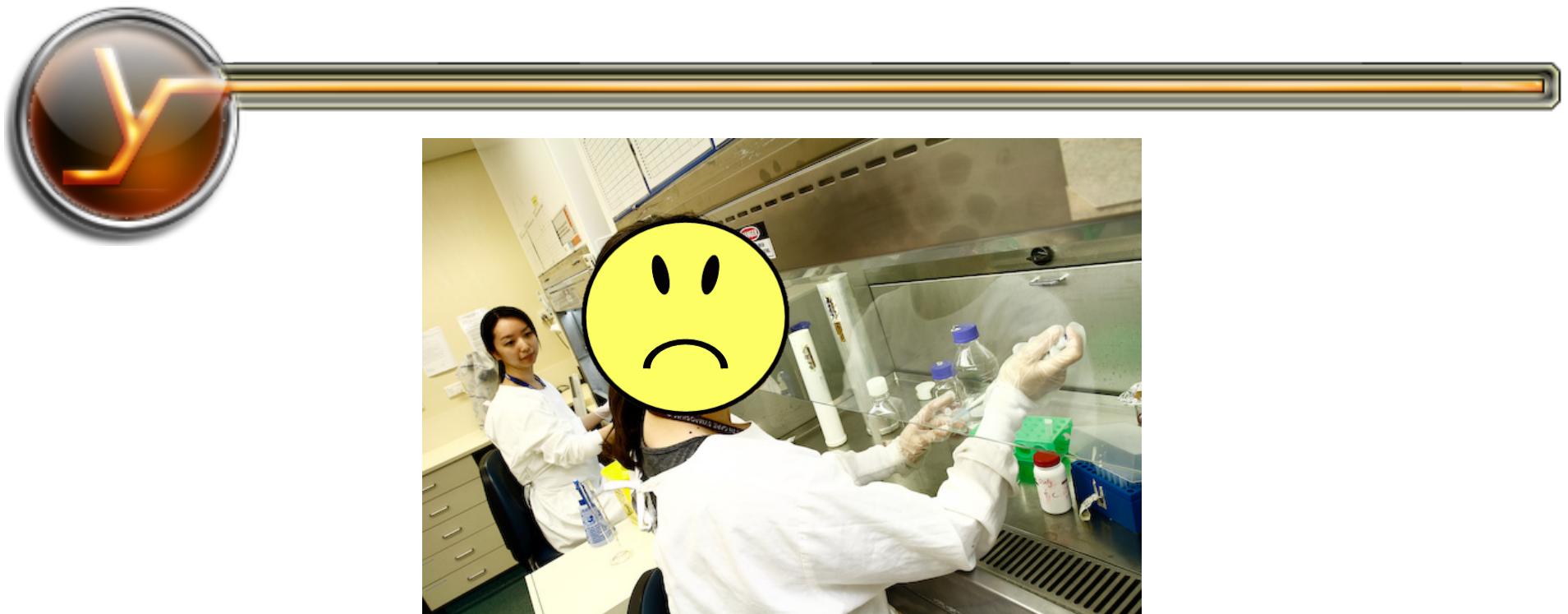


N



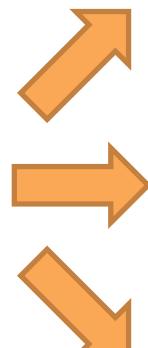








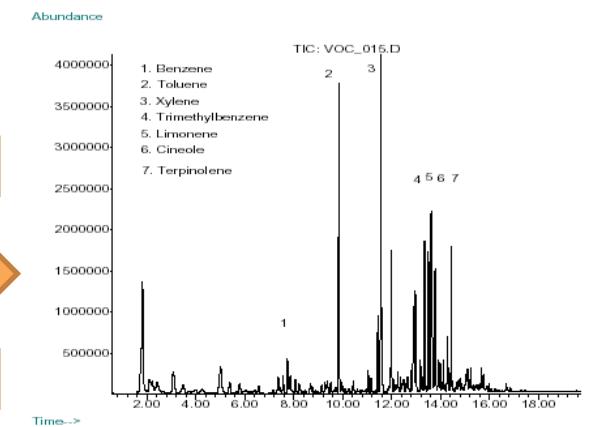
$$(x + a)^n = \sum_{k=0}^n \binom{n}{k} x^k a^{n-k}$$

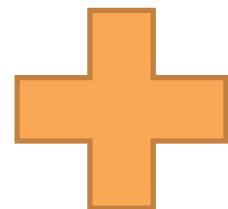


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[Only] a few of the proposed approaches [...] are currently used in practice due to the unavailability of the software or due to difficulties with incorporating the new tools in the existing data analysis pipelines.

- Nesvizhskii10



Hypotheses

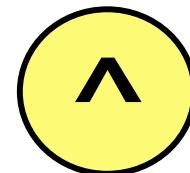
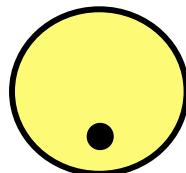
- Haskell is easy
- But performance (lists) stinks
- Using a DSL we can recover some “C” performance
- We think the trade-off is acceptable
- Based on this, we can address the richer MS computation domain with ease and performance.





Whole Array Per-Element

/ Index



- Shift .<<<
- Add .+
- Multiply .*

- Shift ^<<<
- Add ^+
- Multiply ^*



2	4	5	7	3	9
---	---	---	---	---	---

*

1	3	1
---	---	---

=

10	19	18	29	25	30
----	----	----	----	----	----



Y

4	5	7	3	9	0
---	---	---	---	---	---

2	4	5	7	3	9	*
---	---	---	---	---	---	---

0	2	4	5	7	3	*	1
---	---	---	---	---	---	---	---

*	1
1	

+	+
---	---



```
-- Sum up all the parts for the final answer.  
convolve filter input = sum convolvedParts  
where  
    -- Convolve the whole array with one filter element only.  
    oneFilterElement shift mul = (input .<<< shift) ^* filter  
    -- Get the filter radius.  
    r = length filter `div` 2  
    -- Do all the shifts and multiplies separately.  
    convolvedParts = zipWith oneFilterElement [-r..r] filter
```



- Using Lists:

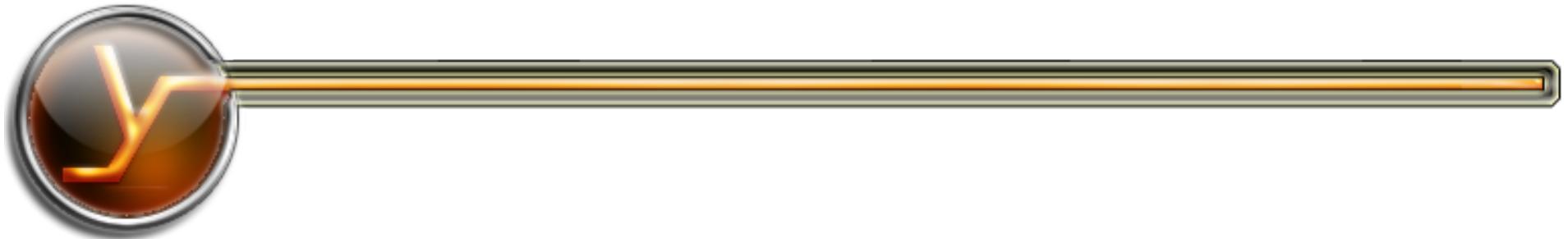
```
convolve :: [Float] -> [Float] -> [Float]
```

- Using PEGGY:

```
convolve :: [Float] -> PYExpr Float target -> PYExpr Float target
```

```
-- Convert the old input to PEGGY GPU data.
```

```
peggyInput = toArray listInput
```



```
data PYExpr a b = (PYCode a b) (PYMem a b)
```

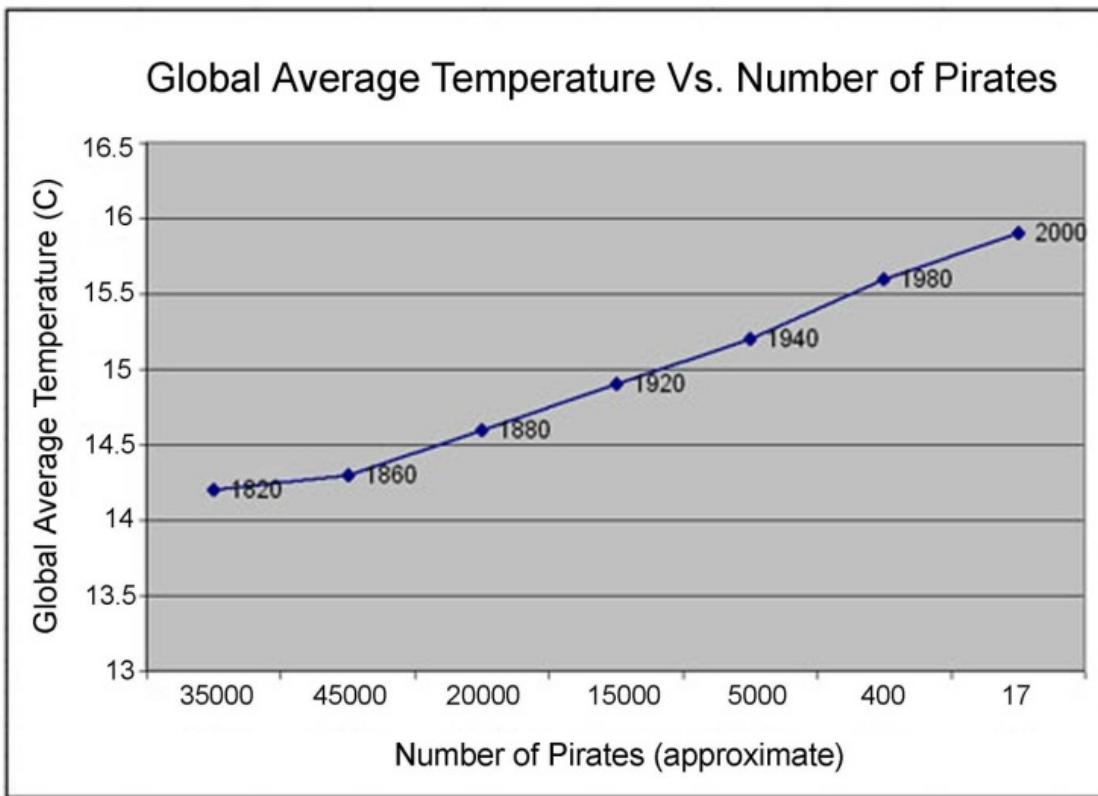
```
data instance PYMem a TargetHaskell = [a]
```

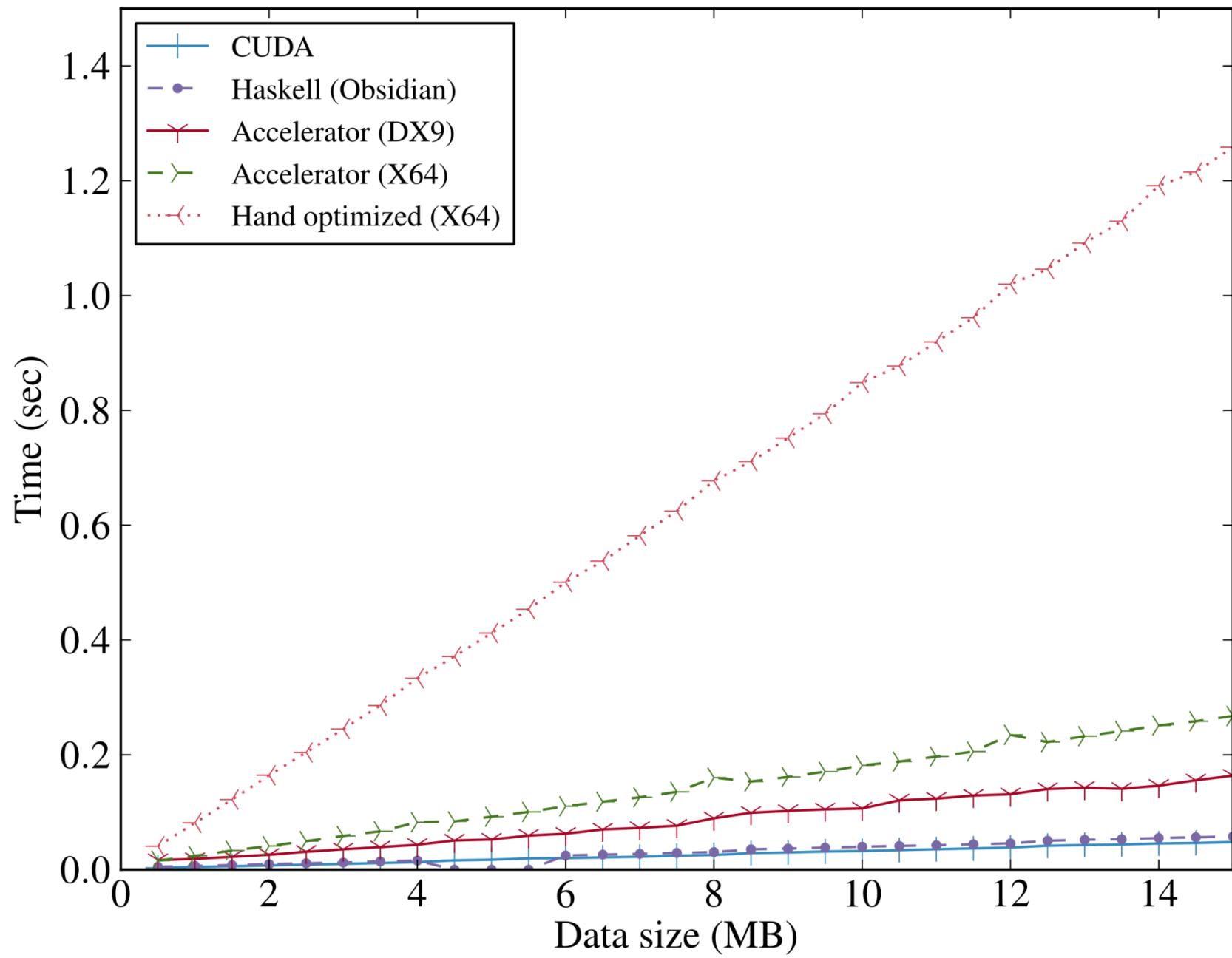
```
instance PYCode a TargetHaskell where
```

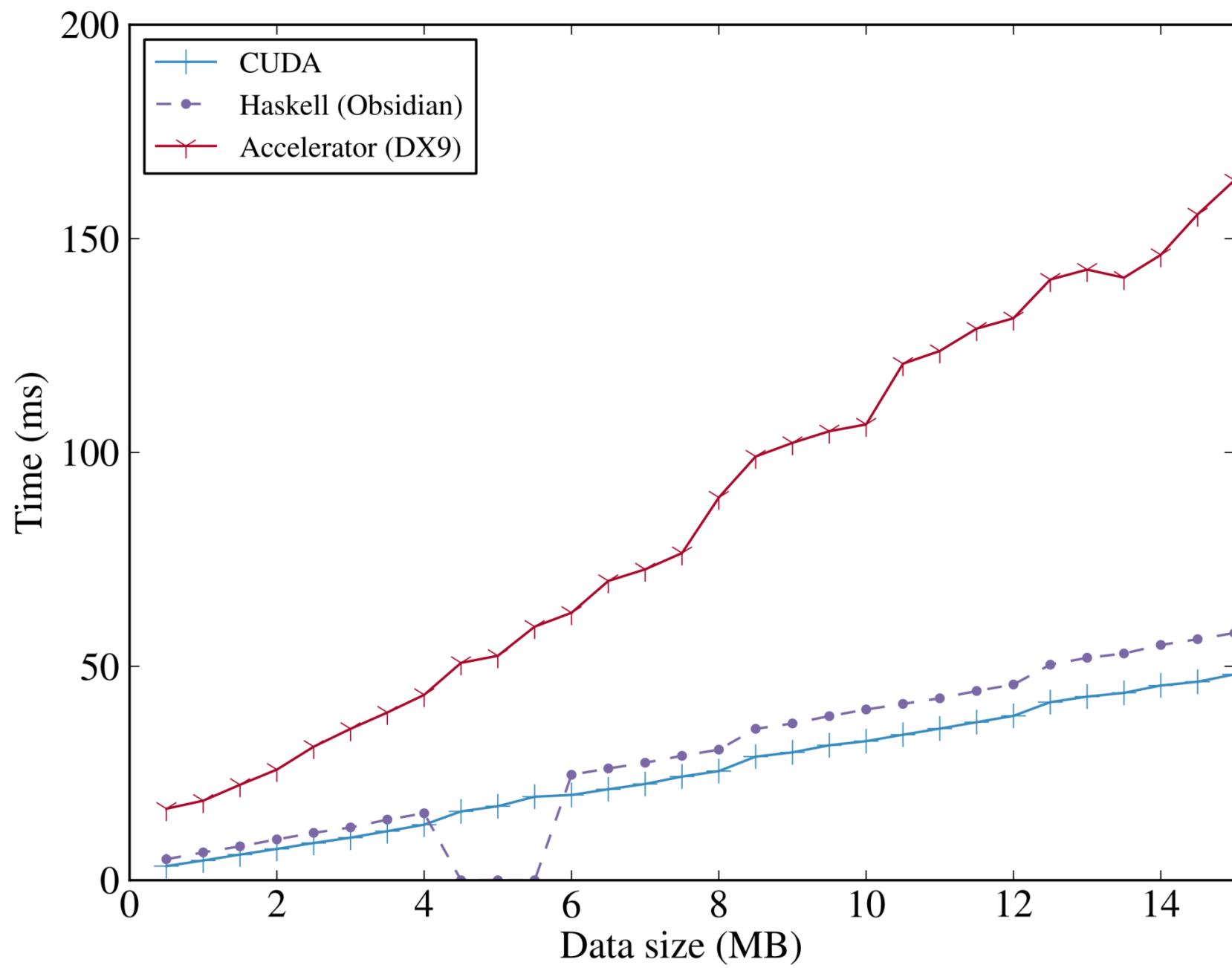
```
  (^+) x y = zipWith (+) x y
```

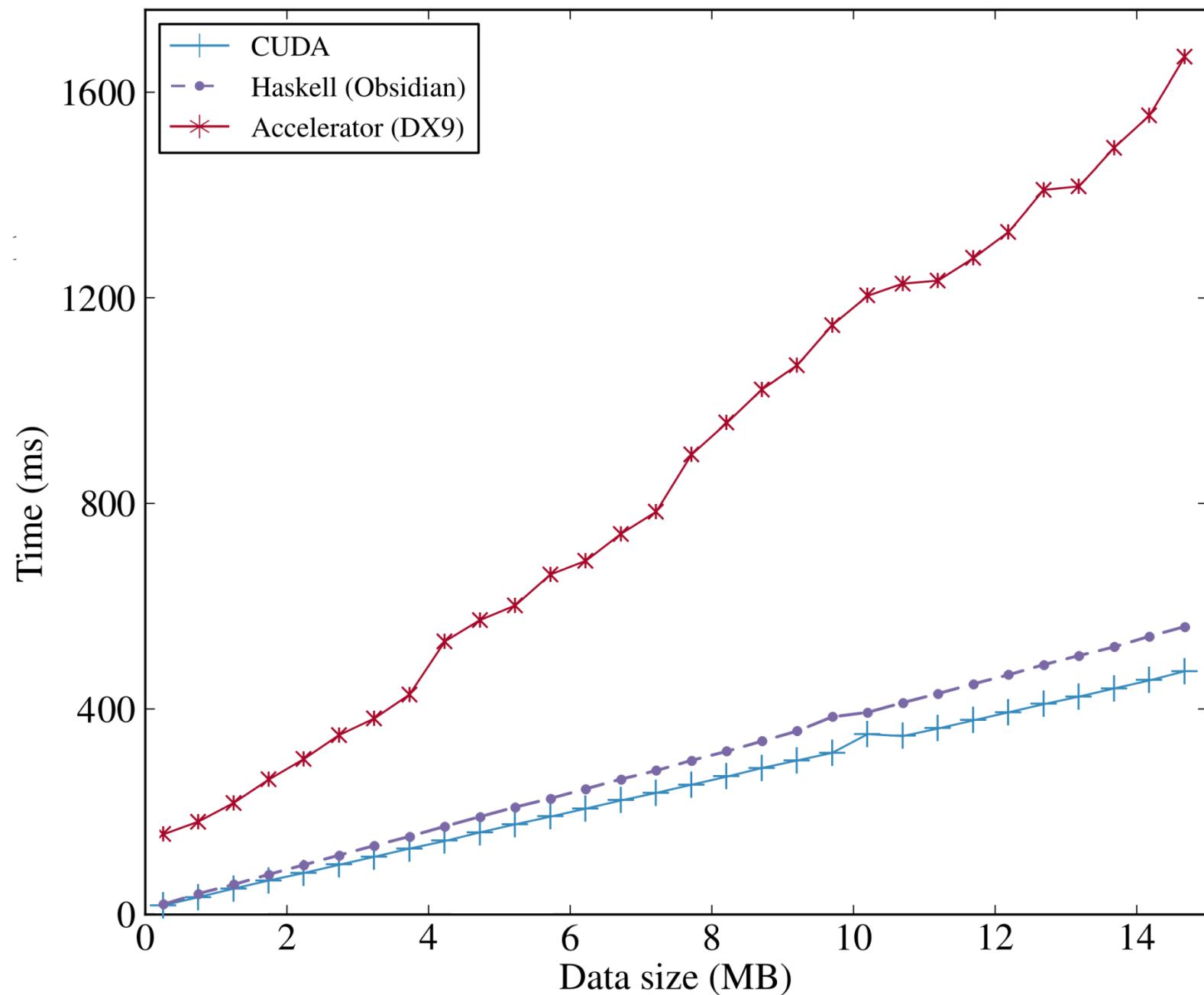


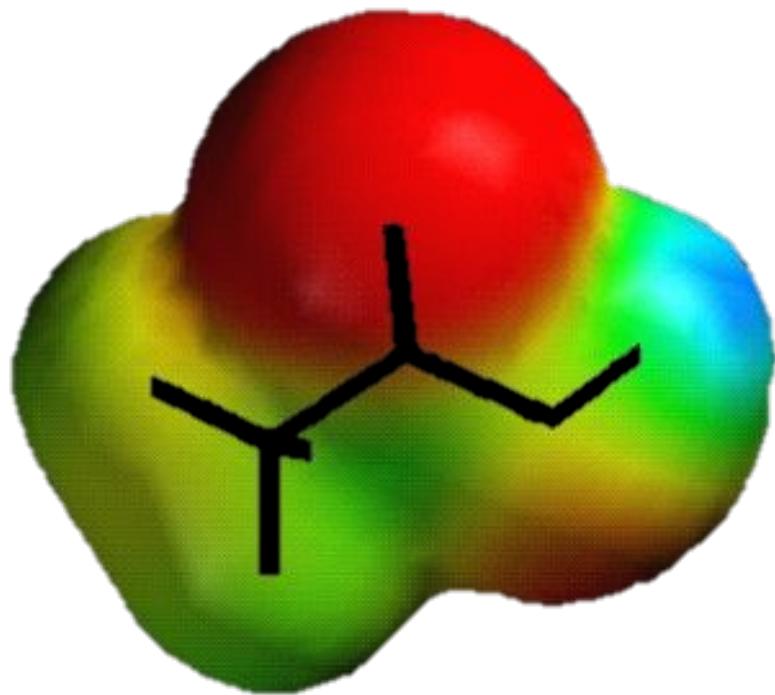
STOP GLOBAL WARMING: BECOME A PIRATE

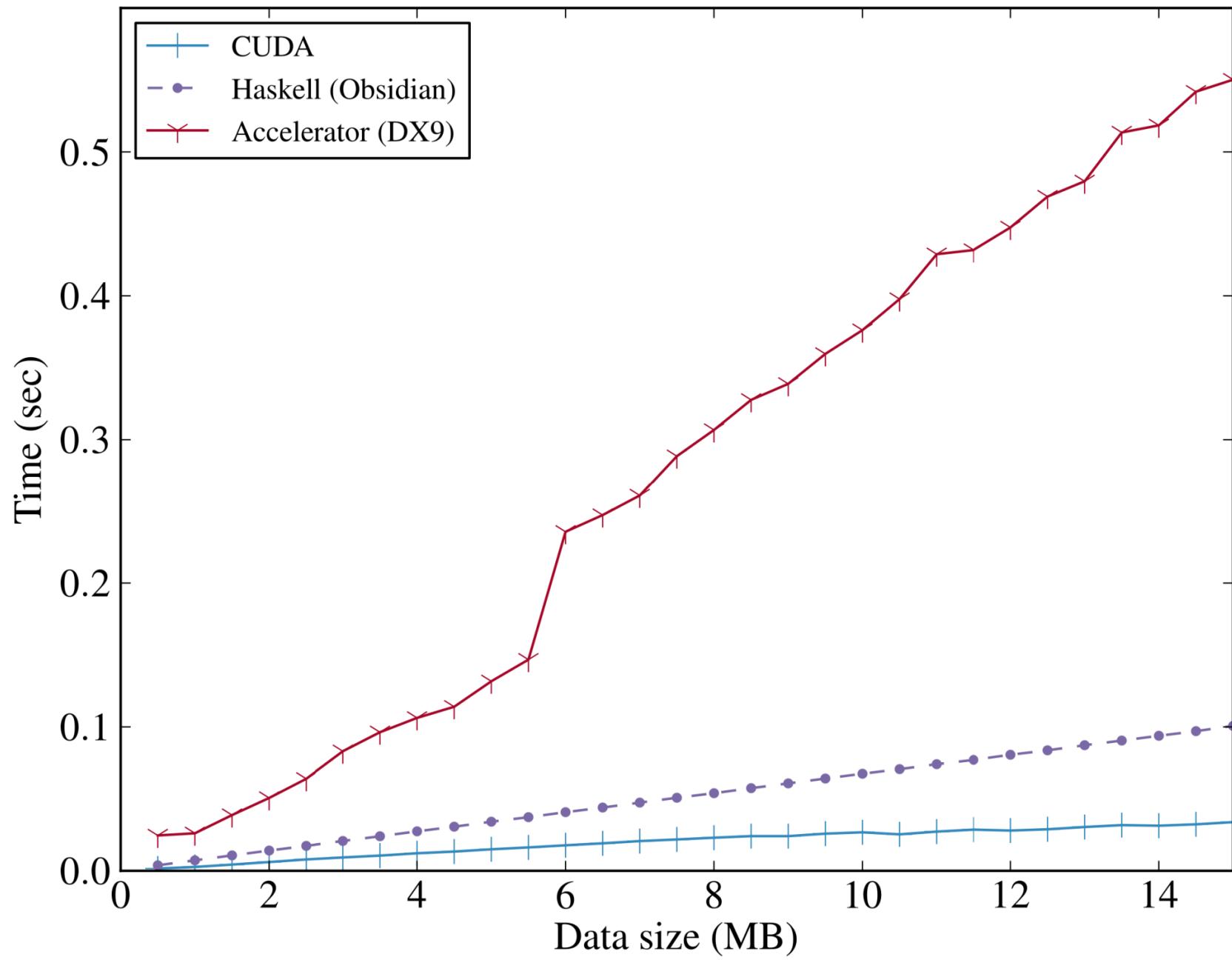














DATA

* f1 =

* f2 =

LOW FREQUENCY

* f1 =

* f2 =

HIGH FREQUENCY

LOW FREQUENCY

HIGH FREQUENCY

* f1 =

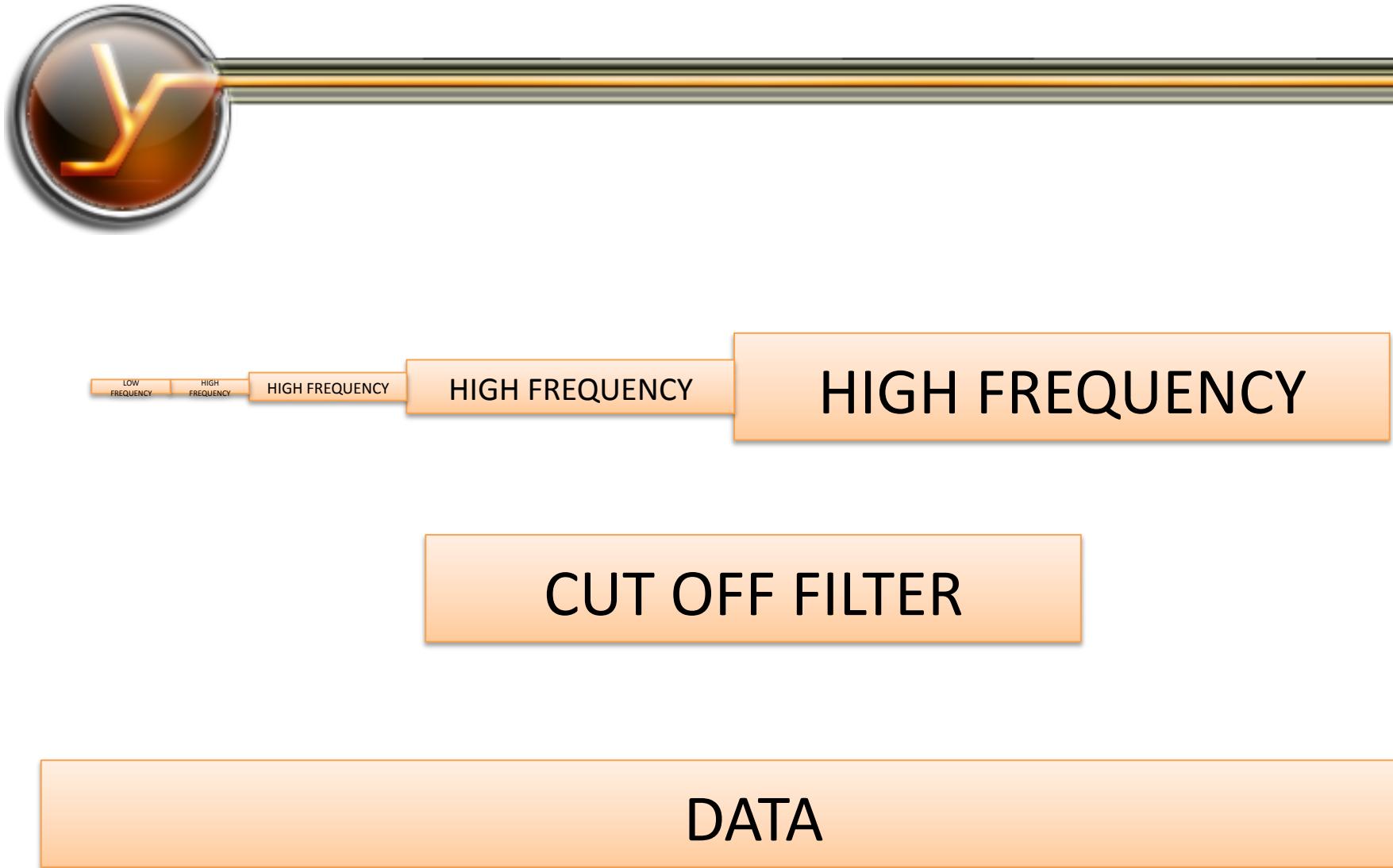
* f2 =

LOW FREQUENCY

HIGH FREQUENCY

f1
LOW
FREQUENCY

f2
HIGH
FREQUENCY





DATA

* f3 =

* f4 =

LOW FREQUENCY

HIGH FREQUENCY

* f3 =

* f4 =

LOW FREQUENCY

HIGH FREQUENCY

* f3 =

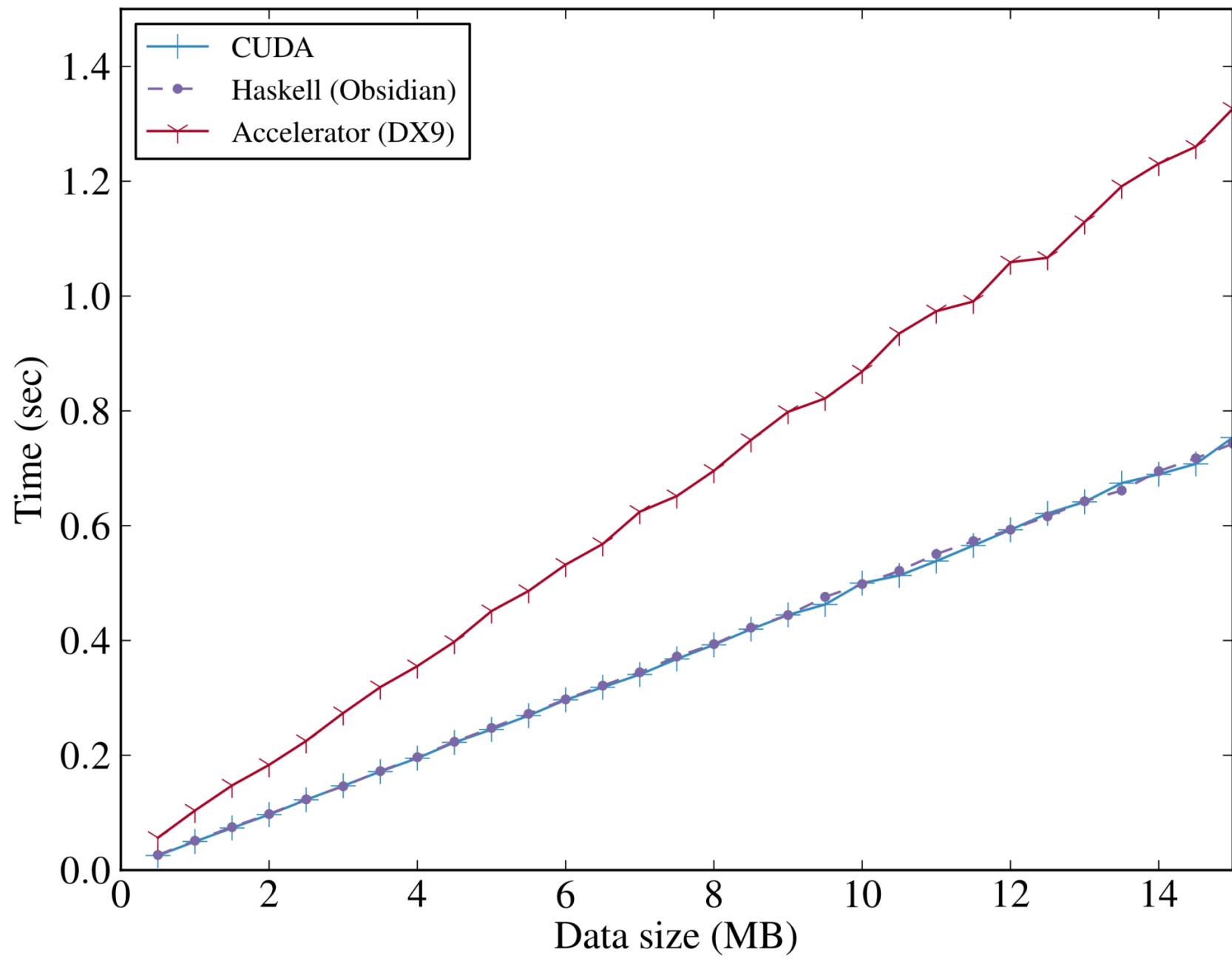
* f4 =

LOW FREQUENCY

HIGH FREQUENCY

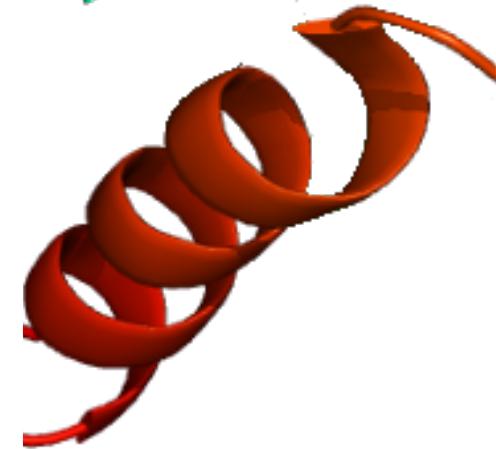
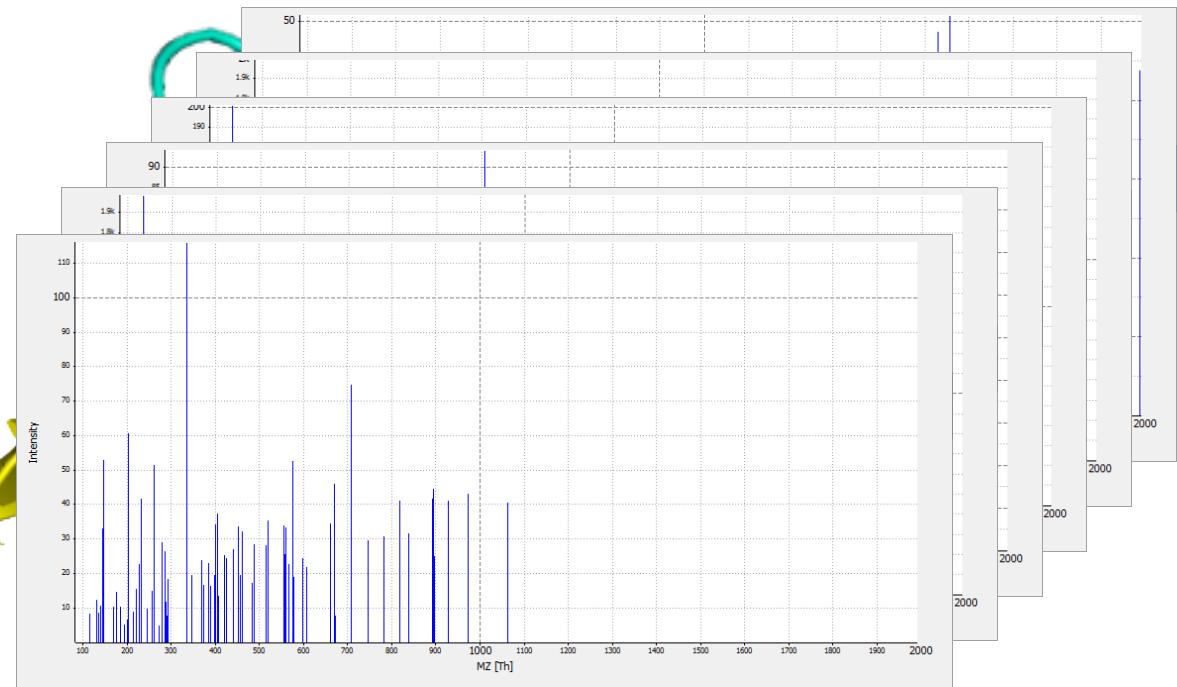
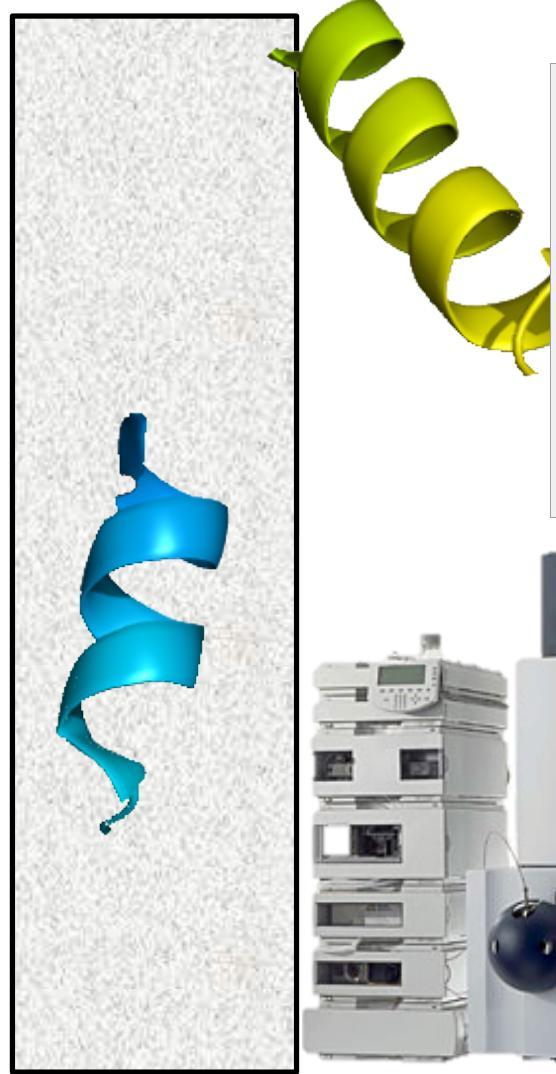
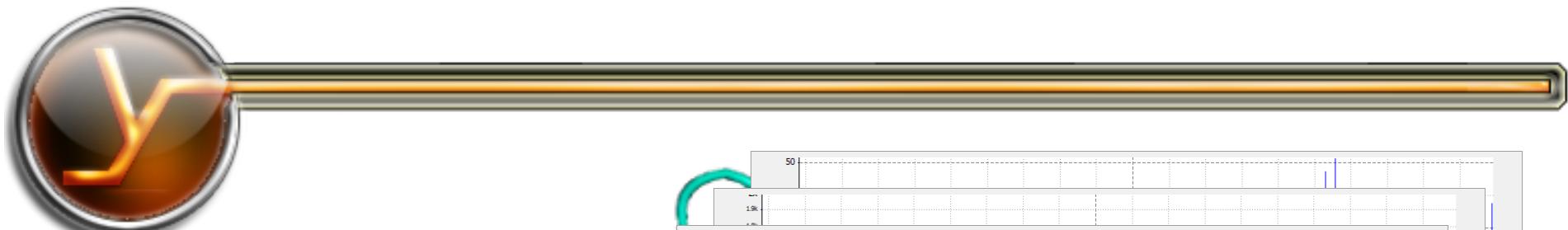
f3
LOW
FREQUENCY

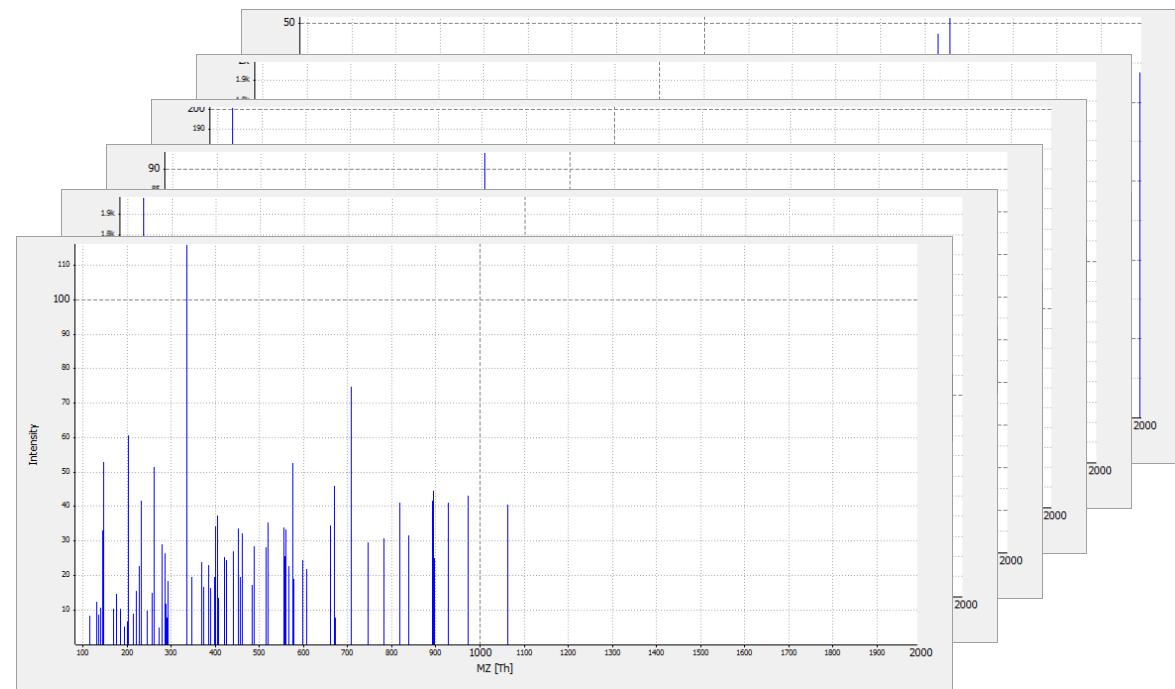
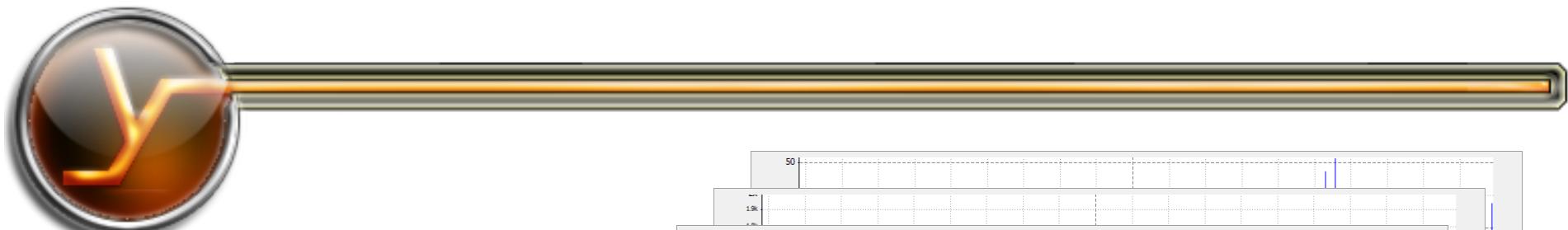
f4
HIGH
FREQUENCY

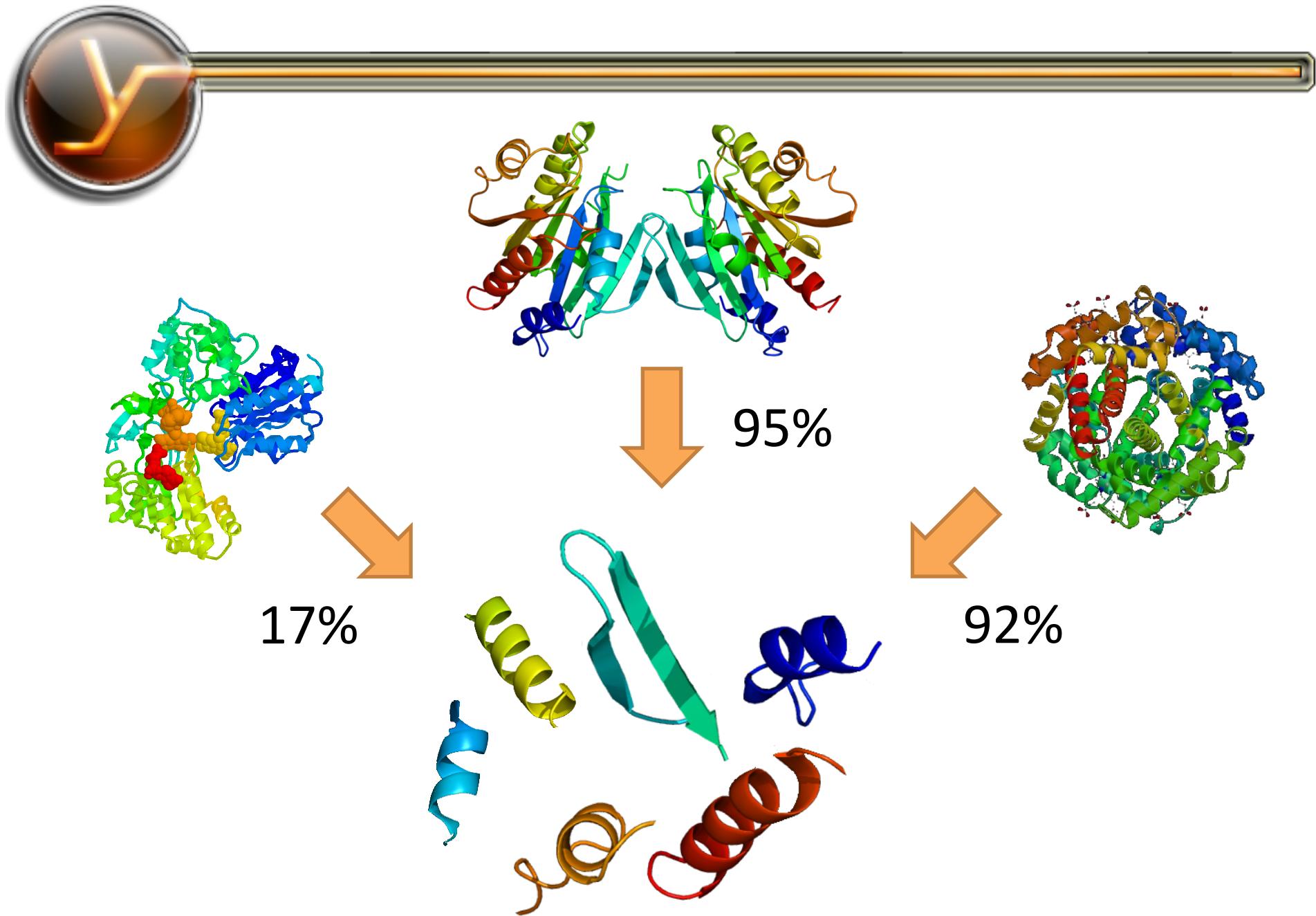














Overview

- Backend with proven potential
- Complete MS analysis implementation
- Abstract to a DSL
- Improved performance





Nesvizhskii10:

“A survey of computational methods and error rate estimation procedures for peptide and protein identification in shotgun proteomics.” Alexey Nesvizhskii, *Journal Of Proteomics*, 2010