Synthesising Graphics Card Programs from DSLs

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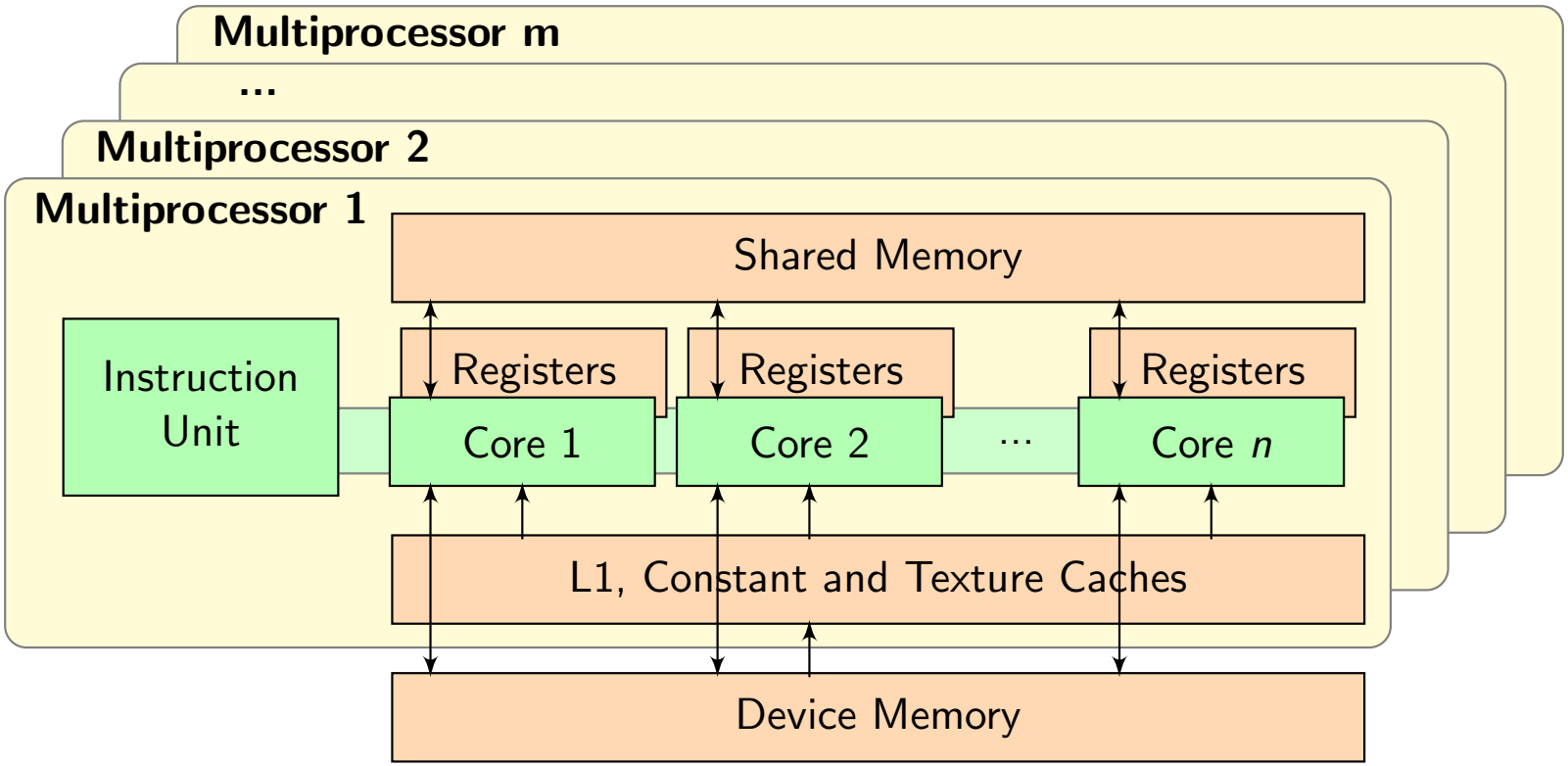
GPU development is difficult



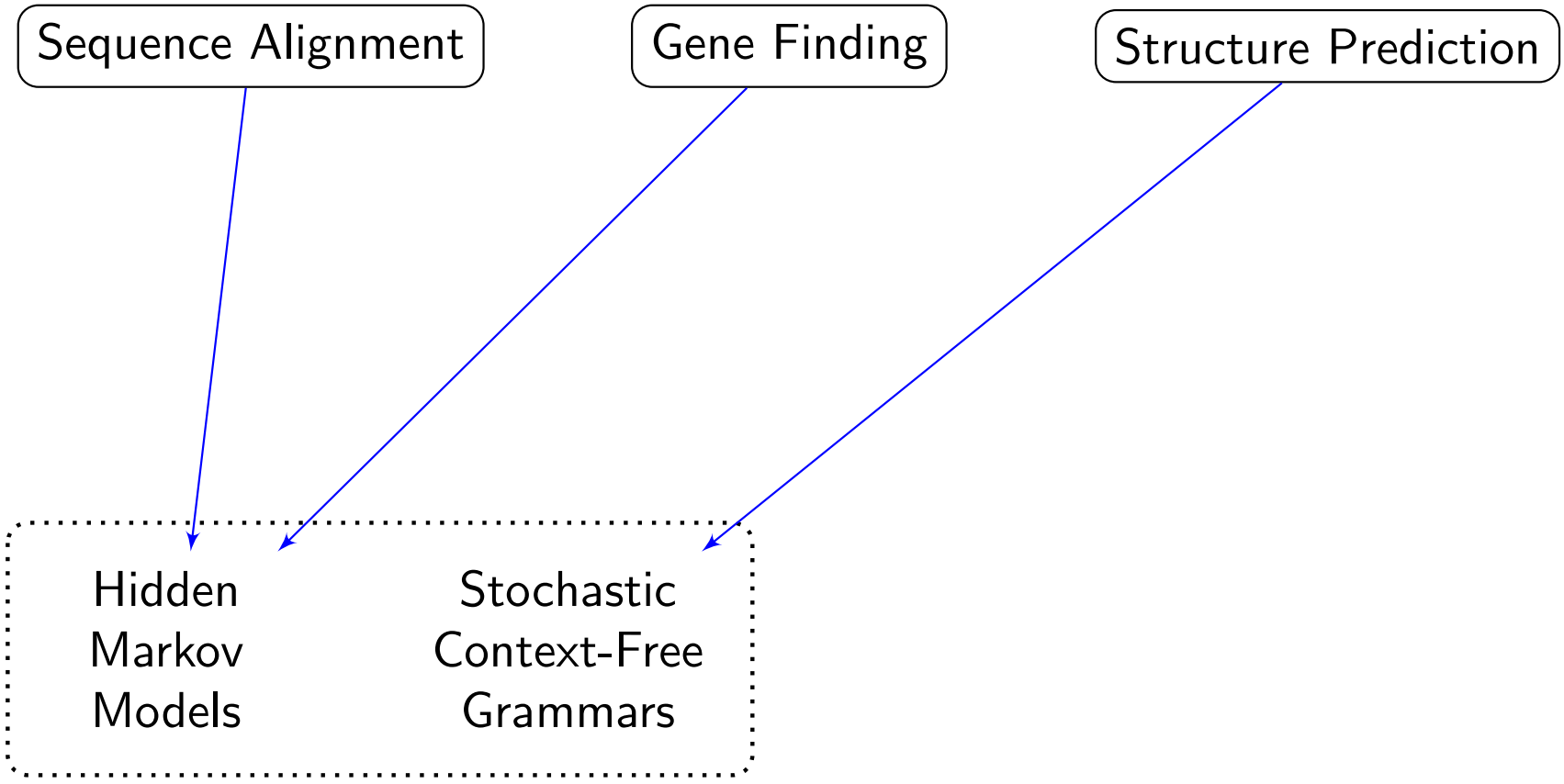
Case Study in Bioinformatics

Sequence Alignment

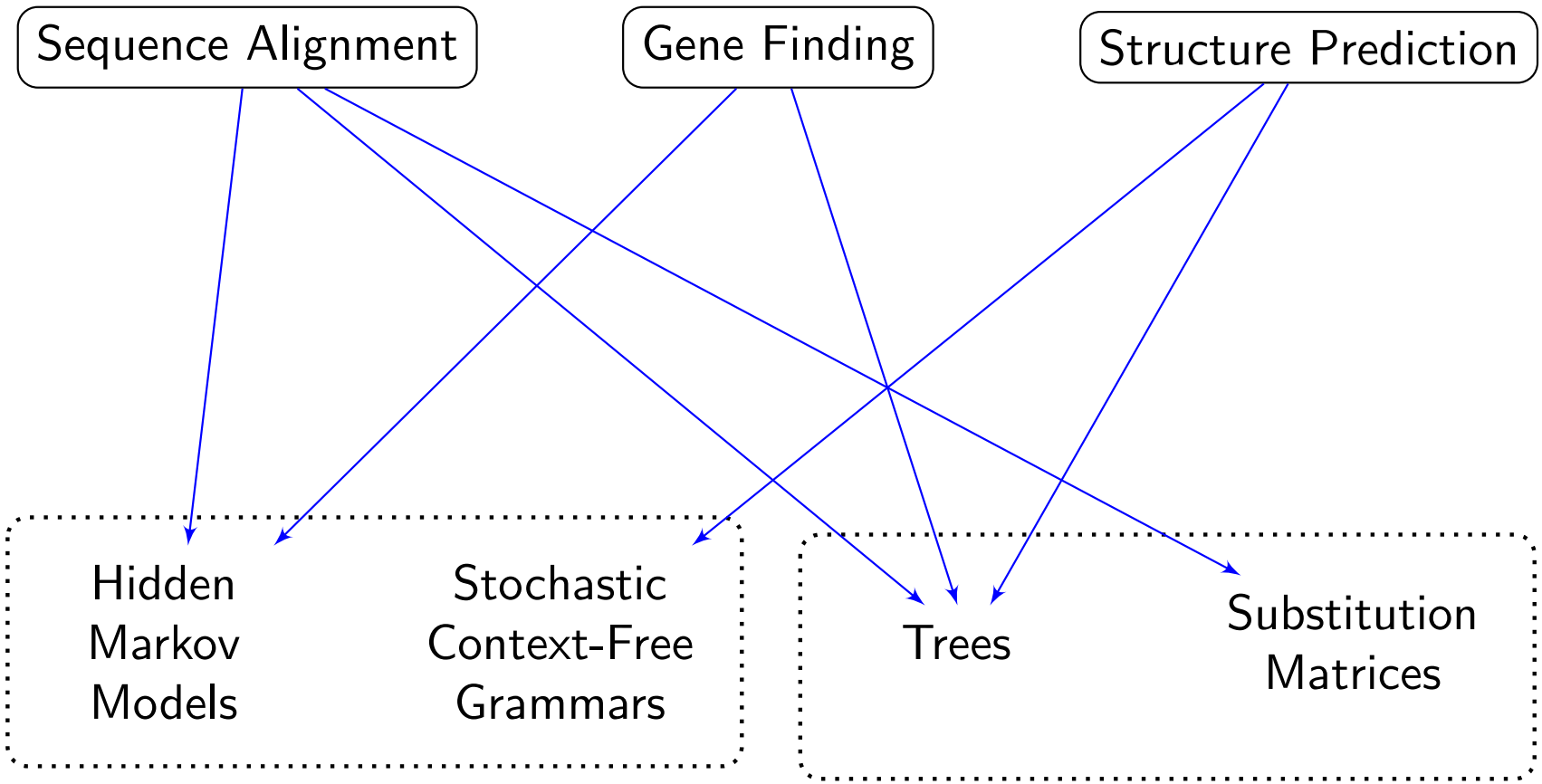
Gene Finding

Structure Prediction

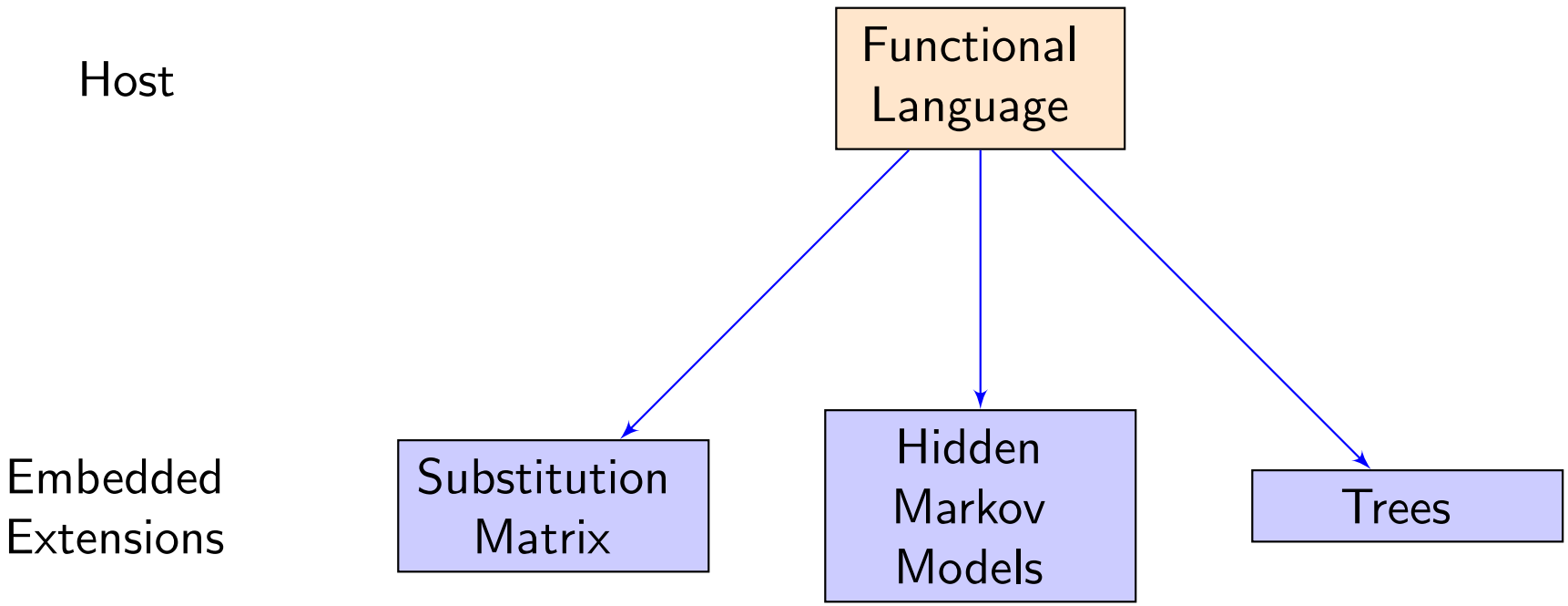
Case Study in Bioinformatics



Case Study in Bioinformatics



Bioinformatics DSL Framework



Language example - edit distance

$$d(i,j) = \begin{cases} i & \text{if } j = 0 \\ j & \text{if } i = 0 \\ d(i-1,j-1) & \text{if } s[i] = t[j] \\ min \begin{pmatrix} d(i-1,j), \\ d(i,j-1), \\ d(i-1,j-1) \end{pmatrix} + 1 & \text{otherwise} \end{cases}$$

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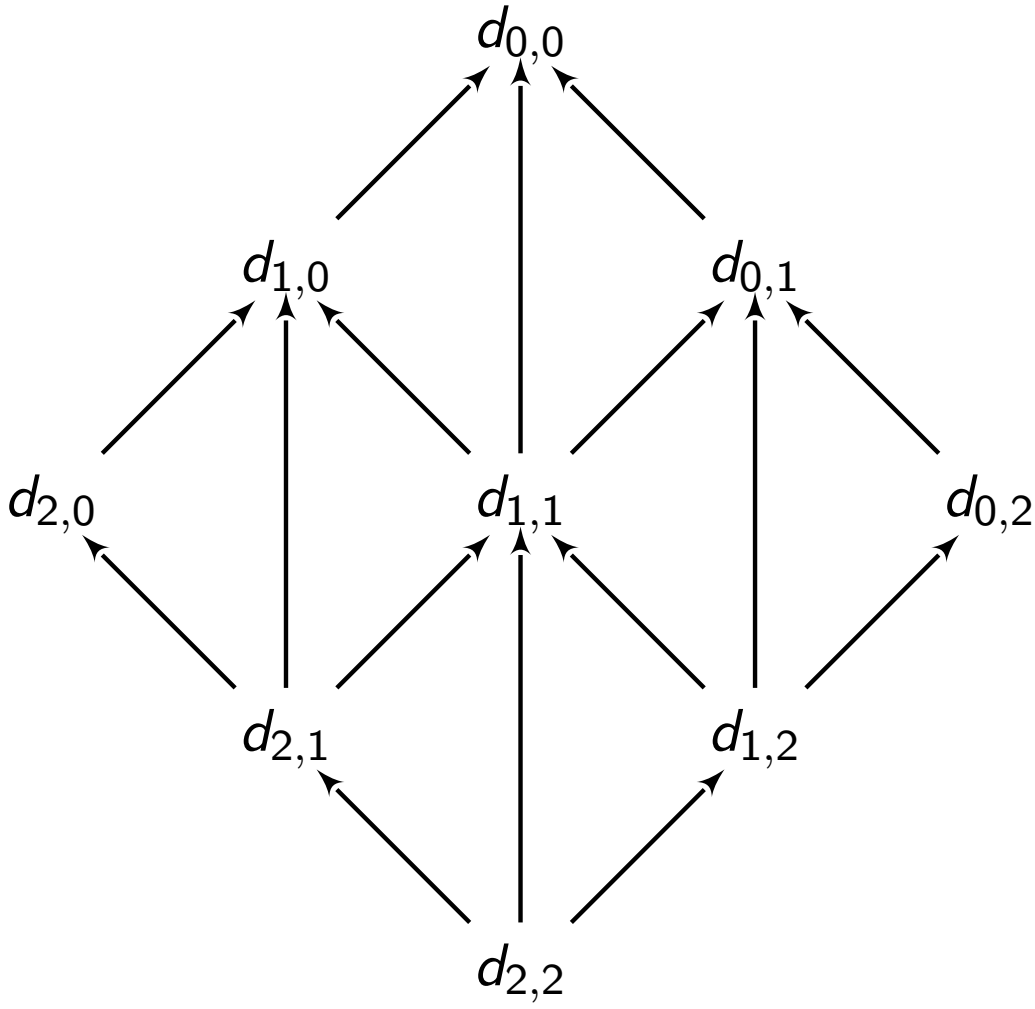
```
int d(seq[en] s, index[s] i, seq[en] t, index[t] j) =
   if i == 0 then
      j
   else if j == 0 then
      i
   else if s[i - 1] == t[j - 1] then
      d(i - 1, j - 1)
   else
      (d(i - 1, j) min d(i, j - 1) min d(i - 1, j - 1)) + 1
```

Dependency Graph



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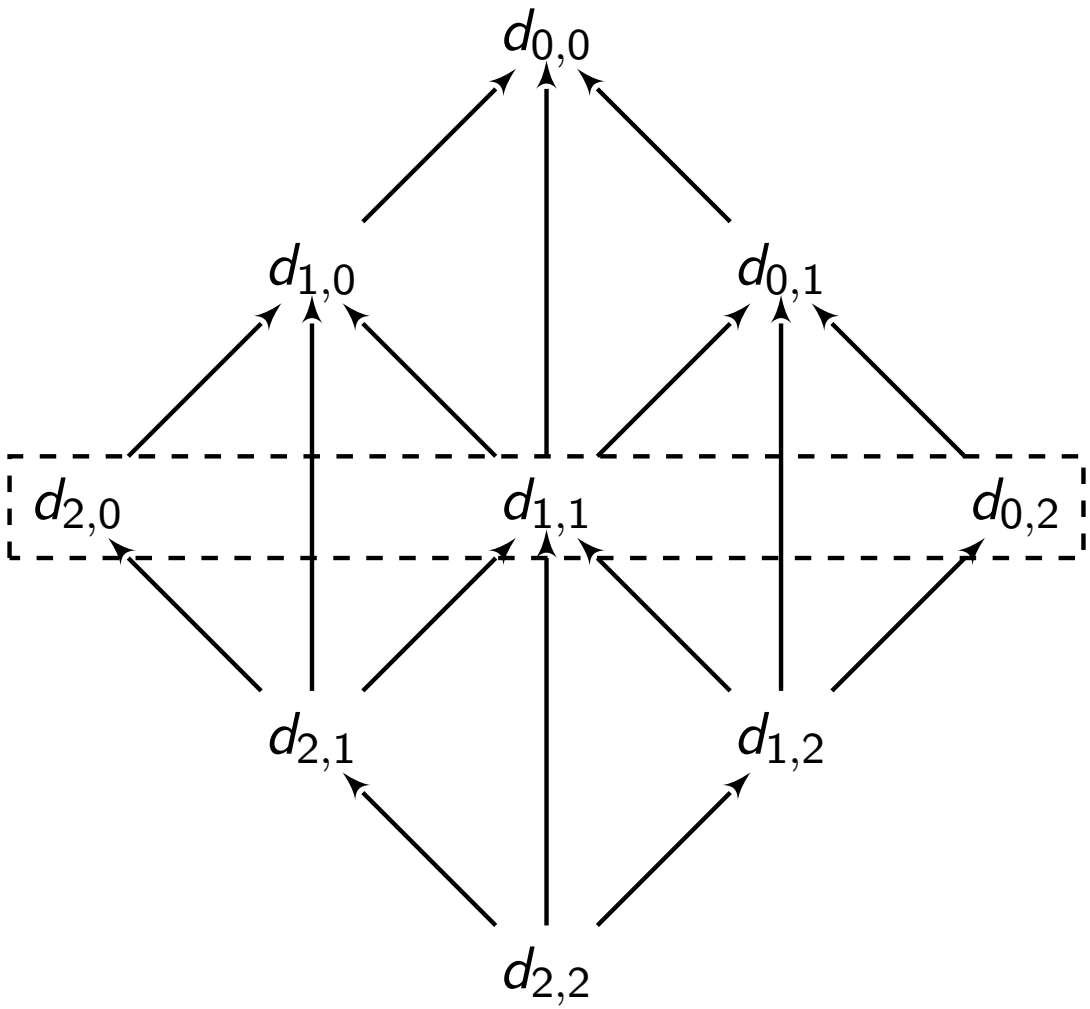
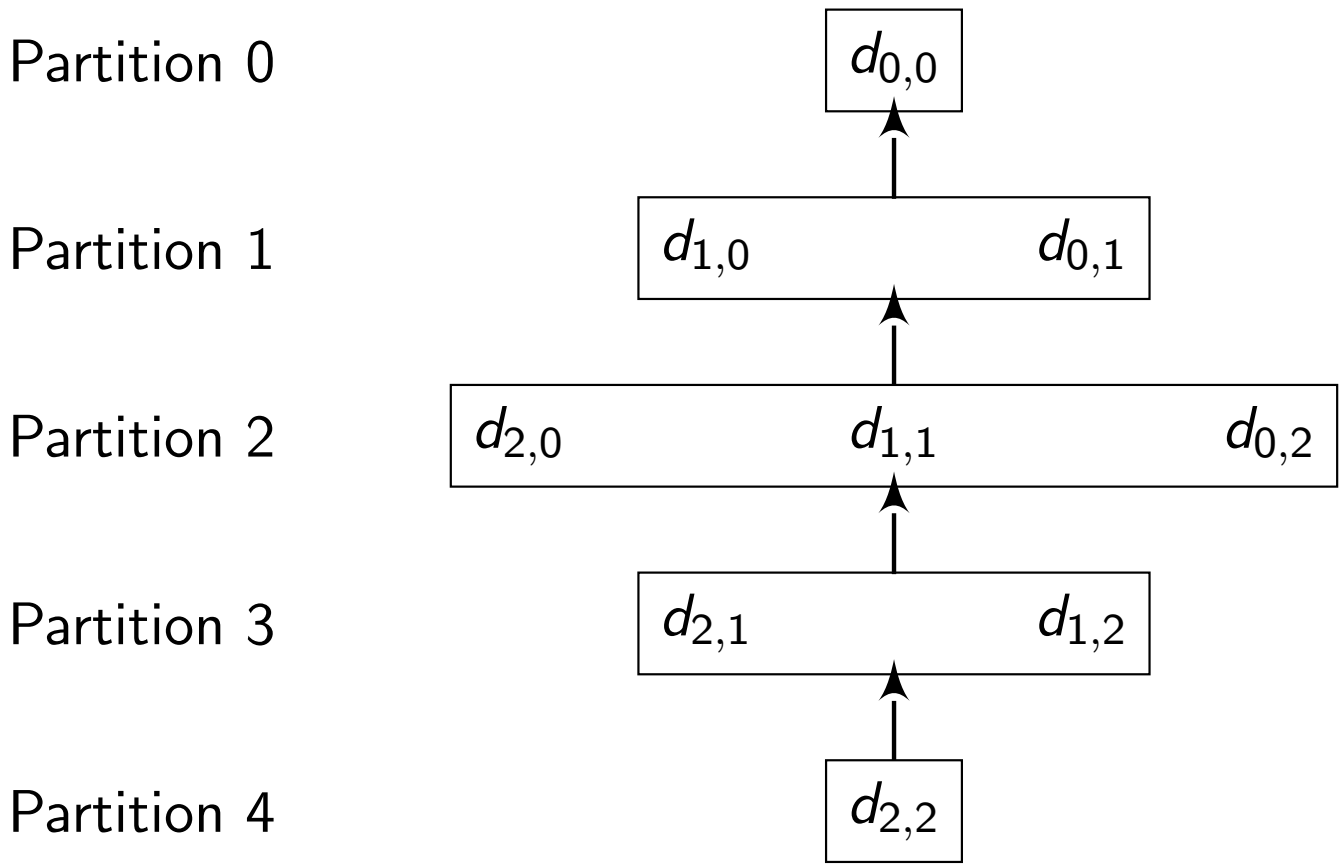


Schedule

Linear function that describes partitions of **independent** values.

e.g $S_d(i, j) = i + j$



Valid Schedules

Partition Ordering

$$\forall (i_1, j_1) \in P, (i_2, j_2) \in Q : (i_1, j_1) \rightsquigarrow (i_2, j_2) \implies P > Q$$

Where $\rightsquigarrow$ is the transitive closure of dependencies ($\rightarrow$)

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Valid schedules adhere to: $\forall i, j, d(i_r, j_r) : S_d(i, j) > S_d(i_r, j_r)$

Identify a schedule

Problem: Find a $S_d(i,j) = a_1 i + a_2 j$.

Step 1: Identify criteria on S_d

For each $d(i,j) = \ldots d(i_r, j_r) \ldots$ use $S_d(i,j) > S_d(i_r, j_r)$

Example:

$$S_d(i,j) > S_d(i-1,j)$$

$$\equiv$$

$$a_1 i + a_2 j - (a_1(i-1) + a_2 j) > 0$$

$$\equiv$$

$$a_1 > 0$$

Identify a schedule 2

Step 2: Construct a CSP to choose a *valid* and *efficient* schedule

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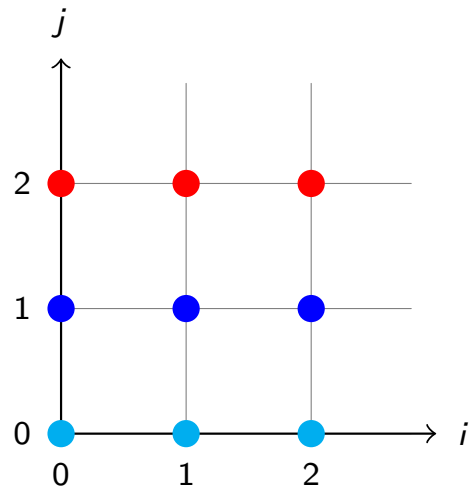
Finds $S_d(i, j) = i + j$ in edit distance example.

Polyhedral model

Given a schedule + original function, we can generate code using the **polyhedral model**.

Domain of recursion: $\{0 \leq i \leq n, 0 \leq j \leq m\}$
Schedule: $S_d(i,j) = i + j$



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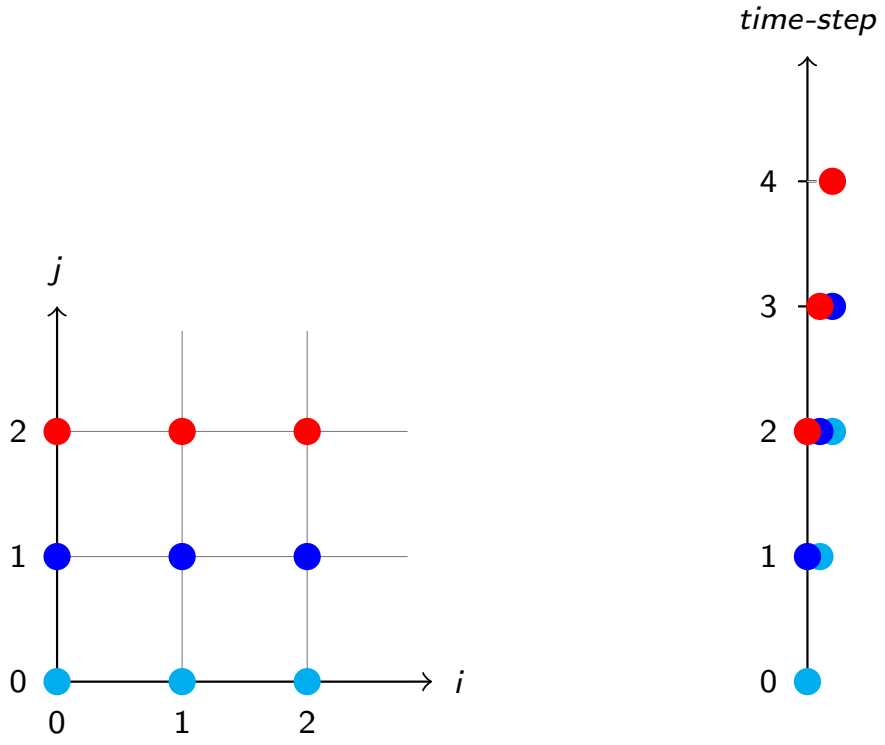

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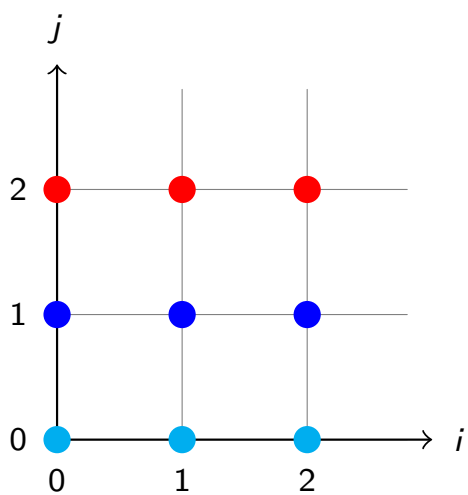
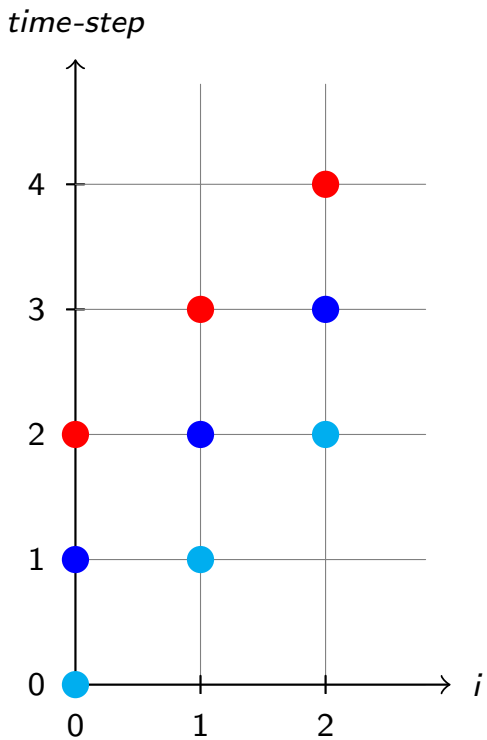




Edit Distance Program Synthesis

We use the polyhedral code generator CLooG to produce a set of nested loops that iterate over the transformed domain.

```
for (p=0;p<=m+n;p++) {
  for (i=max(0,p-m);i<=min(n,p);i++) {
    S1(i,p-i);
  }
}
```

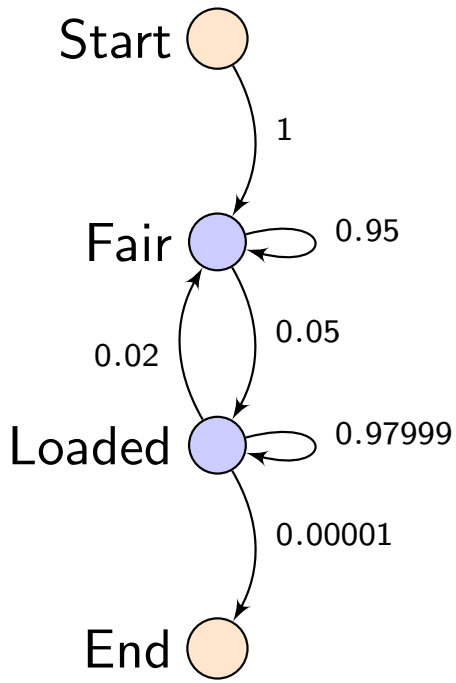
C. Bastoul: Code Generation in the Polyhedral Model is Easier Than You Think. PACT 2004

GPU Program Synthesis

Block size: *tn* threads

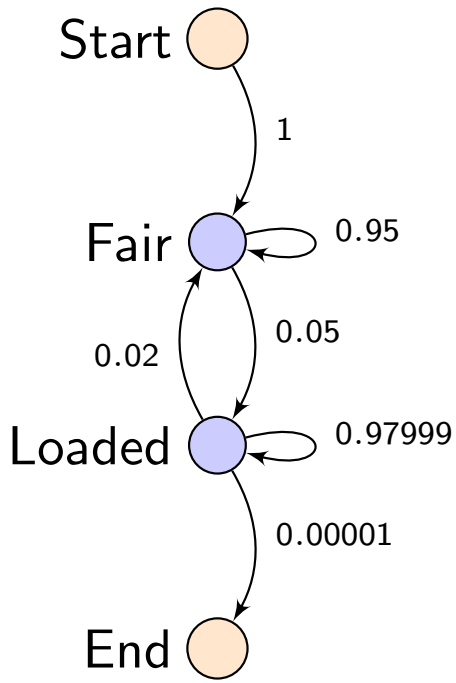
```
parfor threads t in 0..tn {
  for (p=0;p<=m+n;p++) {
    for (i=t+max(0,p-m);i<=min(n,p);i+=tn) {
      j = p - i;
      darr[i,j] = d(i,j);
    }
    sync;
  }
}
```

DSL Extensions - Hidden Markov Models



$$F(q,i) = \sum_{p:a_{p,q}>0} a_{p,q} e_{q,s[i]} F(p, i-1)$$

DSL Extensions - Hidden Markov Models



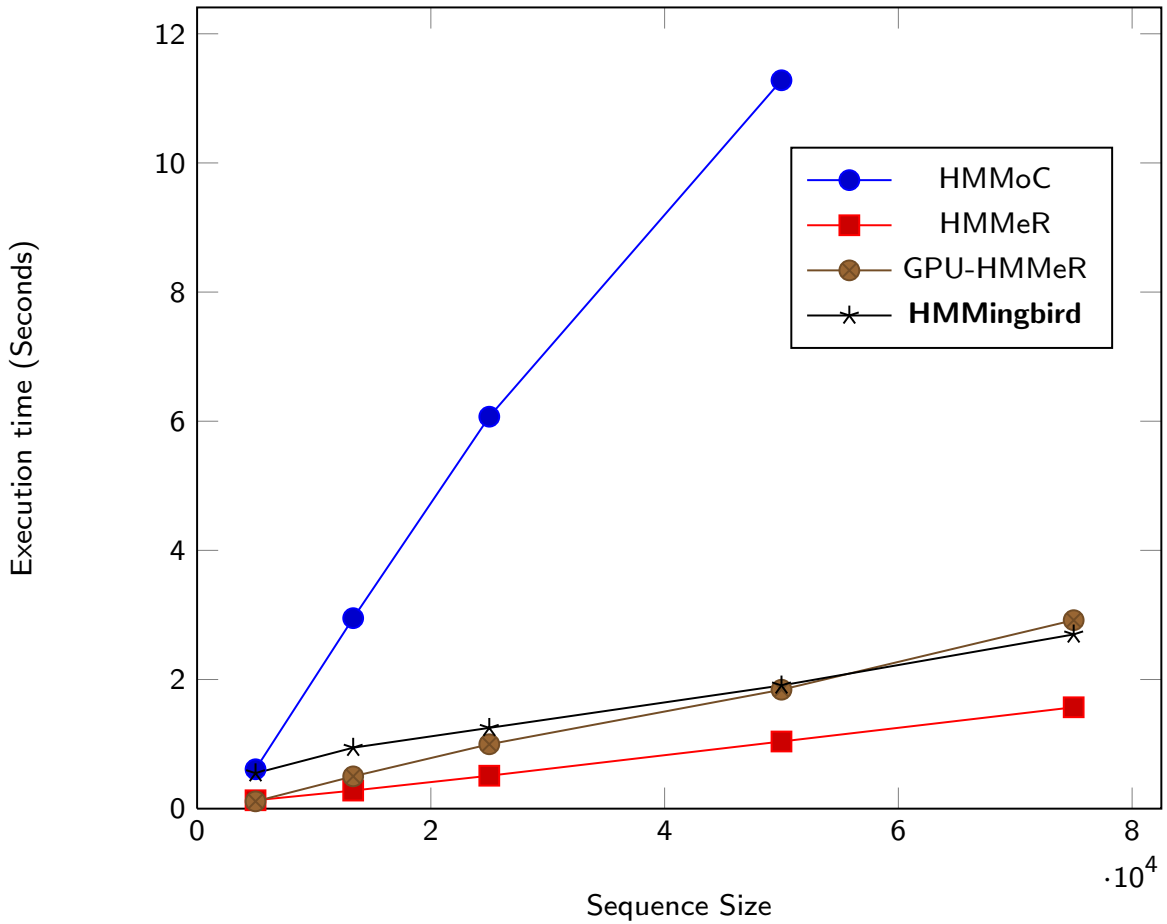
$$F(q,i) = \sum_{p:a_{p,q}>0} a_{p,q} e_{q,s[i]} F(p, i-1)$$

```
define alphabet dice [1,2,3,4,5,6]

define hmm casino {
   alphabet dice;
   startstate start;
   state fair emits fairemission;
   state loaded emits loadedemission;
   endstate end;
   start -> fair 1;
   fair -> fair 0.94999;
   fair -> loaded 0.05;
   fair -> end 0.00001;
   loaded -> loaded 0.97999;
   loaded -> fair 0.02;
   loaded -> end 0.00001;
   emission fairemission =
      [1/6, 1/6, 1/6, 1/6, 1/6, 1/6];
   emission loadedemission =
      [0.1, 0.1, 0.1, 0.1, 0.1, 0.5];
}

prob forward(hmm h, state[h] s, seq[*] x, index[x] i) =
   if i == 0 then
      if s.isstart then 1.0 else 0.0
   else
      sum(t in s.transitionsto :
            forward(t.start, i - 1) * t.prob)
      * (if s.isend then 1.0 else s.emission{x[i-1]})
```

Performance results



Performance for the forward algorithm on a profile HMM model of 10 positions, with varying numbers of sequences.

Conclusion

- We can have our cake and eat it too.
- Automatic parallelisation of first-order, call-by-value functional language.
- High-level approach can provide both an efficient implementation and happy users.