Bellman's GAP - A Declarative Language for Dynamic Programming

Georg Sauthoff Stefan Janssen Robert Giegerich

Universität Bielefeld
Technische Fakultät, 33501 Bielefeld, Germany
{gsauthof, sjanssen, robert}@techfak.uni-bielefeld.de

Abstract

Dynamic programming is a well-established technique to solve combinatorial optimization problems. In several areas of applied computer science, such as operations research, natural language processing, or biosequence analysis, dynamic programming problems arise in many variations and with a considerable degree of sophistication. The simple way dynamic programming problems are normally presented in computer science textbooks – as a set of table recurrences – scales poorly for real world problems, where the search space is deeply structured and the scoring model is elaborate. Coming up with pages of correct recurrences is difficult, implementation is error-prone, and debugging is tedious. *Algebraic* Dynamic Programming (ADP) is a language-independent, declarative approach which alleviates these problems for a relevant class of dynamic programming problems over sequence data.

Bellman's GAP implements ADP by providing a declarative language (GAP-L) with a Java-reminiscent syntax, and a compiler (GAP-C) translating declarative programs into C++ code, which is competitive to handwritten code, and arguably more reliable. This article introduces the GAP-L language, demonstrates the benefits of developing dynamic programming algorithms in a declarative framework by educational example, and reports on the practice of programming bioinformatics applications with Bellman's GAP.

Categories and Subject Descriptors D.3 [*PROGRAMMING LANGUAGES*]: Language Classifications—Specialized application languages

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1. Introduction

Difficulties with dynamic programming Dynamic programming is a widely used technique to solve combinatorial optimization problems. Often, it allows to evaluate a search space of exponential size in polynomial time. Variations of the basic algorithm return not only an optimal solution, but may also report co- or near-optimal solutions, or compute synoptic properties of the search space as a whole, such as its size or sum of all scores. They may sample the search space stochastically, or partition it into certain classes of interest and perform either one of the above analyses class-wise, and so on.

In several areas of applied computer science, such as operations research, natural language processing, or biosequence analysis, dynamic programming problems arise in many variations and with a considerable degree of sophistication. The simple way in which dynamic programming problems are normally presented in computer science textbooks – as a handful of table recurrences – scales poorly for real world problems, where the search space is deeply structured, the scoring model elaborate, and multiple objective functions may be used in combination. Coming up with several pages of correct recurrences is difficult, their implementation is error-prone, and debugging is tedious. For efficiency reasons, optimization is a separate first phase, followed by a backtracing stage to retrieve the solution associated with the optimal score. More comprehensive analyses, such as complete backtracing for the p percent near-optimal solutions, or optimization in a class-wise fashion, considerably add to the implementation effort.

Separating concerns *Algebraic* Dynamic Programming (ADP) [9] is a language-independent, declarative approach that alleviates these problems for a relevant class of dynamic programming algorithms, namely those over sequence data. The remedy is a perfect separation of four concerns that are traditionally expressed in the recurrences in an intermingled fashion: search space definition, candidate scoring, optimization objective, and tabulation issues (the last determines runtime and space efficiency). The central idea behind the algebraic approach can be introduced by a simple example: consider two strings $x = x_1 \dots x_m$ and $y = y_1 \dots y_n$. Their edit distance can be computed via the recurrences

$$dist(0,0) = 0 \tag{1}$$

$$dist(i,0) = dist(i-1,0) + del(x_i), 1 \le i \le m \tag{2}$$

$$dist(0,j) = dist(0,j-1) + ins(y_j), 1 \le j \le n \tag{3}$$

$$dist(i,j) = \min \begin{cases} match(x_i,y_j) & + dist(i-1,j-1) \\ del(x_i) & + dist(i-1,j) \\ ins(y_j) & + dist(i,j-1) \end{cases} \tag{4}$$

Here, del and ins are the scoring functions for deletions and insertions, and $match$ scores character replacements. The boundary conditions, Equations 1-3, indicate structural recursion over the two input sequences, but where does the three-fold case distinction in Equation 4 come from? It reflects the structure of a solution candidate, i.e. an alignment that edits x into y. It recurs on an invisible data structure, which is evaluated without being constructed. To

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make this view explicit, the last equation can be rewritten into

$$\begin{aligned} dist(\eta) &= \min\left[dist(\eta_1), dist(\eta_2), dist(\eta_3)\right] = \\ &\min \begin{cases} match(x_i, y_j) + dist(\zeta_1) \\ del(x_i) + dist(\zeta_2,) \\ ins(y_j) + dist(\zeta_3) \end{cases} \\ \text{where } \eta_1 &= Match(x_i, \zeta_1, y_j) \\ \eta_2 &= Del(x_i, \zeta_2) \\ \eta_3 &= Ins(\zeta_3, y_j) \end{aligned}$$

Here, η denotes the invisible candidate(s) for a subword, and ζ the invisible candidate on which a right-hand side call to $dist$ recurs. Note that the use of subscripts with η and ζ becomes implicit, since, if η is derived from subproblem $(x_i..., y_j...)$, it is clear in each case which characters x_i or y_j are consumed by the local case analysis, and that ζ is derived from the remaining subproblem.

The ADP approach makes the invisible candidate structure explicit. Candidates are modeled as trees. The function symbols used at inner tree nodes reflect the designer's case analysis. They are seen as tree constructors on the specification level, and will be interpreted (called) as scoring functions at runtime. They are collected in a signature which serves as the interface between two (otherwise) independent specification components: grammar and algebras.

The search space is defined by a tree grammar. Candidate scoring is done by an evaluation algebra, implementing the score functions and the optimization objective. Tabulation issues are hidden from the programmer, thus there are no subscripts any more, and hence no subscript errors. Different tree grammars may share evaluation algebras, or different evaluation algebras may be used with one grammar. In particular, products of evaluation algebras give rise to new evaluation algebras, a feature providing re-use of components and a great convenience in practice. An implementation of this approach must take responsibility to generate efficient dynamic programming code, given these declarative constituents.

The Bellman's GAP system *Bellman's GAP* implements ADP. It provides a declarative language (GAP-L) with a Java-reminiscent syntax, in which the programmer specifies tree grammars and evaluation algebras. The language provides three types of evaluation algebra products, allowing to derive more sophisticated analyses from tested components without the need for any reprogramming. Furthermore, it includes a number of pragmatic extensions to the ADP approach, such as generic evaluation algebras and multi-track input. The Bellman's GAP compiler (GAP-C) translates declarative programs into C++ code, which is competitive to handwritten code, and arguably more reliable. It performs extensive optimization to achieve optimal asymptotic space and time efficiency, with reasonable constant factors.

In this article

- we recall (in a compact form) the principles of ADP, and report on their extension by new product operations,
- we introduce the GAP-L language, which bridges the gap between the abstract definitions and the practice of ADP,
- we report on the experiences with ex-bedding ADP from Haskell,
- we demonstrate the benefits of program development in Bellman's GAP by educational example,
- we report from the practice of programming bioinformatics software in GAP-L,
- we conclude with a short list of theoretical and practical research topics which emerge from our experience with Bellman's GAP, and
- the optimizations of the GAP-C compiler are described elsewhere [10].

Relation to previous work During the early development of ADP, the approach was implemented as a combinator language in Haskell [7, 8]. Efficiency concerns with applications emerging around 2004 [12, 18, 19] motivated the implementation of a compiler, which translated the Haskell-embedded notation into more efficient C code [11]. However, the Haskell syntax turned out to be an obstacle to the wider acceptance of the method within the bioinformatics community, in spite of the evident increase in programmer productivity. Also, the fragile borders of an embedded language encouraged algorithm designers to incorporate non-ADP features from the host language, resulting in an unfortunate mixture of automated translation and subsequent hand-patching. Hence, Bellman's GAP was designed to free ADP from its Haskell embedding, and at the same time to incorporate new features that had evolved after publication of [9].

Outside the realm of the algebraic approach, related work is for example the *Dynamite* system [3] for biosequence analysis, or, in the natural language processing community, the DYNA language [5]. DYNA is based on a general, Prolog-style backtracking scheme, allowing the programmer to concentrate on the logic of the parsing algorithm, rather than its implementation. Neither of these approaches achieves a separation of search space construction and evaluation. In both cases, unfortunately, it must be said that these approaches have worked well only in the hands of their creators. Since the gain in abstractness is not large enough, they have not found more widespread use. This holds also, albeit for different reasons as described above, for our early efforts with Haskell-embedded ADP. With Bellman's GAP, we hope to break this barrier.

2. GAP-L semantics

Signatures, tree grammars and evaluation algebras This paragraph recalls, in a very terse format, the basic definitions of ADP, following the literature [9]. Let $\mathcal{A}$ be an alphabet and $\mathcal{A}^*$ be the set of strings or sequences over $\mathcal{A}$. A *signature* Σ over $\mathcal{A}$ is a set of function symbols and a datatype place holder (sort) S. The return type of an $f \in \Sigma$ is S, each argument is of type S or $\mathcal{A}$. T_Σ denotes the term language described by the signature Σ and $T_\Sigma(V)$ is the term language with variables from the set V. A Σ-*algebra* or *interpretation* $\mathcal{E}$ is a mathematical structure given by a carrier set $S_\mathcal{E}$ for S and functions operating on this set for each $f \in \Sigma$, consistent with their specified type. Interpreting a term $t \in T_\Sigma$ by $\mathcal{E}$ is denoted $\mathcal{E}(t)$ and yields a value in $S_\mathcal{E}$.

A *regular tree grammar* $\mathcal{G}$ over a signature Σ is defined as tuple $(V, \mathcal{A}, Z, P)$, where V is the set of non-terminals, $\mathcal{A}$ is an alphabet, $Z \in V$ is the axiom, and P is the set of productions. Each production is of form

$$v \rightarrow t \text{ with } v \in V, t \in T_\Sigma(V) \quad (5)$$

The *language* generated by a regular tree grammar $\mathcal{G}$ is the set of trees

$$\mathcal{L}(\mathcal{G}) = \{t \in T_\Sigma | Z \Rightarrow^* t\} \quad (6)$$

where $\Rightarrow^*$ is the reflexive transitive closure of $\rightarrow$. By construction, $\mathcal{L}(\mathcal{G}) \subseteq T_\Sigma$. Its elements are seen as trees when it comes to constructing them, and as formulas when it comes to their evaluation.

Symbols from $\mathcal{A}$ reside on the leaves of these trees. The symbol y denotes the *yield function* and is of type $T_\Sigma \rightarrow \mathcal{A}^*$. It is defined as $y(a) = a$, where $a \in \mathcal{A}$ and $y(f(x_1, \ldots, x_n)) = y(x_1) \ldots y(x_n)$, for $f \in \Sigma$ and $n \geq 0$. The yield language $\mathcal{L}_y(\mathcal{G})$ of a tree grammar $\mathcal{G}$ is defined as

$$\mathcal{L}_y(\mathcal{G}) = \{y(t) | t \in \mathcal{L}(\mathcal{G})\} \quad (7)$$

Regular tree grammars as we use here pose a special type of parsing problem: given $x \in \mathcal{A}^*$, we construct the *search space* $\{t | t \in \mathcal{L}(\mathcal{G}), y(t) = x\}$. This process - computing the inverse of y – is called *yield parsing*. A Bellman's GAP programmer does not need to care about how yield parsing works.

The candidate trees constitute the "invisible" data structure mentioned in our introductory remarks. They allow us to effectively separate search space construction from search space evaluation. Note that the candidate trees, the elements of $y^{-1}(x)$, are not parse trees. Each candidate tree *has* a parse tree by $\mathcal{G}$, but it *is* a terminal tree in $L(\mathcal{G})$. Basing candidate evaluation on parse trees directly might be feasible, but would create interdependence between search space construction and evaluation.

An *evaluation algebra* is a Σ-algebra augmented with an objective function $h : [S] \to [S]$, where the square brackets denote multisets (in theory, and lists in practice).

An *ADP problem instance* is specified by a regular tree grammar $\mathcal{G}$, evaluation algebra $\mathcal{E}$ and input sequence $x \in \mathcal{A}^*$. Its solution is defined by

$$\mathcal{G}(\mathcal{E}, x) = h_{\mathcal{E}}[\mathcal{E}(t) | t \in \mathcal{L}(\mathcal{G}), y(t) = x] \tag{8}$$

The square brackets in Equation 8 denote a multiset. This is required because in practice, we often ask for all co-optimal solutions, or all solutions within a percentage of optimality. The notation $\mathcal{G}(\mathcal{E}, x)$ suggests the use of the regular tree grammar $\mathcal{G}$ (more precisely, its yield parser) as a function called with evaluation algebra $\mathcal{E}$ and input x as parameters. Internally, however, Equation 8 is not executed literally. Rather, the application of the objective function is amalgamated with the evaluation of the candidate trees, which are not constructed explicitly. (In functional language terminology, this is a case of deforestation.) Also, tabulation of intermediates is used where appropriate, to avoid exponential blow-up. The prerequisite for correct and efficient computation of the solution in this way is Bellman's Principle of Optimality [2], which is defined by Equations 9 and 10 in the ADP framework

$$\begin{aligned} &h_{\mathcal{E}}[\, f_{\mathcal{E}}(x_1, \ldots, x_k) \mid x_1 \leftarrow X_1, \ldots, x_k \leftarrow X_k \,] = \\ &h_{\mathcal{E}}[\, f_{\mathcal{E}}(x_1, \ldots, x_k) \mid x_1 \leftarrow h_{\mathcal{E}}(X_1), \ldots, x_k \leftarrow h_{\mathcal{E}}(X_k) \,] \end{aligned} \tag{9}$$

$$h_{\mathcal{E}}(X_1 \cup X_2) = h_{\mathcal{E}}(\, h_{\mathcal{E}}(X_1) \cup h_{\mathcal{E}}(X_2)\,) \qquad \text{and} \qquad h_{\mathcal{E}}[\,] = [\,], \tag{10}$$

where X_i denote multisets. Note that these equations imply less general criteria which are found in the literature. When h is minimization or maximization, it implies (strict) monotonicity of each $f \in \Sigma$ [15]. When the evaluation algebra holds only a single, binary and commutative function f, (h, f) forms a semiring where h distributes over f [17].

When compiling an ADP algorithm coded in GAP-L, it is always assumed that the evaluation algebra used satisfies Bellman's Principle. This is the developer's responsibility. However, in some cases, the compiler can notice that this principle is violated, and issues a warning.

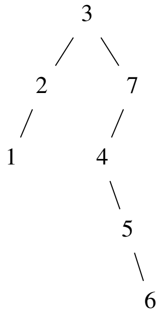
Example We present an ADP version of the classic optimal binary search tree algorithm [4] to demonstrate the ADP concepts from the previous paragraph. Given a set of keys and their access probabilities, the algorithm computes the binary tree with minimal mean access time. Why is this a *sequence* analysis problem at all? Because in a search tree, the order of leaves is fixed. The yield string of any search tree must hold the keys in sorted order.

With a dynamic programming approach, the minimal expected access time results from the optimization phase, the underlying optimal tree structure is derived via backtracing. With the example input sequence

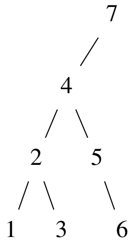
$$\begin{aligned} s = [&(1, 0.05), (2, 0.05), (3, 0.40), (4, 0.10), \\ &(5, 0.20), (6, 0.01), (7, 0.19)] \end{aligned}$$

the two binary trees t_1 and t_2 have a mean access time of 2.18 and 2.98, where the access time is the number of key comparisons in a lookup operation, which corresponds to the depth of the accessed node.

t_1 :



t_2 :

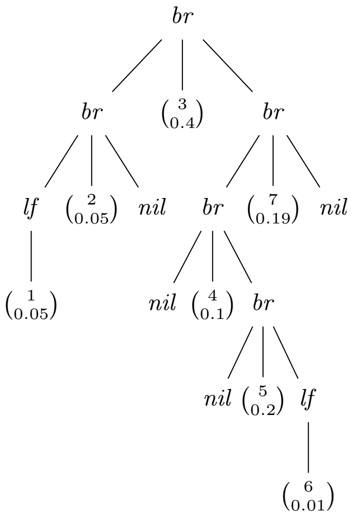


In this example, the candidates of the search space are all possible binary search trees. The *signature* requires a branching symbol br, a leaf symbol lf and a symbol that represents an empty subtree nil.

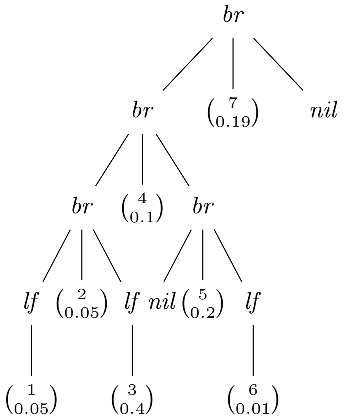
$$\begin{aligned} br &: T \times \mathcal{A} \times T && \to T \\ \mathit{lf} &: \mathcal{A} && \to T \\ \mathit{nil} &: && \to T \end{aligned}$$

Using these symbols, the following *candidate trees* represent t_1 and t_2:

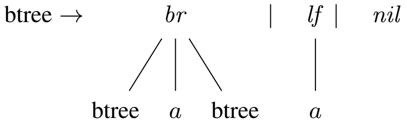
t'_1 :



t'_2 :



The following tree grammar *btrees* (axiom is btree) generates all possible binary search trees using the function symbols from the signature:



where $a \in \mathcal{A}$. The *alphabet* $\mathcal{A}$ is $K \times P$, where K is the set of keys and $P = [0, 1]$.

Computing the mean access time is done via the evaluation algebra *mean*. The place-holder (sort) T is mapped to $\mathbb{R} \times \mathbb{R}$, where the first component of a result is the mean access time of the candidate and the second component is sum of the probabilities of the yield of the candidate tree. The evaluation functions are implemented by

$$\begin{aligned} br(l,(k,p),r) = &\quad (l_1 + r_1 + l_2 + r_2 + p, l_2 + r_2 + p) \\ lf((k,p)) = &\quad (p,p) \\ nil = &\quad (0,0) \\ h = &\quad min \end{aligned}$$

The objective function h is minimization, to choose the binary tree with the minimal access time. Thus, a call to $btrees(mean, s)$ computes the minimal mean access time for the example sequence s:

$$btrees(mean, s) = [(1.96, 1)]$$

i.e. the minimal mean access time for the input sequence s is 1.96.

The non-optimizing *printing algebra*, by convention named *print*, transforms a candidate tree into a textual notation, i.e. T is mapped to the domain of character sequences.

$$\begin{aligned} br(l,(k,p),r) = &\quad \text{“(”} + l + \text{“)”} + str(k) + \text{“(”} + r + \text{“)”} \\ lf((k,p)) = &\quad str(k) \\ nil = &\quad \text{“”} \\ h = &\quad id \end{aligned}$$

where *str* converts its argument to a string representation and + means string concatenation. Note that we choose to represent only the key, not its probability.

Evaluating $btrees(print, s)$ enumerates the complete search space of 2,128 candidates, including strings for both example candidates:

$$t_1 \rightarrow \text{((1)2())3((()4(()5(6)))7())}$$
$$t_2 \rightarrow \text{(((1)2(3))4(()5(6)))7()}$$

With a slightly more elaborate *print* algebra, we generate the LaTeX code for tree graphics as depicted above.

Computing both, minimal mean access time and the structure of the candidate which achieves it, is done via a *product algebra*: $btrees(mean * print, s)$ returns a list of optimal structures with minimal mean access time, e.g.

$$[((1.96, 1), \text{“(()1(2))3((4)5((6)7()))”})]$$

This example also demonstrates how the “separation of concerns” mentioned above is achieved in practice: The signature defines a universe of candidates, algebras define different ways to score them, objective functions capture the intended goal of the analysis, and tree grammars define the candidate space arising from given input. Efficiency concerns related to tabulation have been eliminated completely, as this issue is automated by the compiler. An immediate benefit of this separation of concerns is that we can build more sophisticated analyses from simpler ones by operations on evaluation algebras.

Products of algebras If combinatorial optimization is to be performed under multiple objectives, one could design algebras which operate on tuples of scores and apply the multiple objectives. A much faster and safer way to achieve this is often possible via *product algebras*. They allow to describe different objectives independently, and to afterwards combine them in various fashions, avoiding a lot of redundant and error-prone coding. With algebras A and B already available, one simply calls $\mathcal{G}(A * B, x)$, with no extra programming or debugging effort.

We present three kinds of products here. The “lexicographic” product has been introduced and studied in [22], the other two are new.

We need to introduce two properties of algebras, which are prerequisites for well-defined products. An algebra is called *unitary*, if its evaluation functions return lists of results holding at most one element. A *generic* algebra $A(k)$ has a parameter $k > 0$ such that it returns the k best solutions under its objective function. Naturally, $A(1)$ is unitary.

Let A and B be unitary evaluation algebras over Σ. The *cartesian product* $A \times B$ is an evaluation algebra over Σ. Its functions take arguments of the form $(a, b) \in \mathcal{S}_A \times \mathcal{S}_B$ or $z \in \mathcal{A}$. For simplicity, we define the functions of $A \times B$ for the case of a binary function f with one argument of either kind, and leave the general case to the reader.

$$f_{A\times B}((a,b),z) = (f_A(a,z), f_B(b,z))) \tag{11}$$

The objective function of $A \times B$ is

$$\begin{aligned} h_{A\times B}[(a_1,b_1),\ldots,(a_m,b_m)] = [\,(l,r) \mid l \leftarrow h_A[a_1,\ldots,a_m], \\ r \leftarrow h_B[b_1,\ldots,b_m]\ ]. \end{aligned} \tag{12}$$

The algebras are required to be unitary, because otherwise, Bellman's Principle would be violated and the answer sets would blow up exponentially, without adding information. The cartesian product has little use by itself, because the results returned from A and B are independent – according to Eq. 12 they are drawn from different candidates in the search space. Thus, instead of $\mathcal{G}(A \times B, x)$ one might call $\mathcal{G}(A, x)$ and $\mathcal{G}(B, x)$ separately, which gives the same result, albeit more slowly. However, in combinations with other products, we have found the cartesian product useful, and we will see examples of this later.

The *lexicographic product* $A * B$ is an evaluation algebra over Σ and has the functions

$$f_{A*B} = f_{A\times B} \tag{13}$$

for each $f \in \Sigma$, and the objective function

$$\begin{aligned} h_{A*B}[(a_1,b_1),\ldots,(a_m,b_m)] = [\,(l,r) \mid \\ l \leftarrow \mathrm{set}(h_A[a_1,\ldots,a_m]), \\ r \leftarrow h_B[\,r' \mid (l',r') \leftarrow [(a_1,b_1),\ldots,(a_m,b_m)],\ l' = l\,]\ ]. \end{aligned} \tag{14}$$

Here, $\mathrm{set}(X)$ reduces the multiset X to a set. This product gets its name from the fact that if both algebras optimize, then it implements the lexicographic ordering of the two independent criteria as its objective. However, this product is not restricted to the case of two optimizing algebras, and exhibits a surprising versatility of use [22]. For example, a product $A * P$, where P is an algebra that produces an external "print" representation of the candidate, specifies a backtracing phase after optimization with A.

Our third product combines the objective functions in a more sophisticated way. Assume we have the generic $MinPrice(k)$ algebra which returns the k cheapest pizzas in our search space, and algebra $Kind$ which evaluates pizzas as “vegetarian”, “meat”, “seafood”, or “other”, but does not make any choices. Then, the use of $(Kind \otimes MinPrice)(2)$ is defined to yield the two cheapest pizzas such that each is of a different kind.

Let A be a Σ-algebra and $B(k)$ a generic Σ-algebra. The *interleaved product* $(A \otimes B)(k)$ is a generic Σ-algebra and has the functions

$$f_{A\otimes B} = f_{A\times B} \tag{15}$$

for each $f \in \Sigma$, and the objective function

$$\begin{aligned} & h_{(A\otimes B)(k)}[(a_1,b_1),\ldots,(a_m,b_m)] = \\ & \quad [\,(l,r) \mid (l,r) \leftarrow U, p \leftarrow V, p = r] \\ & \text{where} \\ & \quad U = h_{A*B(1)}[(a_1,b_1),\ldots,(a_m,b_m)] \\ & \quad V = \text{set}(h_{B(k)}[v \mid (\_,v) \leftarrow U]) \end{aligned} \tag{16}$$

Further generalizations To keep the formalism short, we have ignored several features which are required to turn a concise formalism into a practical programming tool, but do not make the theory deeper. *Generic* algebras may contain parameters, to be instantiated when the algebra is applied. They are not restricted to be a number as in Eq. 16. Signatures and algebras may be many-sorted, if the result types need to be different for subproblems that arise in the input decomposition. The objective function h then splits into a separate function for each result type. Some problems, such as string edit distance, require two input strings rather than one. These issues will be discussed in our description of GAP-L.

3. The Bellman's GAP Language

The design goal of GAP-L is to make it easy to learn for ADP beginners, and powerful to use for ADP experts. To lower the entry barrier for novice programmers, GAP-L uses some concepts that are common in the widespread C/Java-like languages. A signature declaration in GAP-L is similar to an interface declaration in Java. An evaluation algebra *implements* a signature, as a Java class may implement an interface. An algebra may *extend* another algebra and overwrite existing functions, as a Java class is able to extend another class. Tree grammars are specified in a declarative style, where the right hand side of productions contain tree patterns resembling function calls. The algebra code is written as imperative code blocks. In spite of such resemblance, GAP-L is a declarative language for dynamic programming over sequence input.

Space does not allow a full presentation of GAP-L here. The interested reader is referred to [20, 21]. We demonstrate features of GAP-L in two parts. First, we show the notations for the core ADP concepts. Then we present a selection of further language features which are motivated by practical convenience and control of efficiency.

Coding signatures, grammars, algebras and instances

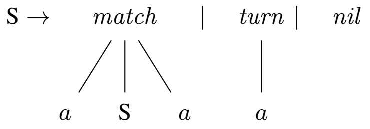
We demonstrate the GAP-L syntax using a simple example. Given string x, we seek a palindromic structure for it, which is optimal under some scoring scheme. This is a toy example, which we will gradually extend to show the building-block style of program development in GAP-L. *Exact* palindromes are strings which read the same forward and backward, i.e. $x = x^{-1}$. We will use several variants of the basic problem, such as approximate palindromes (allowing errors), nested palindromes, or finding the sub-string with the best palindrome score under a given scoring model.

We first decide which function symbols we need to model the candidate terms in the search space, i.e. we define the signature, and then proceed (in any order) to define algebras and grammars. Our first signature is

```
signature paliS(alphabet, answer) {
  answer match(alphabet, answer, alphabet);
  answer nil(void);
  answer turn(alphabet);
  choice [answer] h([answer]); }
```

where answer denotes the sort symbol, and function symbols are $\{match, nil, turn\}$. They cover the cases of two matching characters, and the mid-point of a palindrome of even or odd length. The signature declaration resembles a Java interface declaration and the [] brackets denote a list type. The **choice** keyword marks the function symbol h as the objective function.

We describe the search space of all palindrome candidate terms with Grammar *Pali1*, axiom is S



where the first two rules are shorthands for $|\mathcal{A}|$ rules each, one for each $a \in \mathcal{A}$.

In GAP-L syntax the tree patterns are written like function applications:

```
grammar Pali1 uses paliS(axiom = S) {
  S     = match(CHAR, S, CHAR) with equal |
          turn(CHAR) |
          nil(EMPTY) # h ; }
```

The underlying signature and the axiom are specified in the header of the grammar definition. The **#** operator specifies where the objective function should be applied to the rules' alternatives (**#** binds more weakly than |). While it could be applied by default with every production, there are situations which require exceptions from this default, and we decided to give the programmer full control by an explicit **#** operator. Terminal symbol/parser names are written in upper case, such as CHAR for a single character from the alphabet, and STRING for a string.

The first alternative of non-terminal S uses *syntactic filtering*, i.e. the left hand side of the **with** keyword is only parsed if the *equal* filter returns true for the parsed sub-word. The *equal* filter tests if the first and last character of the sub-word are equal. This filtering reduces the search space, rather than penalizing non-palindromes with a large cost. As a consequence, the *match* algebra function does not need to check the characters. Without syntactic filtering, we would need to duplicate the match rule for every character of the alphabet.

Next, we define a simple scoring scheme:

```
algebra score
    implements paliS(alphabet = char,
                     answer = int) {
  int match(char a, int b, char c)
    { return b + 3; }
  int turn(char l) { return 0; }
  choice [int] h([int] x)
    { return list(maximum(x)); } }
```

The syntax of the algebra definition resembles the definition of a Java class. The header contains the mapping between alphabet and sort symbol to concrete data types.

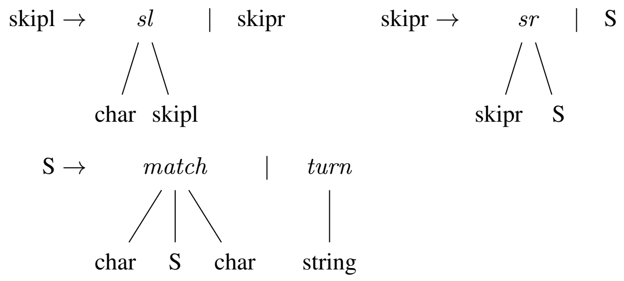
Perfect palindromes do not pose an optimization problem. The search space is empty if x is not a palindrome, and otherwise, it is $[t]$, with $score(t) = (|x| \; div \; 2) \cdot 3$. No dynamic programming is needed – a simple loop is sufficient that checks for character matches in x outside to inside. In fact, the optimizations within GAP-C recognize such a special case and generate a simple loop without allocating any tables.

To make the example more interesting, we want to search the input for *local* palindromes. They may hold a (non-palindromic) turn of any length, and may be embedded somewhere in a longer string. We extend the signature for this:

```
signature paliS(alphabet, answer) {
  answer match(alphabet, answer, alphabet);
  answer turn(int);
  answer sl(char, answer);
  answer sr(answer, char);
  choice [answer] h([answer]); }
```

sl and *sr* allow for leading or trailing characters around the palindrome and *turn* allows for a region of several unmatched characters.

We extend the grammar towards local palindromes:
grammar *Pali2*, axiom is *skipl*



Here *string* is a terminal symbol denoting an arbitrary string over $\mathcal{A}$, and *char* denotes a character.

We write the *Pali2* grammar in GAP-L as:

```
grammar Pali2 uses paliS(axiom = skipl) {
  skipl = skipr |
          sl(CHAR, skipl) # h ;
  skipr = skipr(sr, CHAR) |
          S               # h ;
  S     = match(CHAR, S, CHAR) with equal |
          turn(SEQ0)      # h ; }
```

The SEQ0 terminal parser accepts an arbitrary sub-word of the input and returns its length.

In our simple scoring scheme, skipping characters in the beginning or end or in the middle turn is for free:

```
algebra localscore
    implements paliS(alphabet = char,
                     answer = int) {
  int match(char a, int b, char c)
    { return b + 3; }
  int turn(int l) { return 0; }
  int sl(char c, int x) { return x; }
  int sr(int x, char c) { return x; }
  choice [int] h([int] x)
    { return list(maximum(x)); } }
```

Our scoring ignores the length of the "turn", but since SEQ0 passes the length of the subword to the function turn, we could have penalized long turns with a score of, say, $-0.2 \cdot l$.

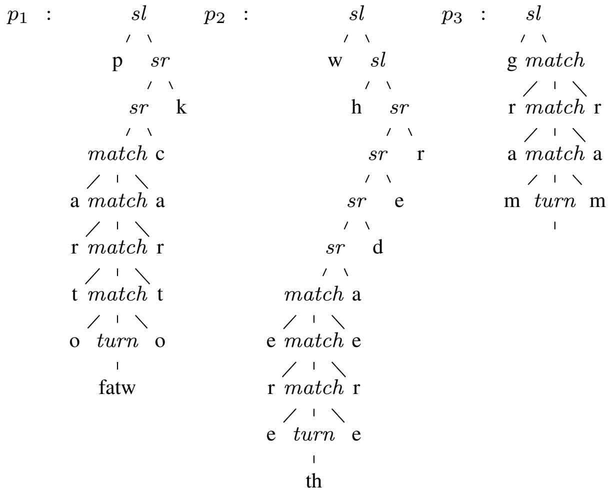
With grammar *Pali2*, the palindromic structure of a string is no longer unique. If we depict alternative structures using parenthesis for matched characters, '+' for characters constituting the turn, and '-' for leading/trailing characters, three candidate solutions (out of many, resulting from applying *Pali2* to the source text of this article) can be depicted as

```
    partofatwotrack
p1: -((((++++))))--

    wherethereader
p2: --(((++)))----

    grammar
p3: -((()))
```

As elements of $\mathcal{L}(Pali2)$, they are represented as trees



where the reader may verify (using Eq. 8) that *Pali1*(*score*, "grammar") = [], and *Pali2*(*localscore*, "grammar") = [9], where this optimal score is derived from the candidate p_3.

In many situations, the size of the search space for given input is of interest. It can be determined by a *counting* algebra, which scores every candidate by 1 and the objective function sums over all candidates. Care must be taken to write the algebra in a way such that it satisfies Bellman's Principle. Since there is a schematic way to achieve this, a counting algebra can be automatically derived from the signature. The syntax to request a counting algebra in GAP-L is:

```
algebra howMany auto count ;
```

The compiler generates an algebra named *howMany* which is equivalent to following explicit algebra definition:

```
algebra count
    implements paliS(alphabet = char,
                     answer = int) {
  int match(char a, int b, char c)
    { return b; }
  int turn(int l) { return 1; }
  int sl(char c, int x) { return x; }
  int sr(int x, char c) { return x; }
  choice [int] h([int] x)
    { return list(sum(x)); } }
```

This is a particularly simple example, but the automatic generation works for any signature.

A *print* algebra does not optimize an objective nor does it do synoptic analysis of the search space, but it specifies how a candidate structure is mapped to a string representation. The following algebra marks gaps with - characters, matches with parentheses and an unmatched position with a + character, such as -(((+++)))-. The objective function is the identity.

```
algebra print
    implements paliS(alphabet = char,
                     answer = string) {
  string match(char a, string x, char b) {
    string r; append(r, ’(’);
    append(r, x); append(r, ’)’);
    return r;
  }
  string turn(int l) {
    string r; append(r, ’+’, l);
    return r;
  }
  string sl(char b, string x) {
    string r; append(r, ’−’);
    append(r, x); return r;
  }
 string sr(string x, char b) {
    string r; append(r, x);
    append(r, ’−’); return r;
  }

  choice [string] h([string] x)
    { return x; }
}
```

Bellman’s GAP requires the programmer to specify in advance which combinations of grammars and algebras will be called. This is because the compiler can perform extensive optimizations and produce specialized code when the instances are known.

As part of the GAP-L program we add two instance definitions for the products we want to use:

```
instance scorecnt =
            pali2( localscore * count ) ;
instance scoreprt =
            pali2( localscore * print ) ;
```

This example displays the versatility of the lexicographic product. According to Eq. 14, the first instance computes the number of co-optimally scoring palindromes in the search space. The second instance computes the optimal palindrome score and the print string of (all) their associated candidate structures. If you ever have programmed a backtracing phase to retrieve the candidate behind the optimal score, you will appreciate getting it without programming effort in this way.

The product operators $\times$ and $\otimes$ are written as % and / characters in GAP-L.

Multi-track input GAP-L supports dynamic programming on multiple sequences. An example of a multi-track DP algorithm is the pairwise sequence alignment algorithm, i.e. the optimal sequence of edit operations to transform one sequence into the other. We write a sequence alignment grammar to exemplify the GAP-L multi-track syntax. It implements our introductory edit-distance example.

First, an input declaration specifies a two track program:

```
input < raw, raw >
```

The raw keyword means that no preprocessing of the input sequence is done. Otherwise, some character transformations may be specified.

In the grammar, the <> brackets start input track bifurcations:

```
grammar Align uses alignS(axiom = ali) {
  ali = match(<CHAR, CHAR>,   ali)  |
        ins(<EMPTY, CHAR>,    ali)  |
        del(<CHAR, EMPTY>,    ali)  |
        nil(<EMPTY, EMPTY>)          # h ; }
```

The non-terminal ali is a two-track non-terminal, i.e. it is part of a two-track context. The <> parentheses enclose as many components as the number of tracks in the current context. Each component is in a one-track context. In this example, the one-track contexts only contains terminal parser calls, but it is also possible to call one-track non-terminals from multi-track bifurcations. A use case for this is the minisatellite alignment problem [1], but the model is too complex to be included here.

The <> parentheses are also used in the signature declaration and algebra definition to access the different tracks:

```
signature alignS(alphabet, answer) {
  answer match( < alphabet, alphabet >,
                answer); ...  }
algebra affine implements
    alignS(alphabet = char, answer = int) {
  int match(<char a, char b>, int m)
  { ... } ...  }
```

Filters, parameters, and more We have already seen *syntactic filtering*, using the **with** keyword followed by filtering function defined by the programmer. This boolean function is applied to an input sub-word before it is parsed, and no parse is made if the filter is false. This implements a syntactic pruning of the search space. *Semantic filtering* is also possible using the keyword **suchthat**. It tests on values derived for a candidate by the given algebra. In this case, the candidate is parsed and scored, but may be eliminated from further consideration, for any reason we specify via the semantic filter function.

Sometimes, a grammar requires many rules with renamed non-terminal symbols, but isomorphic in structure. In this case, GAP-L allows the use of nonterminal symbols that pass parameters from the left-hand to the right-hand side.

Although subscripts are completely banned in ADP programming, sometimes scoring requires access to positions in the input, for example, when a match of two characters near the ends is to be scored more highly than near the middle. To this end, GAP-L provides a parser *LOC* which recognizes an empty subword and returns its position in the input. Positions so obtained become regular arguments to the algebra functions.

Finally, for programming in the large, GAP-L provides a module concept and allows to mix several algebras, signatures and grammars in one program.

4. Ex-bedding Experience

As described in the introduction, ADP was first implemented as domain specific language (DSL) embedded in Haskell. With Bellman’s GAP we have chosen to ex-bed ADP from Haskell into the GAP-L language and have created the optimizing GAP-C, which translates GAP-L into efficient C++ code. [10] The reasons for the ex-bedding are threefold.

First, like with other DSLs embedded into a host language, error reporting and diagnostics are problematic in the ADP Haskell embedding. Small errors, like a missing parameter or an accidental indenting (offside rule) may lead to several screen pages of type inference errors. Effectively, to program in the embedded language one has to know how to program in Haskell and implementation details of the client language. Haskell-literacy in bioinformatics is marginal. We designed GAP-L and GAP-C with this in mind. The syntax is Java-like and algebra functions are written as imperative code. GAP-C includes some efforts for user friendly reporting of warnings and diagnostics regarding syntax and semantic errors.

Second, the performance of the Haskell embedding is limited. The runtime is several magnitudes greater in comparison with handwritten code. For several algorithms, the memory usage is

Table 1. program variations for different palindrom problems.

program	features	opt. score	answer
input $x =$ `ababdcdaaadacda`			
$Pali_1(score * print, x)$	exact palindrome	-	
$Pali_2(score * print, x)$	longer turn, free ends	6	`----((++++++))-`
$Pali_3(score * print, x)$	unmatched characters anywhere	7	`----(({{()}}))-`
$Pali_4(score * print, x)$	several adjacent palindromes	15	`(+)-(+)()((++))`
$Pali_5(score * print, x)$	nested palindromes	18	`((-)((((+))-)))`

Table 2. the results of the Pali5 grammar and two classifying example products.

grammar	Pali5$(trns * count, x)$	Pali5$(trns * score * print, x)$
input	`ababdcdaaadacda`	`ababdcdaaadacda`
results	`( 1 , 26632 )`	`( ( 1 , 15 ) , --(-((((+))-))) )`
	`( 2 , 60684 )`	`( ( 2 , 15 ) , ((+)-(((+))-)-) )`
	`( 3 , 16896 )`	`( ( 3 , 15 ) , ((+)(+)-)((++)) )`
	`( 4 , 200 )`	`( ( 4 , 10 ) , {}({}(-()(+))-) )`

very high, such that they can only be used for short sequences [10]. GAP-C includes several optimizations such that the generated imperative code is competitive with handwritten code. Since the compiler is specialized to the domain of dynamic programming, memory management is not a problem in the generated code.

Third, new language features of GAP-L, e.g. multitrack DP and filters are problematic to implement in the embedding, because of the danger of bulky parser combinators and inter-parser interactions.

However, we still maintain the Haskell embedding, because it proves to be useful in several respects. We use it as reference implementation of the ADP core. The testsuite of GAP-C includes several parallel test cases against it. Also, it is advantageous rapid prototyping of new language ideas in some cases, e.g. new product variants. Rewriting large parts of the compiler for a language extension, where it is unclear if it pays off, is not feasible.

5. Program development in Bellman's GAP

We further extend our palindrome example to demonstrate the ease of developing dynamic programming algorithms in GAP-L. See Table 1 for an overview. We rely on the reader's intuition to evaluate the extend to which such convenience carries over from our toy to real-world applications.

Four variations on palindromes Proceeding from *Pali2* to *Pali3*, we merely drop the syntactic filter, and thus leave it to the scoring functions to score two equal, or similar, characters positive, the others negative:

```
grammar Pali3 uses paliS(axiom = skipl) {
   skipl = sl(CHAR, skipl) |
           skipr           # h ;
   skipr = sr(skipr, CHAR) |
           S               # h ;
   S = match(CHAR, S, CHAR)|
       turn(SEQ0)          # h; }
```

The $localscore$ scoring algebra is changed such that mismatches are penalized:

```
   int match(char a, int b, char c) {
     if (a == c) return b + 3;
            else return b − 1; }
```

Next, we change the grammar to allow for multiple successive palindromes in the input. For this, we need to add a new nonterminal to the grammar which also becomes the axiom, and we need to add another alternative rule to S to append only non-empty palindromes:

```
grammar Pali4 uses paliS(axiom = A) {
  A = skipl |
      app(skipl, S) # h ;
   ...
  S = match(CHAR, S, CHAR) |
      match(CHAR, turn(SEQ0), CHAR) # h ; }
```

The new function symbol app extends the signature. It is responsible for scoring the case of two adjacent (sub-)palindromes. We extend algebra *localscore* with a line

```
  int app(int x, int y) { return x + y; }
```

Adding one more alternative rule for S, we can allow for nested palindromes, i.e. the "turn" of a palindrome can recursively contain palindromes:

```
grammar Pali5 uses paliS(axiom = A) {

  A = skipl | app(skipl, S) # h ;

   skipl = skipr          |
           sl(CHAR, skipl) # h ;

   skipr = sr(skipr, CHAR) |
           S               # h ;

  S = match(CHAR, S, CHAR)             |
      match(CHAR, turn(SEQ), CHAR)     |
      match(CHAR, sl(CHAR, A), CHAR)   |
      match(CHAR, sr(A, CHAR), CHAR)  # h; }
```

At this point, the grammar already resembles a simplified RNA secondary structure prediction grammar. We will build this in the next section on "real world" examples.

In Table 1 we give an overview of different results.

Splitting the search space into classes Let us assume we want to understand our search space more deeply, and compute several near-optimal structures, which are subject to the condition that they hold a different number of local palindromes. We leave it to the reader to design the evaluation algebra $trns$ which counts the number of "turns" in a candidate structure. (Hint: use $app(x, y) = x + y, match(a, x, b) = x$.) Using this algebra $trns$ in the two products shown in Table 2, we obtain the count of structures for each number of turns, as well as the optimal score/structure for each number.

This simple example demonstrates a general method: *any* analysis $\mathcal{G}(B, x)$ can be refined with respect to a classification attribute that can be computed by yet another algebra A, simply by calling $\mathcal{G}(A * B, x)$.

An $O(n^6)$ time, $O(n^4)$ space algorithm To give an example for an algorithm of higher complexity, let us seek optimal *joint* palindrome structures for two sequences, as exemplified by

```
MI-SSISSIPPI
+( ((+)))()
PAPPALAPAPP-
```

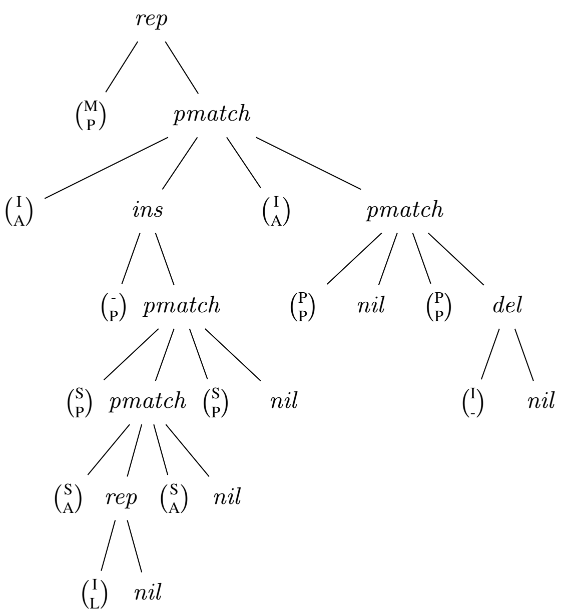
We extend the grammar $Align$ by a production which derives a matching character pair in either sequence, where the two pairs need not be the same. This case is scored by the new function $pmatch$. (The extended signature align2 is not shown).

```
grammar PaliJoint uses align2(axiom = pj) {
  pj = rep(<CHAR, CHAR>, pj)     |
       ins(<EMPTY, CHAR>, pj)    |
       del(<CHAR, EMPTY>, pj)    |
       nil(<EMPTY, EMPTY>)       |
       pmatch(<CHAR, CHAR>, pj,
              <CHAR, CHAR>, pj) # h ;
}
```

```
algebra score implements align2(
    alphabet = char, answer = int) {
  int rep(<char a, char b>, int x) {
    if (a==b) return x + 1;
        else  return x − 1;
  }
  int ins(<void, char b>, int x) {
    return x − 1; }
  int del(<char a, void>, int x) {
    return x − 1; }
  int nil(<void, void>) {
    return 0; }
  int pmatch(<char a1, char b1>, int x,
             <char a2, char b2>, int y) {
    if ((a1 == a2) && (b1 == b2)) {
      if (a1 == b1) return x + y + 3;
          else      return x + y + 2;
    } else { return −1000; }
  }
  choice [int] h([int] x) {
    return list(maximum(x));
  }
}
```

Here is one of the two optimal candidates for input strings "MISSISSIPPI" and "PAPPALAPAPP" with score 5.

c_1 :



The new rule in Grammar $PaliJoint$ has the abstract form $pj \rightarrow$ '(' pj ')' pj. Due to insertions and deletions, the position of the split between the two instances of pj is independent in the two input sequences. This leads to an algorithm which requires a four-dimensional table to tabulate non-terminal pj and has asymptotics of $O(n^6)$ time and $O(n^4)$ space. This concludes our expository example series, and we turn to the real world.

6. Practice of declarative programming with Bellman's GAP

Although the Bellman's GAP system has been released just recently [10], there is already a substantial amount of practical experience. Earlier applications developed with the ADP approach were transcribed into GAP-L. Firmly based on ADP theory, recoded grammars and algebras must produce identical results in both implementations. This has been a great testbed for GAP-C. The recoded tools now enjoy the improved efficiency achieved by GAP-C, and have smoothly replaced their earlier versions available for interactive and webservice use at `http://bibiserv.cebitec.uni-bielefeld.de` [1]

In this section, we report how grammars, algebras and products interplay in practice to solve bioinformatics problems in the area of RNA structure analysis.

RNA folding RNA is a chain molecule composed from nucleotides holding the bases A (Alanine) , C (Cytosine), G (Guanine), and U (Uracil). Folding back onto it self, base pairs (A-U), (C-G), and (G-U) making hydrogen bonds create secondary structure. An RNA sequence x has a large set $F(x)$ of possible foldings, its *folding space*. Individual structures are encoded by string representations as in

```
x = AUCGUCGCAAUUGCGUCCAACGCCUUAAUG
    ..((.((((....)))...((....))..))
```

where pairing base positions are indicated by matched parentheses, and dots denote unpaired bases. "Stacks" of successive base pairs give rigidity to the folding. This class of structures resembles our palindromes described by grammar *Pali5*, now taking base pairs for matching characters. A more refined grammar is required, though,

[1] The administration pages of the server collect information about the actual usage of these tools in the bioinformatics community.

because it must accommodate a sophisticated thermodynamic scoring scheme. Based on this thermodynamic model, a structure of minimal free energy (MFE) is computed via dynamic programming, and returned as the predicted structure by established bioinformatics tools such as *Mfold* and *RNAfold* [14, 24].

RNAshapes *RNAshapes* [12] provides a grammar $\mathcal{G}_{\text{MicroStates}}$ (describing $F(x)$) as well as algebras A_{MFE} (implementing the thermodynamic energy model), and $A_{\text{dot-backet}}$ (mapping candidates to their string representations). Hence,

$$\mathcal{G}_{\text{MicroStates}}(A_{\text{MFE}} * A_{\text{dot-backet}}, x)$$

performs "classical" structure prediction by free energy minimization, akin to the aforementioned tools. The unique feature of the program *RNAshapes* is shape abstraction: candidate structures in $F(x)$ are mapped to equivalence classes called shapes, characterized by their arrangement of stacks and unpaired regions, irrespective of their length. The abstract shape of the above example structure would be represented as:

```
[[][]]
```

Shape abstraction is implemented by an algebra A_{shape}, mapping candidates to their shape. The *interleaved product* is used to compute the k best structures of different shape by a call to

$$\mathcal{G}_{\text{MicroStates}}((A_{\text{shape}} \otimes A_{\text{MFE}(k)}) * A_{\text{dot-backet}}, x).$$

This is called *simple shape analysis*.

A second function of *RNAshapes* is to re-scale folding energies into Boltzmann probabilities, which are accumulated over all structures within the same shape. This calls for a simple transformation from the A_{MFE} algebra to A_{BWE}, which computes Boltzmann-weighted energies. It requires a much more refined grammar $\mathcal{G}_{\text{MacroStates}}$ in order not to overcount candidates in the folding space. $\mathcal{G}_{\text{MacroStates}}$ has 26 non-terminal symbols and 67 productions. Trees on the right hand side of some productions have a height > 1 (which is allowed by Eq. 5 but has not occurred in our simpler examples). A call to

$$\mathcal{G}_{\text{MacroStates}}(A_{\text{shape}} * (A_{\text{MFE}} \times A_{\text{BWE}}) * A_{\text{dot-backet}}), x),$$

making use of a cartesian as well as two lexicographic products, computes the probabilities of all shapes which x can fold into, together with the minimal-free-energy structure within each shape. (For backtracing the A_{BWE} values are actually disregarded by GAP-C.) This is called *complete probabilistic shape analysis*; it provides more comprehensive information than simple shape analysis, but is more expensive to compute.

pknotsRG and pKiss So-called pseudoknots in RNA are structures which break the nested (palindromic) pattern of base pairing. Two common classes of pseudoknots, called "H-type" and "kissing hairpin" are exemplified here using different types of matching parenthesis:

```
H-type        ..[[[...{{{....]]]..}}}..
kissing HP    ..[[[...{{{....]]].<<<..}}}...>>>...
```

Such structures, in general, are not context free, but relevant subclasses thereof can be cast into a grammar which leads to recurrences of runtime $O(n^4)$. The tool *pknotsRG* [18] implements RNA folding, allowing for H-type pseudoknots where energetically favourable, and has become a widely used tool for this purpose. Its recent extension *pKiss* also allows for the kissing hairpin motif [23]. Both programs use grammars which extend $\mathcal{G}_{\text{MicroStates}}$ by special productions for pseudoknots, using syntactic filters provided in GAP-L to deal with the non-context-free features. Algebras A_{MFE} and A_{BWE} are extended by energy rules for pseudoknotted structures. We found that biologists often request to find the best structure including a pseudoknot, even when it is not near the energetic minimum. This task is solved by providing a classification algebra A_{knot}, which maps candidate structures to the value set $\{nested, knot, kiss\}$, depending on their character, with $kiss$ dominating $knot$ and $knot$ dominating $nested$. A call to

$$\mathcal{G}_{\text{pKiss}}(A_{\text{knot}} * A_{\text{MFE}} * A_{\text{dot-backet}}, x)$$

returns the structure of minimal free energy of either type.

Rapidshapes: a generator of GAP-L programs The tool *RapidShapes* marks a different type of application. It *generates* RNA folding programs coded in GAP-L. Interesting shapes p are determined by stochastic sampling. *RapidShapes* then generates so-called shape matchers coded in GAP-L, compiles them on-the-fly with GAP-C, and executes them to compute the shape probability $Prob(p)$. This takes $O(n^3)$ runtime per shape p, while complete probabilistic shape analysis (cf. above) requires $O(\alpha^n \cdot n^3)$ for $\alpha \approx 1.13$. The automatically generated grammars have up to several hundred rules, while all share the A_{MFE}, A_{BWE} and $A_{\text{dot-backet}}$ algebras from *RNAshapes*. These large GAP-L programs are typically never seen by a human programmer, and it is essential that GAP-C completely automates table design for grammars of this origin and size.

Further tools to be converted On our present agenda, there are further tools to be converted to Bellman's GAP, along with implementing planned enhancements. One is the approach of [1] for the comparison of minisatellites, which are repetitive genomic regions used in population studies. This problem is methodically interesting as it combines single-track analysis (for the construction of duplication histories of individual minisatellites) with two-track analysis (for the alignment of two minisatellite sequences) in a single grammar. This algorithm was originally coded the hard way, since ADP implementations prior to Bellman's GAP did not support single- and multitrack combinations.

The second candidate for conversion is the tool *RNAhybrid* [19], which predicts hybridization sites between a (very short) microRNA and (much longer) protein-coding RNA molecules. Today, the regulatory role of these microRNAs is intensively studied because of its medical implications, and the tool *RNAhybrid* has become the busiest tool on our server. The microRNA target prediction task is a two-track problem, with a relatively small grammar akin to $\mathcal{G}_{\text{MicroStates}}$, but with a large number of options to be set by the tool user, since the precise mechanism of interaction between microRNA and target is different between e.g. animals and plants.

7. Conclusion

Declarative dynamic programming with Bellman's GAP suggests a diverse agenda of research topics, both on the theoretical and on the practical side. Let us mention a few of these.

Theoretical questions relate to *properties of algebra products*. Products are associative (modulo re-grouping of tuples), and generally not commutative. Some conditions are known when a product preserves Bellman's Principle, especially the frequent case of $A * B$, when both are optimizing algebras, or when A computes a classification attribute. More general results are lacking. Bellman's GAP clearly states that it is the programmers's responsibility to prove that Bellman's principle is actually satisfied by a product algebra – but our programmers, who no longer have to deal with the amalgamation of search space construction and optimization, tend to forget about this fundamental prerequisite of dynamic programming.

Several *efficiency improving transformations* are known, which can reduce the runtime complexity by an order of magnitude. In general, they require a joint transformation of grammar and algebra(s); the precise preconditions have not been formulated.

As defined by Equations 6 – 10, algebraic dynamic programming is restricted to sequence input, and to a recursive pattern which follows the subword structure of the input. There are other types of recursion in dynamic programming: information flow may go from the context of a subword to the inside. Recursion may be based not on the input data structure, but on the score values achieved by candidates, e.g. with knapsack-type problems. Furthermore, the input data structure may be trees rather than strings, as occurs in RNA structure comparison. Such extensions of the algebraic approach are yet to be studied.

On the practical side, we have started to recreate the *Infernal* tool [16] in Bellman's GAP. This software creates structure-based covariance models for families of RNA sequences, which are collected in the Rfam data base [6] and widely used in RNA gene finding. Making use of product algebras, we plan to explore different, novel semantics [13] that can be associated with stochastic grammars.

Finally, as algebraic dynamic programming has started to enter (bio)informatics curricula at other universities, we feel obliged to enhance our suite of educational materials[2], migrating our collection of educational examples to GAP-L. These examples include typical problems such as the edit distance problem on strings, in many variants, optimal matrix chain multiplication, El Mamun's caravan, and satisfiability, aside from classical bioinformatics problems. We hope to solicit further examples from the community.

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