

On Solving the Multiple Variable Gapped Longest Common Subsequence Problem

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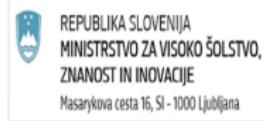
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Introduction

- Objects we deal with: sequences (strings) over finite alphabet Σ
 - DNA/RNA over {A, T, G, C/U}
 - Proteins over 20 (canonical) amino acids: {A, C, D, E, P, Q...}
- **One of central tasks in computational biology:**
 - sequence comparison, finding common motifs between sequences
 - compare structurally but also semantically/functionality
- **Subsequences:** reveal structural similarities → **Longest common subsequence problem** variants (studied 50 years already)

Longest common subsequence problem (LCSP)

Definition (LCSP)

Input: Given an arbitrary set of sequences $S = \{s_1, \dots, s_m\}$

Task: Find a subsequence s **common** for all sequences from S with maximum possible length ($|s|$).

Example

Input: $S = \{\text{AATTGC, ATTAC}\}$

LCS solution: $s = \text{ATTC}$

LCS: Literature & Problem Variants

- For $m = 2$, polynomially solvable: [Dynamic programming](#), Hunt-Szymanski, Hirschenberg, ...
- When m arbitrary large – \mathcal{NP} -hard:
 - approximation, meta-heuristic, but also exact approaches

Problem-related practical variants:

- repetition-free, filled LCS problem, ...
- **Gapped LCS problem**

The gapped LCS problem (Peng and Yang, 2012)

Definition (A gap sequence)

Given is a sequence s and an assigned function $G_s: \{1, \dots, |s|\} \mapsto \mathbb{N}$. A pair (s, G_s) is called a gap sequence.

Definition (A gapped subsequence)

Sequence \tilde{s} is a **gapped subsequence** of (s, G_s) iff

- \tilde{s} is a subsequence of s
- the gap constraint G_s fulfilled w.r.t. *positions of embedding* (letters of) \tilde{s} in s :
 - suppose $i_1 < \dots < i_{|\tilde{s}|}$ are those **positions**
 - $(\forall j = 2, \dots, |\tilde{s}|) i_j - i_{j-1} \leq G_s(i_j) + 1$ (consecutive positions respect gap distances)

Problem definition

Example

$s = \text{AATTGC}$, $G_s(\cdot) = 1$

- $\tilde{s} = \text{ATG}$, the embedding: AATTGC (**valid** gapped subsequence)
- $\tilde{s} = \text{ATG}$, the embedding: AATTGC (**invalid** gapped subsequence)

Definition (The multiple (variable) gapped LCS problem – MVGLCSP)

Input: Given is a set of gapped sequences $\{(s_1, G_{s_1}), \dots, (s_m, G_{s_m})\}$.

Task: Find the longest subsequence \tilde{s} so that

- \tilde{s} is common subsequence of each s_i ;
- \tilde{s} fulfills all gap constraints G_{s_i} ($i = 1, \dots, m$)

Note: when $G_{s_i} = n$ (the length of longest sequence) \Rightarrow VGLCSP = LCSP.

Literature & Motivation for VGLCSP

- Peng and Yang (2012, 2014): studied $m = 2$ version by **three dynamic programming** (DP) approaches (basic and two advanced)
- Manea et al. (2024): complexity analysis investigated
- **NP-hard** under arbitrary large m

Motivation:

- **Genetics and molecular biology**: DNA/protein comparison analysis where structural distances between residues must be respected
- **Time-series analysis**: in settings where events are required to occur within specified temporal delays (Lainscsek et al. (2015))

Methodology

- Based on the significant extension of the **state space graph formulation** for LCS problem (Djukanovic et al. (2020))
- **Gap constraints:** incorporated to cut-off invalid extensions (edges) among the LCS extensions immediately
- **Many root/source nodes** in the state graph (the position of leading letter in each common gapped subsequence free to select)

Root-based state graph formulation: rough idea

- Each **state** $v = (p^L, l^v)$: one or more feasible partial solutions where
 - a vector of positions p^L refer to the positions of suffixes of input sequences relevant to further expand these sols (subproblem)
 - the length of current partial solution l^v
- **Expansion** of v : extend (concatenate) partial solutions feasibly (and non-dominantly) by one letter in all possible ways, respecting gap constraints
- **Non-expandable nodes**: complete solutions;

Decision: select appropriate (matches) p^L for start (empty solution)

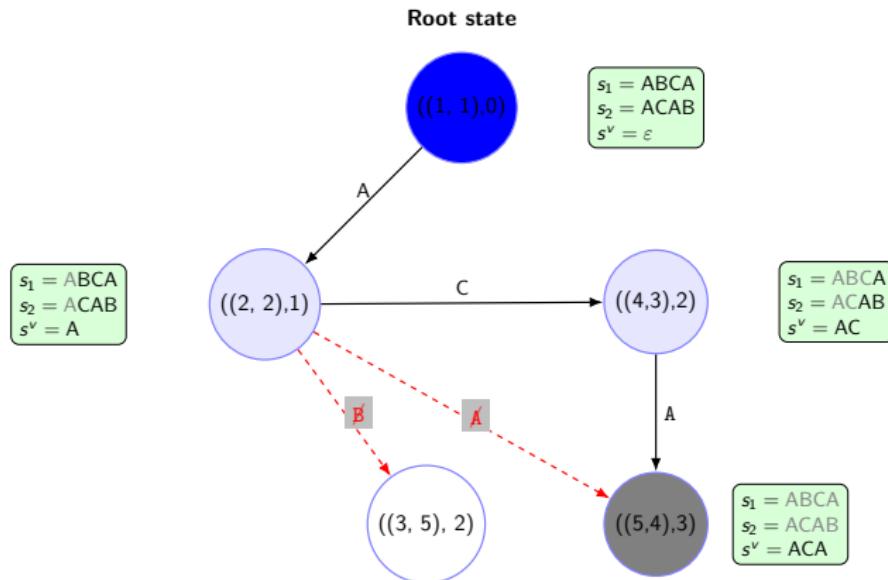
⇒ possibly (**exponentially**) many root nodes

$\text{Space}(p^L)$: root-based state (sub) graph induced by root node $(p^L, 0)$.

Root-based state graph formulation: example

Given $s_1 = \boxed{A}BCA$, $s_2 = \boxed{A}CAB$, assuming $G_1 = G_2 = 1$, match $p^L = (1, 1)$;

Space((1, 1)):

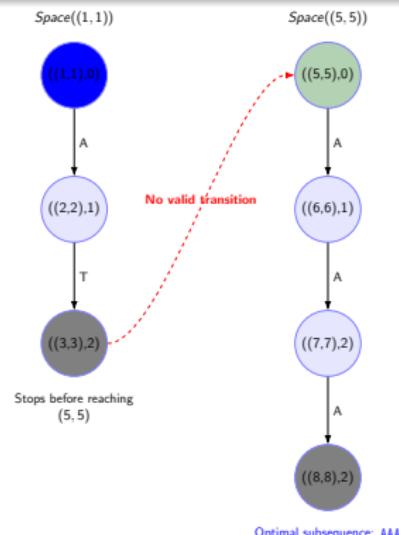


Space((1, 1)) \Rightarrow ACA

An issue with the root-state-space formulation: disconnected components

Example

$S = \{s_1 = \text{ATGG}[\text{A}]AA, s_2 = \text{ATCC}[\text{A}]AA\}$, with $G_{s_1} = G_{s_2} = 1$.



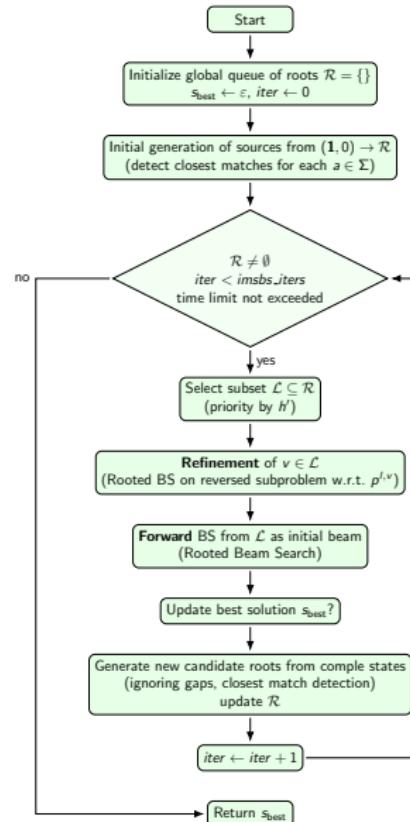
Observation: $((5, 5), *) \notin \text{Space}((1, *))$

On solving the VGLCSP

Iterative multi-source beam search (IMSBS) strategy

- Explicitly enumerating all root states computationally prohibitive ($O(n^m)$ time)
- **IMSBS** (rough idea of exploring space of root nodes):
 - ① **Exploitation** of $\text{Space}(p^L)$: given to **beam search** (BS) — limited breadth-first-search (BFS) strategy; parameter β controls the number of nodes at each level to be further pursued
 - ② **Exploration** of promising regions ($\text{Space}(p^L)$) of the state space
 - **Iteratively identify** a set of **promising** candidate root states during BS
 - allow some (non-) root node: effective *refinement* (find distant root predecessors to reach that node)

Workflow of the IMSBS



Heuristic guidances in BS

Three LCS heuristic guidances:

- ① UB₁: “Look-ahead” for the remaining sequence length
- ② UB₂: *Character Frequency Alignment* score
 - sum up the maximum possible occurrences of each letters in remaining subsequences
- ③ h_{prob} : *probability-based heuristic* guidance (matrices of probabilities (Mousavi and Tabataba, 2012))

Experimental Evaluation: arbitrary large m -case

- Bs: a baseline beam search, executes a **single iteration** of IMSBS (utilizing a huge β)
- IMSBS-GREEDY: fix **beam-width** $\beta = 1$ for the forward BS, perform a large number of IMSBS iterations
 - impact of iterations on the overall performance of IMSBS
- IMSBS: a **tuned version**; configured to use an average runtime comparable to that of Bs

Benchmark set RANDOM

For each combination of instance parameters

- $n \in \{50, 100, 200, 500\}$
- $m \in \{2, 3, 5, 10\}$
- $|\Sigma| \in \{2, 4\}$

10 random problem instances are generated (sequences uniformly at random).

Gap constraints generated from $G_s(\cdot) \in \mathcal{U}(\{[0.5 \cdot |\Sigma|], \dots, [1.5 \cdot |\Sigma|]\})$.

⇒ A total of **320 problem instances** is generated.

Parameter tuning of IMSBS

We fixed less sensible params (preliminary tests): beam width in backward BS, $|\mathcal{L}|$, h'

Tuned parameters:

- β (in BS-forward)
- Heuristic guidance in BS (forward)
 - $\{\text{UB}_1, \text{UB}_2, h_{prob}\}$

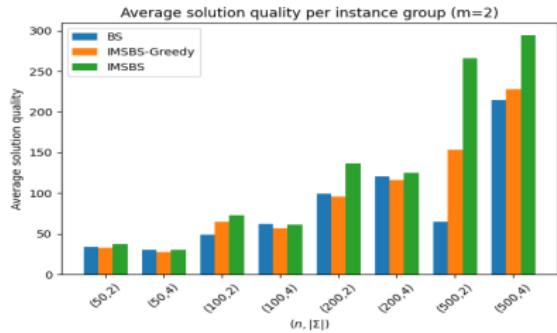
Grid search used for tuning; avg. solution quality over all (320) instances!

The results of tuning

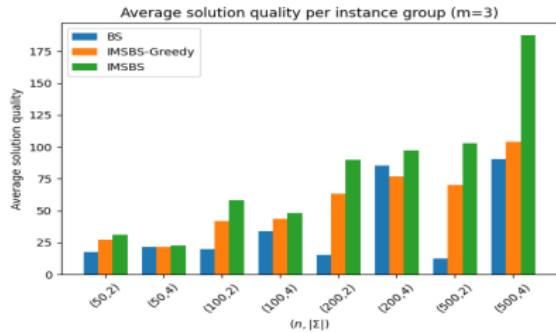
- **(Baseline)** Bs $\Rightarrow \beta = 10,000$ and $h = h_{\text{prob}}$
- IMSBS $\Rightarrow h = \text{UB}_2$, $\beta = 500$, and $\text{imsbs_iter} = 100$
- IMSBS-GREEDY: $\beta = 1$, $\text{imsbs_iter} = 10,000$

Numerical results

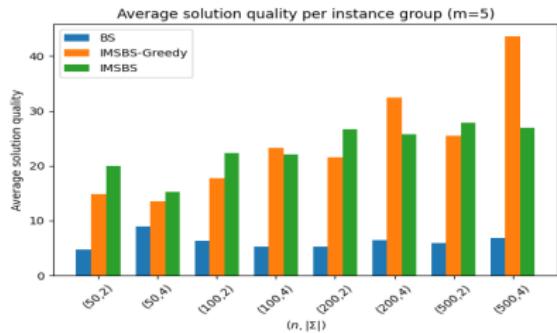
$m = 2$



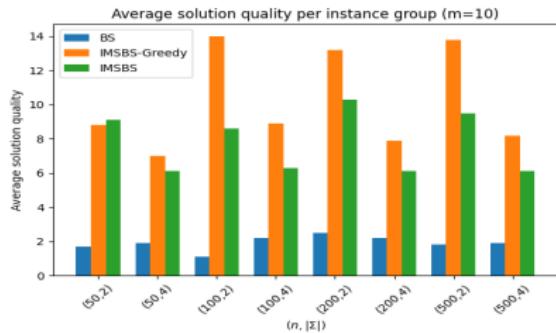
$m = 3$



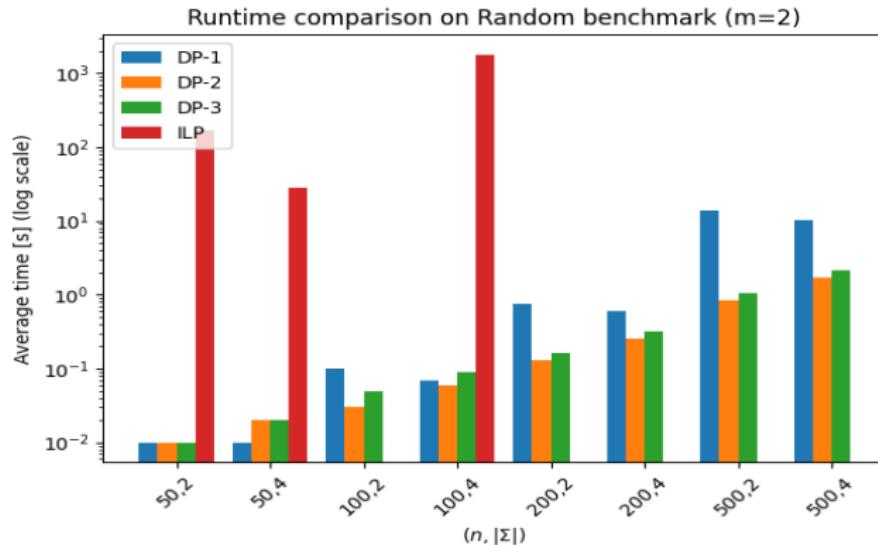
$m = 5$



$m = 10$

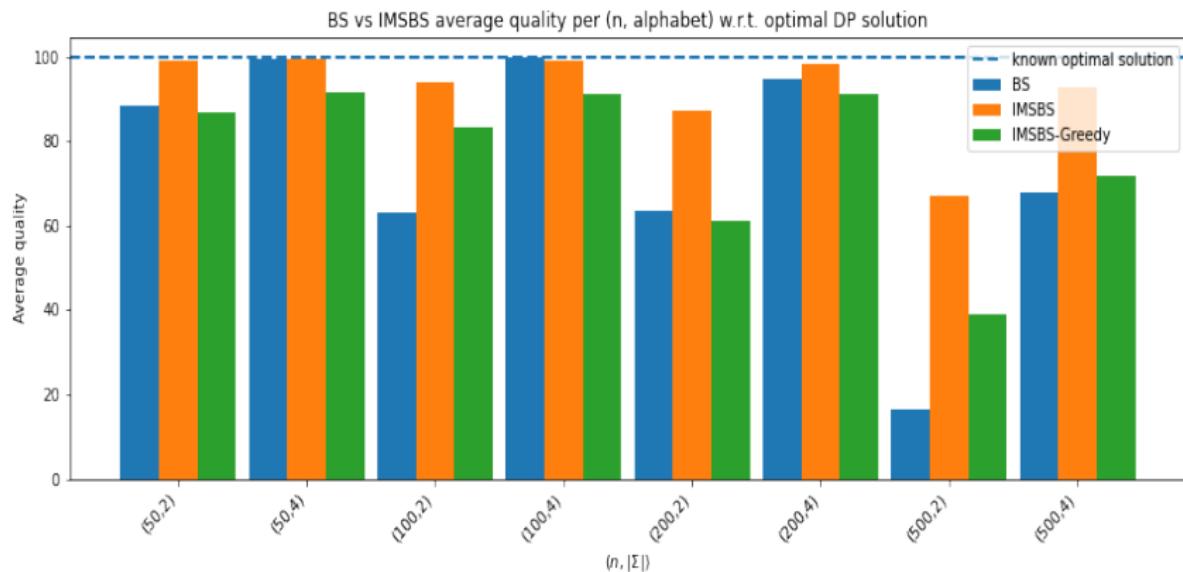


Numerical results for $m = 2$



- The first known empirical study for the $m = 2$ (80 instances)
- ILP: proposed in this work

The $m = 2$ case: heuristic performance vs. optimal solution



Relative solution quality achieved by the heuristic approaches compared to the optimal solutions (shown in %).

Conclusions and Future Work

- Proposed a **general heuristic framework** IMSBS to solve the multiple VGLCS problem
- Combines consecutive Beam search calls which induce refinement of sources, source node generation for further iterations
 - balance between intensification and diversification
- Empirical studies conducted for the first time on the **synthetic instances**: IMSBS outperforms the baseline Beam search

Future work:

- **Real-world** instance-case scenario
- Lack of more advanced heuristic guidance: **Data-driven/ML heuristic** involving various local and global features (NN-based)

Thank you for your attention!