

# On Solving the Multiple Variable Gapped Longest Common Subsequence Problem

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# Introduction

- Objects we deal with: sequences (strings) over finite alphabet  $\Sigma$ 
  - DNA/RNA over  $\{A, T, G, C/U\}$
  - Proteins over 20 (canonical) amino acids:  $\{A, C, D, E, P, Q, \dots\}$
- **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:  $S = \{\text{AATTGC}, \text{ATTAC}\}$

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

# LCS: Literature & Problem Variants

- For  $m = 2$ , polynomially solvable: **Dynamic programming**, Hunt-Szymanski, Hirschberg, ...
- 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 = allowed *num. letters inbetween*)

# 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)  $\Rightarrow \text{VGLCSP} = \text{LCSP}$ .

# 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))

- 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)**

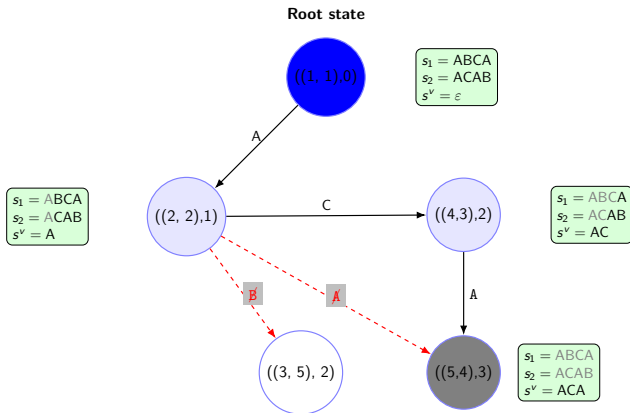
⇒ possibly (**exponentially**) many root nodes

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** $((1, 1))$ :

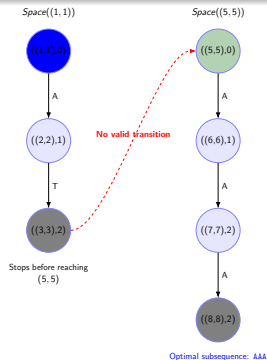


**Space** $((1, 1)) \Rightarrow ACA$

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

## Example

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

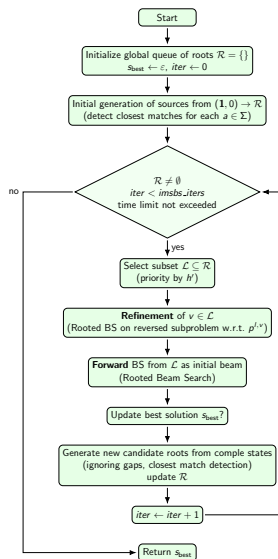


**Observation:**  $((5,5), *) \notin \text{Space}((1,1))$ , The optimal solution: AAA.

# 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  $\beta$  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 ancestors** to reach that node)

# Workflow of the IMSBS



# Heuristic guidances in BS

Three LCS heuristic guidances:

- 1  $UB_1$ : “Look-ahead” for the remaining sequence length
- 2  $UB_2$ : *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: general $m$ -case

- BS: a baseline beam search, executes a single iteration of IMSBS (utilizing a huge  $\beta$ )
- 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

The IMSBS framework implemented in **Python** 3.11.

# 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  $G_s(\cdot) \in \mathcal{U}(\{\lfloor 0.5 \cdot |\Sigma| \rfloor, \dots, \lfloor 1.5 \cdot |\Sigma| \rfloor\})$ .

$\implies$  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:

- $\beta$  (in BS-forward)
- Heuristic guidance in BS (forward)
  - $\{UB_1, UB_2, h_{prob}\}$

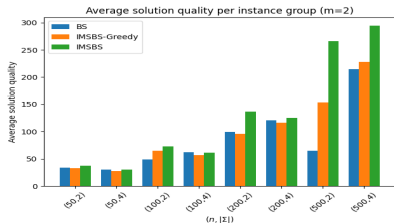
**Grid search used for tuning; avg. solution quality over all (320) instances!**

# The results of tuning

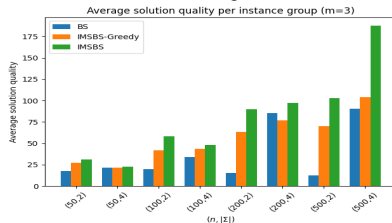
- **(Baseline)**  $B_S \implies \beta = 10,000$  and  $h = h_{\text{prob}}$
- $IMSBS \implies h = UB_2$ ,  $\beta = 500$ , and  $imsbs\_iter = 100$
- $IMSBS\text{-}GREEDY: \beta = 1$ ,  $imsbs\_iter = 10,000$

# Numerical results

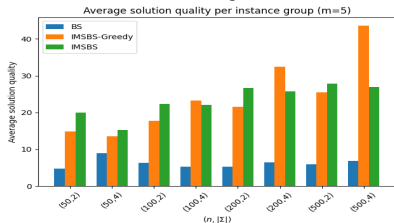
$m = 2$



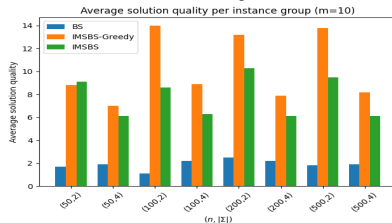
$m = 3$



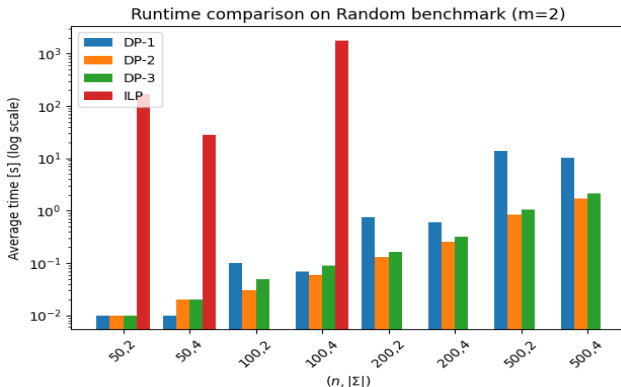
$m = 5$



$m = 10$

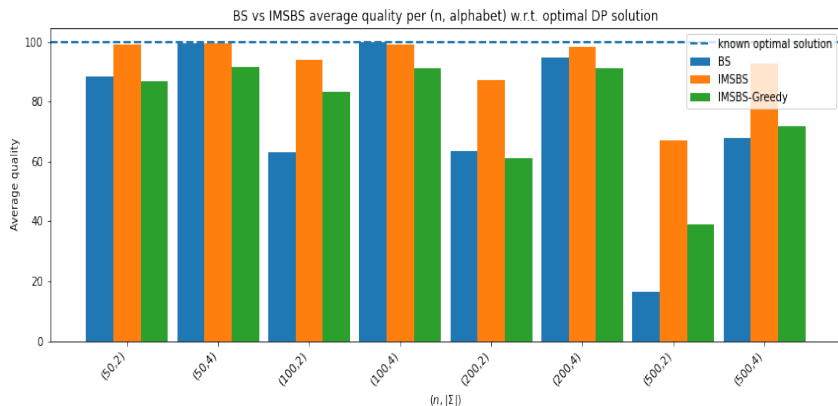


# Numerical results for $m = 2$



- 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!**