RISC-V ARCHITECTURE

UE21EC352A

UNDERSTANDING RISC-V ASSEMBLY: LONGEST COMMON SUBSEQUENCE

AKASH RAVI BHAT
PES1UG21EC025

The Longest Common Subsequence (LCS) problem has various real-life applications, and one notable example is in bioinformatics, particularly in the field of DNA sequence analysis.

1.DNA Sequence Alignment:

1. In bioinformatics, scientists often deal with the comparison of DNA sequences from different organisms or individuals. The LCS algorithm can be applied to find the longest common subsequence between two DNA sequences. This information is valuable for understanding genetic similarities and differences between species, studying evolutionary relationships, and identifying common genetic patterns.
2. For example, when comparing the DNA of two individuals or species, identifying the longest common subsequence helps highlight regions of similarity in their genetic makeup. This can be crucial for identifying shared genes, understanding evolutionary relationships, and studying the genetic basis of diseases.
3. LCS algorithms are employed in bioinformatics tools for sequence alignment, where the goal is to find the optimal alignment between two biological sequences, such as DNA or protein sequences. Identifying the longest common subsequence aids in understanding genetic variations, mutations, and functional similarities.

2.Version Control Systems:

In software engineering, version control systems (VCS) like Git use algorithms related to LCS to determine the differences between different versions of source code files. The LCS algorithm helps identify the longest common subsequence of lines or characters between two versions, and the differing elements are used to represent changes (additions, deletions, or modifications).

When you commit changes to a code repository, the version control system needs to efficiently identify the changes made compared to the previous version. LCS-based algorithms help in this process by identifying the common and differing parts of the code.

Efficiently computing the LCS is essential for minimizing storage space and optimizing the speed of operations in version control systems.

These applications highlight the versatility and significance of the Longest Common Subsequence problem in diverse fields, ranging from bioinformatics to software engineering. The problem-solving approach used in LCS algorithms has practical implications for solving complex sequence matching problems in various domains.

1. **Plagiarism Detection:**
    1. In the field of academic and content-related writing, plagiarism detection systems use LCS algorithms to identify similarities between documents. By finding the longest common subsequence between two pieces of text, these systems can highlight potential instances of plagiarism or content reuse.
2. **Speech Recognition:**
    1. In speech recognition systems, the LCS algorithm can be employed to compare spoken words or phrases. By finding the longest common subsequence, the system can identify similarities between the recognized speech and a reference vocabulary, aiding in accurate transcription.
3. **Image Comparison:**
    1. Image processing and computer vision applications use LCS techniques to compare images. The problem can be applied to find the longest common subsequence of pixel values between two images, helping to identify similarities and differences. This is useful in tasks like image recognition and content-based image retrieval.
4. **Network Traffic Analysis:**
    1. In cybersecurity, analyzing network traffic patterns is crucial for identifying potential security threats. The LCS algorithm can be used to compare sequences of network events or patterns, helping to detect anomalies, intrusions, or malicious activities.

1. **Recommender Systems:**
    1. In recommender systems for e-commerce or content platforms, LCS algorithms can be used to analyze user behavior sequences. By finding common subsequences of user interactions, these systems can recommend products or content based on users' historical preferences.
2. **Automatic Summarization:**
    1. In natural language processing and text summarization, the LCS problem can be utilized to identify common phrases or sentences in a set of documents. This can help in generating concise and meaningful summaries by selecting the most relevant content.
3. **Comparing Biological Sequences (Proteins):**
    1. In addition to DNA sequences, LCS algorithms are applied to compare protein sequences. Analyzing the longest common subsequence of amino acids in proteins is crucial for understanding protein structures, functions, and evolutionary relationships.
4. **Code Clone Detection:**
    1. In software engineering, code clone detection involves identifying duplicated or similar code segments in a software project. LCS algorithms can be used to compare code sequences and identify common structures, aiding in the detection of code clones.

There are three types of data hazards:

1. **Read-After-Write (RAW) Hazard:**
    1. Occurs when an instruction tries to read a register or memory location that has been written to by a previous instruction in the instruction pipeline.
    2. Also known as a true dependency or data dependence.
2. **Write-After-Read (WAR) Hazard:**
    1. Occurs when an instruction writes to a register or memory location that is later read by a subsequent instruction.
    2. Also known as an anti-dependency.
3. **Write-After-Write (WAW) Hazard:**
    1. Occurs when two instructions write to the same register or memory location in sequence.
    2. Also known as an output dependency.

These hazards can potentially lead to incorrect program behavior if not handled properly. To resolve RAW hazards, processors often use techniques such as instruction reordering, data forwarding (bypassing), or inserting pipeline stalls (NOP instructions) to ensure that the data dependencies are correctly satisfied. Data hazards are a crucial consideration in the design of pipelined processors to maintain program correctness and achieve optimal performance.

Load-Use (LU) Hazard:

1. Occurs when a load instruction is followed by an instruction that uses the data loaded by the load instruction.
2. The problem arises because the load instruction takes some time to fetch the data from memory, and the subsequent instruction might execute before the data is available.

To mitigate load hazards, processors employ techniques such as:

- **Forwarding (Bypassing):** Forwarding involves directly passing the result of a load operation to the subsequent instruction that needs it without waiting for the data to be stored in a register. This helps to eliminate the need to stall the pipeline and improves overall performance.
- **Pipeline Stalls (NOP Insertion):** In cases where forwarding is not possible or practical, the processor may insert no-operation (NOP) instructions into the pipeline to introduce delays, ensuring that the data is available when needed.

Load hazards are a critical consideration in designing efficient and high-performance pipelined processors. Efficient handling of load hazards contributes to maximizing instruction throughput and maintaining correct program execution.

SOURCE CODE:

```
.data
.align 4
# test pattern
SequenceA: .string "AKASHRAVIBHAT"
SequenceB: .string "AKASHRRGGUTT"
SASize: .word 13
SBSize: .word 12
str: .string "Found LCS length "
newline: .string "\n"
i: .word 0
j: .word 0
L: .word 1024
.text
.global _start
```

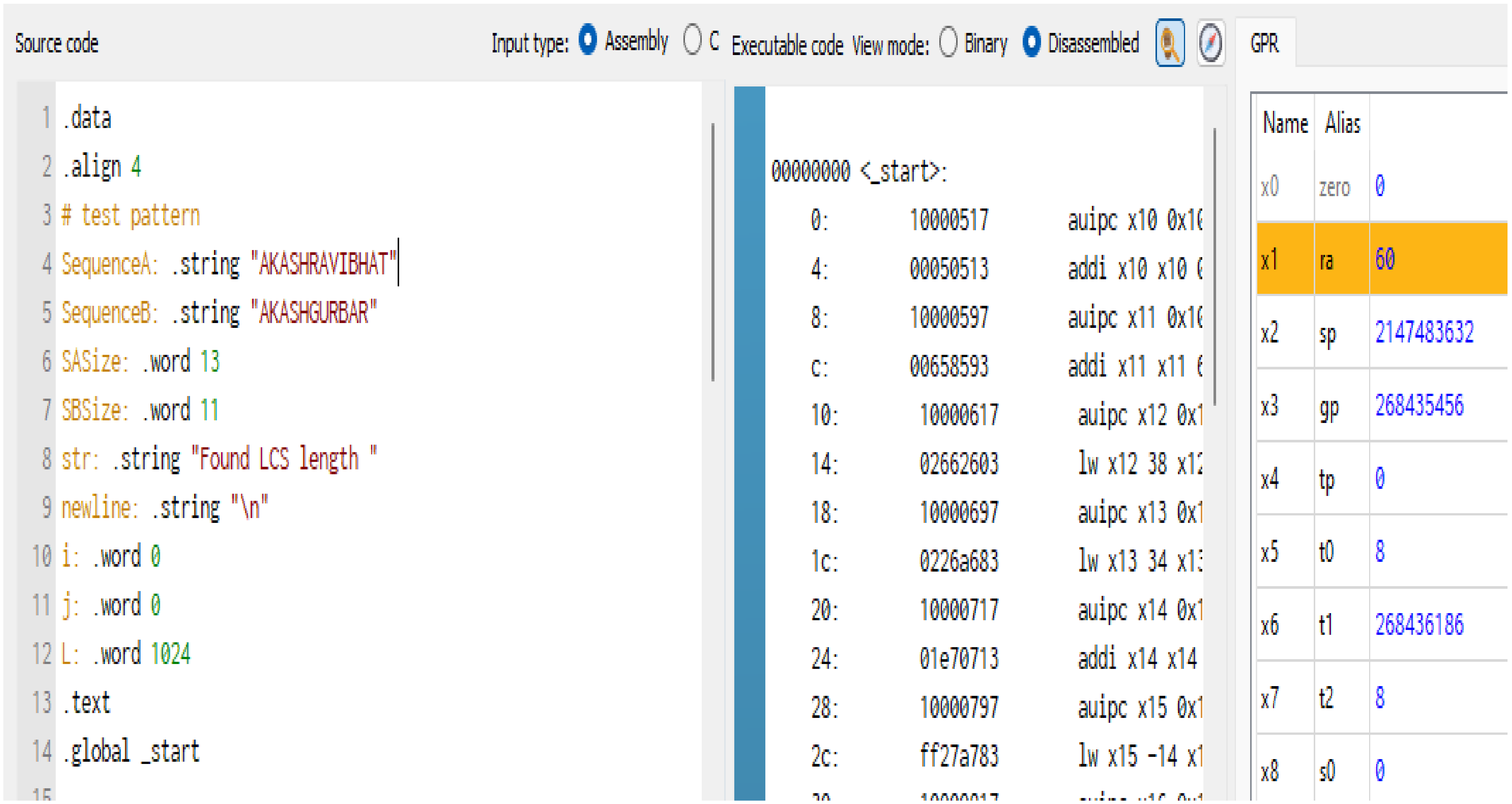
```
_start:
    la a0 SequenceA
    la a1  SequenceB
    lw a2 i
    lw a3 j
    la a4 L
    lw a5 SASize
    lw a6 SBSize
    jal lcs
    #print str
    la a0, str
    li a7, 4
    ecall
    #print a0
    mv a0 t0
    li a7 1
    ecall
    #print \n
    la a0, newline
    li a7, 4
    ecall
    j end
```

```
lcs:
    addi sp, sp, -4
    sw ra, 0(sp) # return address
    addi a2 a2 -1 #set i=-1 first
First_for:
    addi a2 a2 1 #i=i+1
    bgt a2 a5 exit
    addi a3 x0 0 #set j=0
Second_for:
    #jump to First_for if j > SBSize
    bgt a3 a6 First_for
    #jump to condition one if i=0 ||  j=0
    beq a2 zero condition1
    bne a3 zero condition2
condition1:
    addi t0 a6 1
    mul t0 t0 a2 #t0=(SBSize+1)*i
    add t1 t0 a3 #t1=(SBSize+1)*i+j
    slli t1 t1 2 #t1=((SBSize+1)*i+j)*4 RAW Hazard
    add t1 a4 t1 #t1=((SBSize+1)*i+j)*4+a4
    sw x0 0(t1) #L[i][j]=0
    addi a3 a3 1 #j=j+1
    beq x0 x0 Second_for
```

```
condition2:
    addi t2 a2 -1 #t2=i-1
    addi t3 a3 -1 #t3=j-1
    add t0 a0 t2 #t0=SequenceA+i-1
    add t1 a1 t3 #t1=SequenceB+j-1
    lb t0 0(t0) #t0=SequenceA[i-1]
    lb t1 0(t1) #t1=SequenceB[j-1]
    bne t0 t1 condition3

    addi t0 a6 1
    mul t0 t0 a2 #t0=(SBSize+1)*i
    add t1 t0 a3 #t1=(SBSize+1)*i+j
    slli t1 t1 2 #t1=((SBSize+1)*i+j)*4 RAW Hazard
    add t1 a4 t1 #t1=[(SBSize+1)*i+j]*4+a4

    addi t0 a6 1
    mul t2 t0 t2 #t2=(SBSize+1)*(i-1)
    add t3 t2 t3 #t3-[(SBSize+1)*(i-1)+(j-1)]
    slli t3 t3 2 #t3=[(SBSize+1)*(i-1)+(j-1)]*4  RAW Hazard
    add t3 a4 t3 #t3=[(SBSize+1)*(i-1)+(j-1)]*4+a4
    lw t3 0(t3) #t3=L[i-1][j-1]
    addi t3 t3 1 #t3=t3+1
    sw t3 0(t1) #L[i][j]=L[i-1][j-1]+1
```

```
 addi a3 a3 1 #j=j+1
   beq x0 x0 Second_for
condition3:
   addi t0 a6 1 #t0=(SBSize+1)
   mul t0 t0 a2 #t0=(SBSize+1)*i
   add t1 t0 a3 #t1=(SBsize+1)*i+j
   slli t1 t1  2 #t1=((SBSize+1)*i+j)*4 RAW Hazard
   mv t0 t1  #t0=((SBSize+1)*i+j)*4
   add t1  a4 t1  #t1=((SBSize+1)*i+j)*4+a4

   addi t2 a6 1 #t2=(SBSize+1)
   slli t2 t2 2 #t2=(SBSize+1)*4
   sub t2 t0 t2 #t2=[(SBSize+1)*(i-1)+j]*4  RAW Hazard
   add t2 a4 t2 #t2=[(SBSize+1)*(i-1)+j]*4+a4  WAW Hazard
   lw t2 0(t2) #t2=L[i-1][j]   LOAD Hazard

   addi t4 t0 -4 #t4=[(SBSize+1)*i+(j-1)]*4
   add t4 a4 t4 #t4=[(SBSize+1)*i+(j-1)]*4+a4  WAW Hazard
   lw t4 0(t4) #t4=L[i][j-1]   LOAD Hazard
   sub t5 t2 t4
   bge t5 zero index
   sw t4 0(t1) #L[i][j]=t2=L[i][j-1]
   beq x0 x0 exit_condition3
```

```
index:
    sw t2 0(t1) #L[i][j]=t2=L[i-1][j]
exit_condition3:
    addi a3 a3 1 #j=j+1
    beq x0 x0 Second_for
exit:
    addi a5 a5 1
    addi a6 a6 1
    mul t0 a5 a6 #t0=(SASize+1)*(SBSize+1)
    slli t0 t0 2 #t0=(SASize+1)*(SBSize+1)*4
    addi t0 t0 -4 #t0=(SASize+1)*(SBSize+1)*4-4 the last word
    add a4 a4 t0 #a4=a4+t0
    lw a0 0(a4) #a0=L[SASize][SBSize]
    lw   ra, 0(sp) # Reload return address from stack
    add t0 x0 a0
    addi sp, sp, 4 # Restore stack pointer
    jr x1

end:
     nop
```

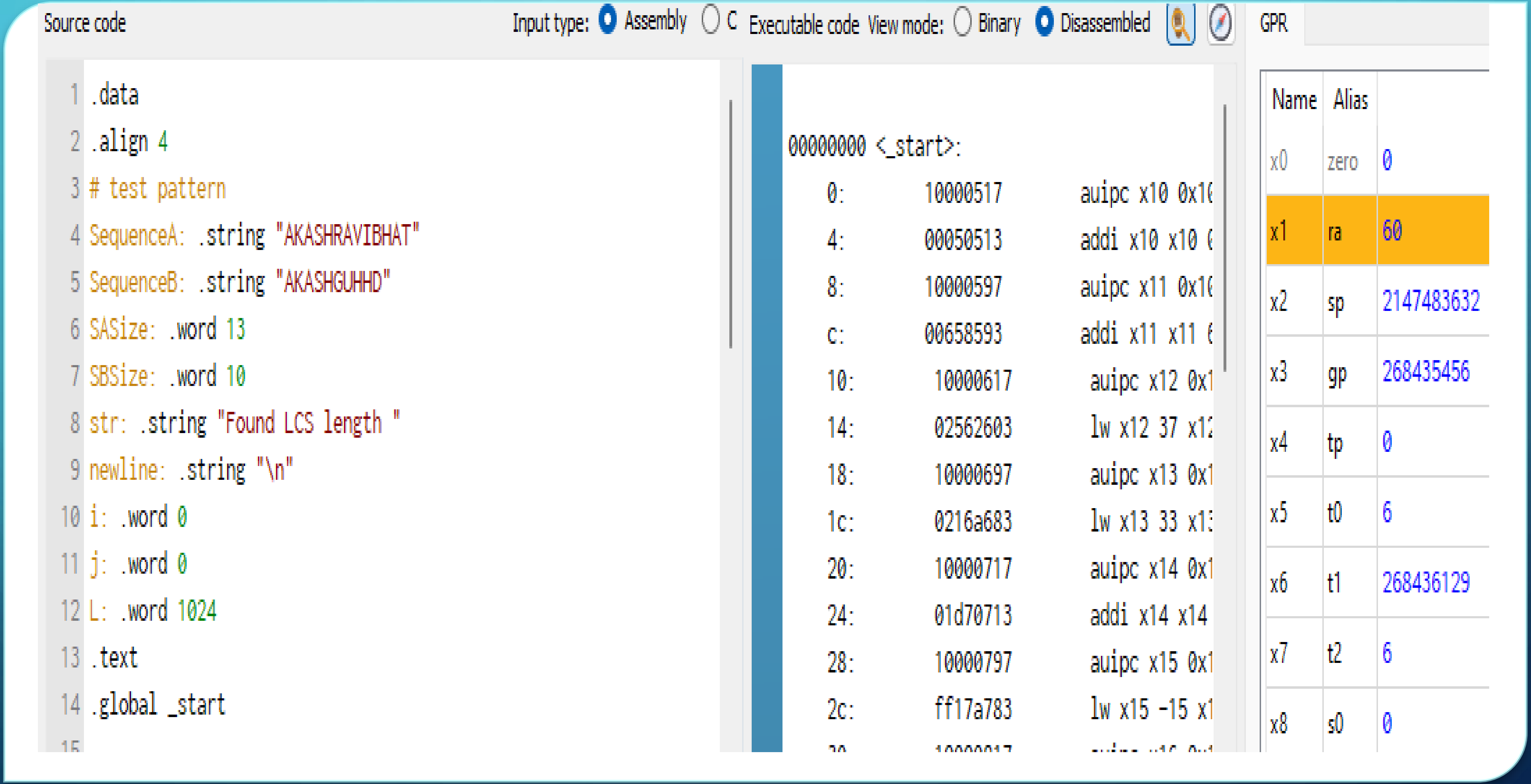


Input type: [✓ Assembly] C
View mode: Binary [✓ Disassembled]

```
.data
.align 4
# test pattern
SequenceA: .string "AKASHRAVIBHAT"
SequenceB: .string "AKASHGURBAR"
SASize: .word 13
SBSize: .word 11
str: .string "Found LCS length "
newline: .string "\n"
i: .word 0
j: .word 0
L: .word 1024
.text
.global _start
```

```
00000000 <_start>:
   0:      10000517      auipc x10 0x1
   4:      00050513      addi x10 x10 (
   8:      10000597      auipc x11 0x1
   c:      00658593      addi x11 x11 (
  10:      10000617      auipc x12 0x1
  14:      02662603      lw x12 38 x12
  18:      10000697      auipc x13 0x1
  1c:      0226a683      lw x13 34 x13
  20:      10000717      auipc x14 0x1
  24:      01e70713      addi x14 x14
  28:      10000797      auipc x15 0x1
  2c:      ff27a783      lw x15 -14 x1
  30:      10000817      auipc x16 0x1
```

Name	Alias	
x0	zero	0
x1	ra	60
x2	sp	2147483632
x3	gp	268435456
x4	tp	0
x5	t0	8
x6	t1	268436186
x7	t2	8
x8	s0	0



Source code

Input type: [✓ Assembly] C

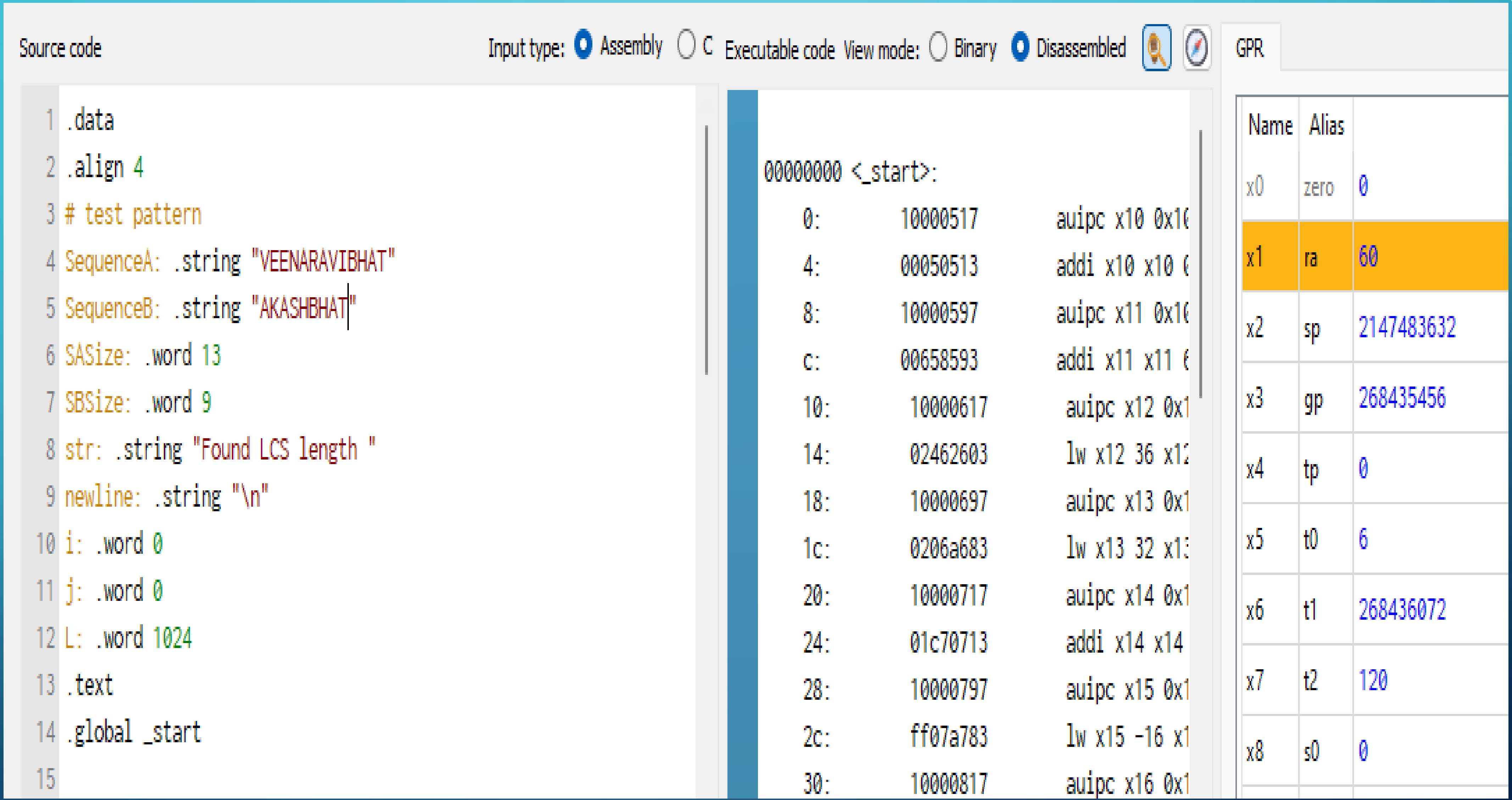
```
.data
.align 4
# test pattern
SequenceA: .string "AKASHRAVIBHAT"
SequenceB: .string "AKASHGUHHD"
SASize: .word 13
SBSize: .word 10
str: .string "Found LCS length "
newline: .string "\n"
i: .word 0
j: .word 0
L: .word 1024
.text
.global _start
```

Executable code View mode: Binary [✓ Disassembled]

```
00000000 <_start>:
    0:      10000517      auipc x10 0x1
    4:      00050513      addi x10 x10
    8:      10000597      auipc x11 0x1
    c:      00658593      addi x11 x11
   10:      10000617      auipc x12 0x1
   14:      02562603      lw x12 37 x1
   18:      10000697      auipc x13 0x1
   1c:      0216a683      lw x13 33 x1
   20:      10000717      auipc x14 0x1
   24:      01d70713      addi x14 x14
   28:      10000797      auipc x15 0x1
   2c:      ff17a783      lw x15 -15 x1
```

GPR

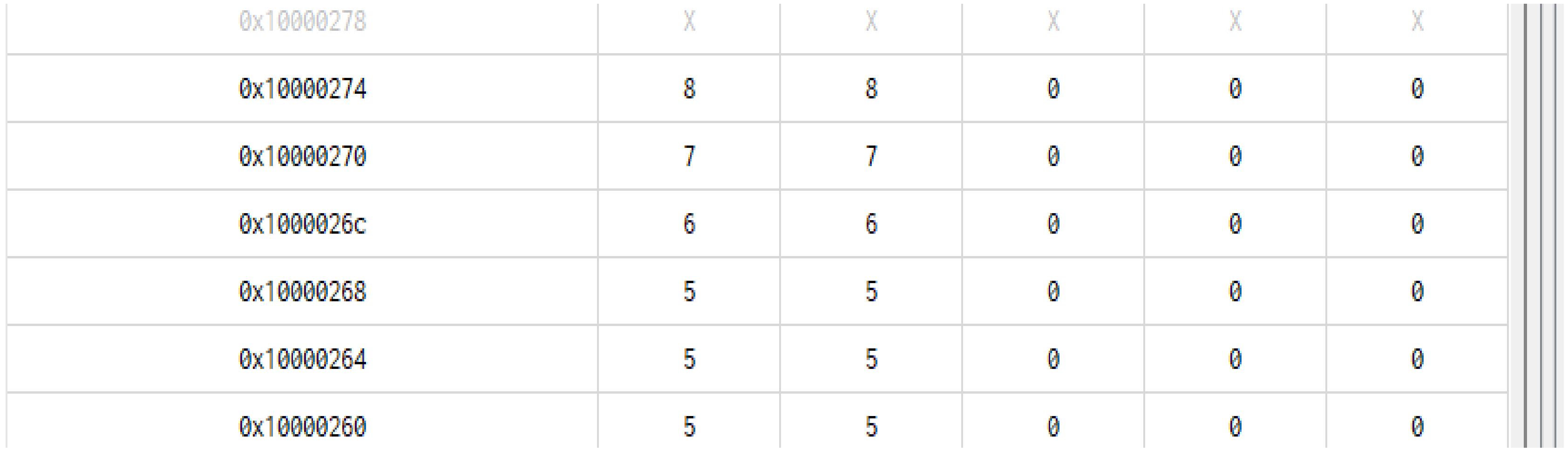
Name	Alias	
x0	zero	0
x1	ra	60
x2	sp	2147483632
x3	gp	268435456
x4	tp	0
x5	t0	6
x6	t1	268436129
x7	t2	6
x8	s0	0


Source code
Input type: [✓ Assembly] C
Executable code
View mode: Binary [✓ Disassembled]
GPR

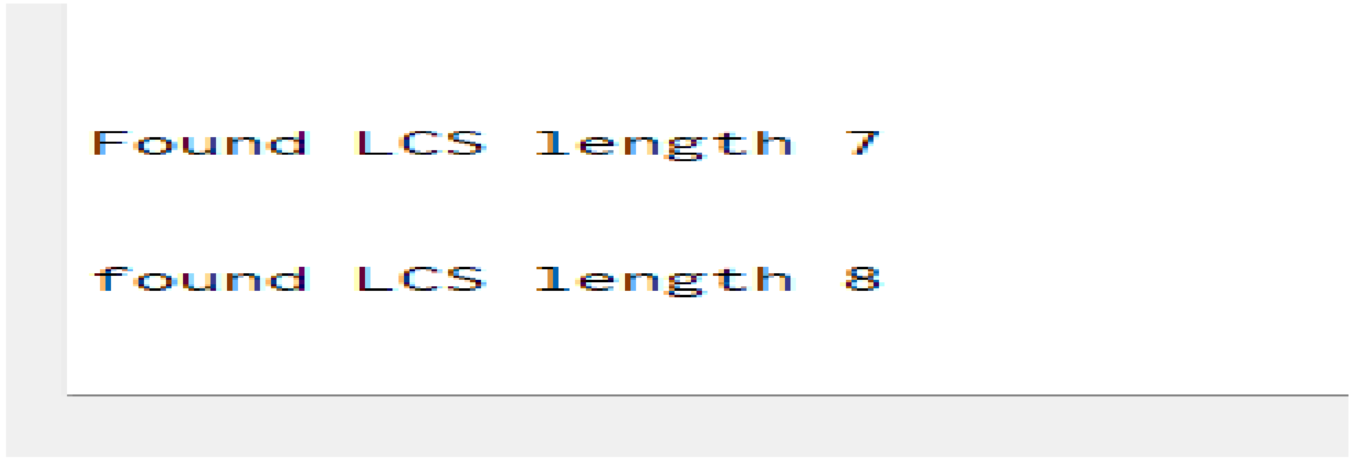
```
.data
.align 4
# test pattern
SequenceA: .string "VEENARAVIBHAT"
SequenceB: .string "AKASHBHAT"
SASize: .word 13
SBSize: .word 9
str: .string "Found LCS length "
newline: .string "\n"
i: .word 0
j: .word 0
L: .word 1024
.text
.global _start

```

```
00000000 <_start>:
    0:        10000517        auipc x10 0x1
    4:        00050513        addi x10 x10
    8:        10000597        auipc x11 0x1
    c:        00658593        addi x11 x11
   10:        10000617        auipc x12 0x1
   14:        02462603        lw x12 36 x12
   18:        10000697        auipc x13 0x1
   1c:        0206a683        lw x13 32 x1
   20:        10000717        auipc x14 0x1
   24:        01c70713        addi x14 x14
   28:        10000797        auipc x15 0x1
   2c:        ff07a783        lw x15 -16 x1
   30:        10000817        auipc x16 0x1
```

Name	Alias	
x0	zero	0
x1	ra	60
x2	sp	2147483632
x3	gp	268435456
x4	tp	0
x5	t0	6
x6	t1	268436072
x7	t2	120
x8	s0	0



0x10000278	X	X	X	X	X
0x10000274	8	8	0	0	0
0x10000270	7	7	0	0	0
0x1000026c	6	6	0	0	0
0x10000268	5	5	0	0	0
0x10000264	5	5	0	0	0
0x10000260	5	5	0	0	0



```
Found LCS length 7

found LCS length 8
```

REFERENCE:

1.Books:

1. "Introduction to Algorithms" by Thomas H. Cormen, Charles E. Leiserson, Ronald L. Rivest, and Clifford Stein.
2. "Assembly Language for x86 Processors" by Kip R. Irvine.

2.Online Documentation:

1. RISC-V ISA specifications: https://riscv.org/specifications/

3.Educational Platforms:

1. Online programming courses or platforms where assembly programming is taught, such as Coursera, edX, or others.

THANK YOU ALL!