BINARY-SEARCH(seq, low, high)

firstSeqPlace <- 0

seqLen <- length(seq)

lastSeqPlace <- seqLen - 1

if low >= high

while firstSeqPlace <= lastSeqPlace and True

middleValue <- seqLen // 2

if seq[middleValue] in range [low, high+1]

return True

else

if seq[middleValue] < low

return BINARY-SEARCH(seq[middleValue+1:], low, high)

else

return BINARY-SEARCH(seq[:middleValue], low, high)