LAB [5], [2/7/2019] MCS 253P

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General Problem Description

Optimal local align two DNA sequences. Input is two DNA sequence strings, and outputs the strings with dash "-" inserted where another nucleotide must be inserted to make them match.

Hint: use Smith-Waterman algorithm or Needleman-Wunsch algorithm.

e.g.,

Input

S1 = ACACACTA

S2 = AGCACACA

Output

S1 = A-CACACTA

S2 = AGCACAC-A

Input

S1 = A

S2 = B

Output

S1 = A

S2 = B

Additional Problem Specifics

- Define <u>substitution matrix</u> and the gap-scoring scheme, I'd better use as API function.
- How will the above parameters be set?
- negative scoring matrix cells are set to zero, for Optimal local align. I agree that in regions of low similarity between distantly related biological sequences, when mutations have added too much 'noise' over evolutionary time, it allows for a meaningful comparison of those regions.
- Traceback procedure starts at the highest scoring matrix cell and proceeds until a cell with score zero is encountered, yielding the highest scoring local alignment.
- Don't require of O(n) space complexity, which means I can first use a matrix for saving the middle results, which, of course, can be recorded to obtain O(n).
- When traceback, begin with the highest score, end when 0 is encountered; rather than begin with the cell at the lower right of the matrix, end at top left cell.
- The only max result;
- The only median value in traceback;
- The ending point is set to be 0, whether it is selected to be the upper, the left, the upper left, it doesn't matter in S-W since it will disregard the last letter.

Proposed Algorithm

#include <iostream>

#include <cstdio>

#include <math.h>

#include <vector>

#include <math.h>

```
using namespace std;
float SubstitutionMatrix(char a, char b ){
  float sub = (a==b)? +3: -3;
  return sub;
}
float Penalty(){
  float pnl = 2;
  return pnl;
bool isstart = false;
float MyMax3(float a, float b, float c){
  float tmp;
  tmp = max(a,b);
  return max(tmp, c);
}
float MyMax4(float a, float b, float c, int d){
  float tmp;
  tmp = MyMax3(a,b,c);
  return max<float>(tmp, d);
void prev(int& i, int& j, vector<vector<float>> H, string& out1, string& out2){
  float a = H[i-1][j-1];
  float b = H[i-1][j];
  float c = H[i][j-1];
  float maxprev = MyMax3(a,b,c);
  if (a == 0 || b == 0 || c == 0)
    isstart = true;
  else{
    if (maxprev == a){
      i = i-1;
       j = j-1;
    else if (maxprev == b){
       i = i-1;
      j = j;
       out2[j] = '-';
    else {
       i = i;
       j = j-1;
       out1[j] = '-';
  }
void BackTracePrint(vector<vector<float>> H, pair<int, int> maxlocation, string S1, string S2){
  int i = maxlocation.first;
  int j = maxlocation.second;
  string out1 = S1.substr(0,i+1);
  string out2 = S2.substr(0,j+1);
  while (isstart == false){
       prev(i,j,H,out1,out2);
  }
```

```
out1 = out1.substr(i, out1.size() - i);
  out2 = out2.substr(j, out2.size() - j);
  cout<<"S1 = "<<out1<<endl;
  cout<<"S2 = "<<out2<<endl;
}
void OptimalLocalAlign(string S1, string S2){
  int size1 = S1.size() + 1;
  int size2 = S2.size() + 1;
  vector<vector<float>> H(size1, vector<float>(size2));
  //initialize
  float maxscore = 0;
  pair<int, int> maxlocation;
  for (int i = 0; i < size1; i++){
    H[i][0] = 0;
  for (int j = 1; j < size 2; j++){
    H[0][j] = 0;
  for (int i = 1; i < size 1; i++){
    for (int j = 1; j < size2; j++){
       H[i][j] = MyMax4(H[i-1][j-1] + SubstitutionMatrix(S1[i],S2[j]),
                H[i][j-1] - Penalty(),
                H[i-1][j] - Penalty(),
                0);
       if (H[i][j] > maxscore){
         maxscore = H[i][j];
         maxlocation = make_pair(i,j);
    }
  }
  cout<<"maxscore: "<<maxscore<<endl;</pre>
  BackTracePrint(H, maxlocation, S1, S2);
}
int main(){
  //string S1 = "ACACACTA";
  //string S2 = "AGCACACA";
  string S1 = "GGTTGACTA";
  string S2 = "TGTTACGG";
  OptimalLocalAlign(S1, S2);
  return 0;
}
```