

Errata for:

(*RNA multiple structural alignment with longest common subsequences*)

1.

The *Maximum Loop Chain* problem (pp. 35-37) can be solved in $O(n^5)$ time. The 2-approximation in fact does not work as it uses a different definition of the original problem.

2.

The *LCSMNL* algorithm (pp. 39) in fact contains some error in the 'Compute D[.]' loop, but can be easily fixed as follows. The error is due to that L[.] and D[.] are computed separately. To fix it, simply do it like in LCSBM. The running time would be the same as before.

```
d=0
if (L[i,j,k,l]=L[i,j-1,k,l]) then
  d=max(d, D[i,j-1,k,l]);
if L[i,j,k,l]=L[i,j,k,l-1] then
  d=max(d, D[i,j,k,l-1]);
if ( $a_j = b_l$  and  $L[i,j,k,l]=L[i,j-1,k,l-1]+1$ ) then
  d=max(d, D[i,j-1,k,l-1]);
if ( $a_i = b_k$  and  $L[i,j,k,l]=L[i+1,j,k+1,l]+1$ ) then
  d=max(d, D[i+1,j,k+1,l]);
if ( $a_i = b_k$  and  $a_j = b_l$  and  $a_i$  matches  $a_j$  and  $L[i,j,k,l]=L[i+1,j-1,k+1,l-1]+2$ ) then
  d=max(d, D[i+1,j-1,k+1,l-1]+1);
D[i,j,k,l]=d;
```

The revised full version of the paper (containing more results and two extra authors) will be available soon.