作业2: 两序列比对

总分: 40

*此封面页请勿删除,删除后将无法上传至试卷库,添加菜单栏任意题型即可制作试卷。本提示将在上传时自动隐藏。

sequence x: GAATTCAGTTA

sequence y: GGATCGA

打分矩阵:

$$s(x_i, y_j) = \begin{cases} 2, & \text{if } x_i = y_j \\ -1, & \text{otherwise} \end{cases}$$

Gap penalty:

extension = opening=-2

请参考课件按照全局比对算法, (1)列出比对矩阵, (2)回溯路径, (3)以及比对后的结果。

2.Please find the best global alignment of following two sequences

- > AGTTGC
- > CAGA

Score matrix

	Α	Т	G	С
Α	2	1	-1	-1
Т	1	2	-1	-1
G	-1	-1	2	1
С	-1	-1	1	2

Gap penalty: open=extension=-2

请参考课件按照全局比对算法,

(1) 列出比对矩阵, (2) 回

溯路径, (3) 以及比对后的

结果

- 3. Please find the best global alignment of following two sequences
 - > AGTTGC
 - > CAGA

Score matrix

	А	Т	G	С
Α	2	1	-1	-1
Т	1	2	-1	-1
G	-1	-1	2	1
С	-1	-1	1	2

Gap penalty: open=-2, extension=-1

请参考课件按照全局比对算法,

(1) 列出比对矩阵, (2) 回

溯路径, (3) 以及比对后的

结果

4*. Write a program to align any two protein sequences with BLOSUM62 matrix, available at:

http://yanglab.nankai.edu.cn/teaching/bioinformatics/BLO SUM62.txt

gap opening=-11

gap extension=-1

To examine whether your program is correct, you can compare your result with the program at

http://zhanglab.ccmb.med.umich.edu/NW-align/