Group A: Random assignment at lecture

- Read sections 1 and 2 and especially section 2.5 *Inexact matching: bounded traversal/backtracking* in the paper
  
  Li, Durbin: *Fast and accurate short read alignment with Burrows–Wheeler transform*.  
  [http://dx.doi.org/10.1093/bioinformatics/btp324](http://dx.doi.org/10.1093/bioinformatics/btp324)

- At study group, discuss the inexact matching method based on the pseudocode in Fig. 3.  
  Hint: The four recursive calls to `InexRecur` correspond to insertion, deletion, substitution, and match.

Group B: Random assignment at lecture

- Read about *general gap penalty model* and *affine gap penalty model* on pages 42–45 of the book:
  
  Sung: *Algorithms in Bioinformatics: A Practical Introduction*.  
  CRC Press 2010.

Copies are distributed at the lecture.

Also watch the short lecture video by Nikolay Vyahhi covering the affine gap penalty:  
[https://youtu.be/Npv180dQ_4Y?list=PLQ-85lQI1PqFNmbPEsMoxb5dM5qtRaVShn](https://youtu.be/Npv180dQ_4Y?list=PLQ-85lQI1PqFNmbPEsMoxb5dM5qtRaVShn)

- At the study group, discuss the basic ideas of the method. How do the tables in the book excerpt correspond to the levels in the video?  
  What is the best global alignment of CGAGAT and CAT using the affine gap model? Use cost +4 for a match, -2 for mismatch, -3 for gap opening, -1 for gap extension. What is the score of the alignment?

Group C: Random assignment at lecture

- Read about *gene prediction by spliced alignment* on pages 203–207 of the book
  
  Jones & Pevner: *An Introduction to Bioinformatics Algorithms*.  

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- At the study group, discuss the basic ideas based on Figure 6.28, and the derivation of the recurrences. What is the running time of the algorithm?