

Algorithms for Bioinformatics (Autumn 2015)

Study Groups 5 (Tue 6.10. 12-14 B222)

Each student should belong to exactly one of the groups A, B and C. The groups are assigned at the lecture on Thu 1.10. If you were not present at the lecture, please contact the lecturer and ask for your group.

Group A: Random assignment at lecture

- Read the subsection titled *Epilogue: Synteny Block Construction* on pages 293–300 in the course book by Compeau & Pevzner.

Also watch the lecture video by Pavel Pevzner at

https://youtu.be/vTbQA8vV31Y?list=PLQ-851Q1PqF0cGz6A3g2ZArRL09Ffpp_N

- At the study group solve the “exercise break” problems and discuss the “STOP and Think” questions in the subsection. What can go wrong with a wrong choice of the parameters `maxDistance` and `minSize`?

Group B: Random assignment at lecture

- Read about an optimal algorithm for sorting by reversals, particularly Sections 4 and 5 in the following article:

Bader, Moret, Yan: **A Linear-Time Algorithm for Computing Inversion Distance between Signed Permutations with an Experimental Study.**

Journal of Computational Biology. October 2001, 8(5): 483-491.

<http://dx.doi.org/10.1089/106652701753216503>

- At study group, discuss the basic ideas of the method based on the Figs. 1 and 2.

Group C: Random assignment at lecture

- Read the section *Methods* in the following article:

Alekseyev & Pevzner: **Breakpoint graphs and ancestral genome reconstructions.**

Genome Research 2009, 19: 943-957.

<http://dx.doi.org/10.1101/gr.082784.108>

- At study group, discuss the basic ideas of the method based on Figure 3.