Try the following exercises from pages 139–140 of the Setubal-Meidanis book:

3, 6, 7, 12, 13, 18, 1

Answers: `http://www.liacs.nl/home/kosters/bio/`

Exercise 3 from Setubal-Meidanis, p. 139:

> What is the smallest value of ϵ such that the layout below is valid under the Reconstruction model?

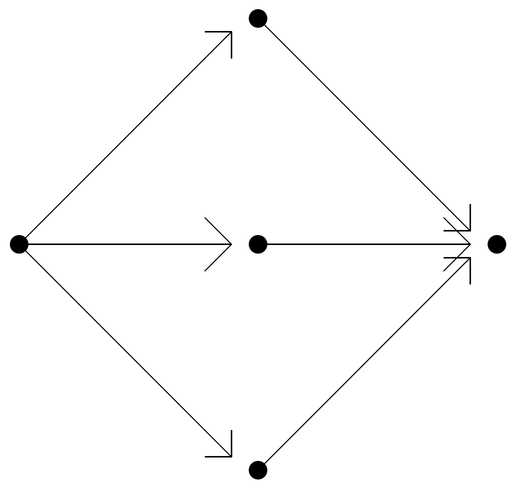
```
ACCGT       --ACCGT--
CGTGC       ----CGTGC
TTAC        TTAC-----
TGCCGT      -TGCCGT--
            _________
            TTACCGTGC
```

Exercise 6 from Setubal-Meidanis, p. 140:

> Construct the overlap graph for $\mathcal{F} = \{\mathtt{AAA}, \mathtt{TTA}, \mathtt{ATA}\}$. Find a shortest common superstring for this collection.

Exercise 7 from Setubal-Meidanis, p. 140:

> Find sequences that give rise to the following overlap graph, where only edges with positive weight are shown. The weights are yours to find/choose.



Exercise 12 from Setubal-Meidanis, p. 140:

> Let $\mathcal{F} = \{\mathtt{ATC}, \mathtt{TCG}, \mathtt{AACG}\}$. Find the best layout for this collection according to the Reconstruction model with $\epsilon = 0.1$ and $\epsilon = 0.25$. Be sure to consider reverse complements.

Exercise 13 from Setubal-Meidanis, p. 140:

> Let $\mathcal{F} = \{\mathtt{TCCCTACTT}, \mathtt{AATCCGGTT}, \mathtt{GACATCGGT}\}$. Find the best set of contigs for this collection according to the Multicontig model with $\epsilon = 0.3$ and $t = 5$. (No reverse complements.)

Exercise 18 from Setubal-Meidanis, p. 140:

> Find a polynomial time reduction of SCS to Reconstruction.

Or: transform a problem instance for the Shortest Common Superstring problem into a problem for the Reconstruction problem, in such a way that solutions "correspond" with each other.

Exercise 1 from Setubal-Meidanis, p. 139:

Suppose we have the following fragments:

$f_1 =$ ATCCGTTGAAGCCGCGGGC
$f_2 =$ TTAACTCGAGG
$f_3 =$ TTAAGTACTGCCCG
$f_4 =$ ATCTGTGTCGGG
$f_5 =$ CGACTCCCGACACA
$f_6 =$ CACAGATCCGTTGAAGCCGCGGG
$f_7 =$ CTCGAGTTAAGTA
$f_8 =$ CGCGGGCAGTACTT

And we know that the length of the target molecule is about 55. Assemble these fragments and obtain a consensus sequence. Think of reverse complements.