1. **Shortest common superstring and ATSP.**
   Solve the shortest common superstring problem on set $S = \{CTTA, TGAT, TACT, GATG\}$ by reducing the problem to asymmetric traveling salesman problem through the prefix graph and dummy vertex as described at the lecture.

2. **Shortest common superstring and minimum weight cycle cover.**
   Simulate the 4-approximation algorithm for shortest common superstring problem on the same set $S$ as above. Visualize also the minimum weight perfect matching corresponding to the minimum weight cycle cover. What is the real approximation factor achieved on this instance?

3. **Graph editing.**
   Eulerian path in a graph is a path that visits all edges exactly once. Insert and delete minimum number of edges to/from the graph below so that it has an Eulerian path.

4. **Sequencing by hybridization.**
   A measurement from a hybridization experiment estimates that the 3-mer spectrum of $s$ would be $\text{Spectrum}(s, 3) = \{GAG, GAT, TAG, ATA, ATA, AGA, TAC\}$. Construct $s$ by the Eulerian path approach described at the course, taking into account that there might be one $\ell$-mer missing from the measured spectrum. **Hint:** Note that because the spectrum contains twice the 3-mer $\text{ATA}$, the graph should have two edges from $\text{AT}$ to $\text{TA}$.

5. **Preprocessing for gene rearrangement study.**
   Consider you have the genome sequences of two species A and B and you would like to study their rearrangement distance. Each gene in A may have several putative homologs with different local alignment score in B, and vice versa. How would you find a one-to-one mapping between all genes in A to genes in B so that the sum of the corresponding local alignment scores is maximized? Here we may assume that A has at most as many genes as B (otherwise their role can be switched). **Hint:** Reduce to a graph problem and add some dummy nodes/edges.