(1) Write a short essay (≤ one page) about the software **PHYLIP**. Who developed **PHYLIP** and why? What does it do and who uses it? Illustrate the use of **PHYLIP** for one example chosen by you.

(2) Consider the following two DNA sequences of length ten:

\[ \sigma^1 = \text{ACGGCTTAGG} \quad \text{and} \quad \sigma^2 = \text{CGACTCTATG}. \]

How many alignments do these two sequences have? Find all alignments of these two sequences that maximize the number of matches.

(3) The sequences in Problem (2) define a polynomial \( f_{\sigma^1, \sigma^2} \) as in equation (2.15) on page 56. Let \( h_{\sigma^1, \sigma^2} \) be the polynomial in three unknowns \( m, x, s \) which is obtained from \( f_{\sigma^1, \sigma^2} \) by specializing \( \theta_{uu} = m, \theta_{uv} = x, \theta_{u-} = \theta_{-u} = s \) for any two distinct nucleotides \( u, v \), and \( \theta'_{kl} = 1 \) for any \( k, j \in \{ H, I, D \} \). Compute the Newton polytope of \( h_{\sigma^1, \sigma^2} \).

(4) Explain the meaning of Figure 7.3 on page 204 in your own words.

(5) Let \( n = 6 \) and determine the metric \( d \) which gives the pairwise distances (in miles) among the six cities Atlanta, Chicago, Houston, Miami, New York and San Francisco. Build a phylogenetic tree on these “taxa” from the data \( d \) by applying the Neighbor-Joining Algorithm (pages 73/74).

(6) The following \( 5 \times 5 \)-matrix \( D \) has two unknown parameters \( x \) and \( y \):

\[
D = \begin{pmatrix}
0 & 4 & 10 & 8 & 7 \\
4 & 0 & 12 & 10 & 9 \\
10 & 12 & 0 & x & 7 \\
8 & 10 & x & 0 & y \\
7 & 9 & 7 & y & 0
\end{pmatrix}
\]

Draw the set of all points \((x, y)\) in the plane such that \( D \) is a metric. In your diagram, mark all points \((x, y)\) such that \( D \) is a tree metric.