# Biopython Workshop

1. Work with DNA sequences:
    - Sequence: AGTCCCAAGAgTGATG
    - Reverse complement the sequence
    - Transcribe and translate the sequence
    - Define your own stop codon
2. Reading FASTA-files:
    - Read file „e_coli_plasmid_p12579.txt“ as fasta file
    - Use the SeqIO for parsing the contents of the file
    - Which information are accessible?
3. Plot the length of the gene sequences from a FASTA-file using pylab
4. Plot the GC content of the gene sequences from a FASTA-file
5. BLAST over the internet
    - BLAST a nucleotide sequence using Bio.Blast
    - Save BLAST result in a xml-file
    - Access the results using NCBIXML
    - Print alignments
    - Which different species were found?
    - BLAST a short and a long DNA sequence, compare the time needed for BLAST
6. Optional: Take a known sequence and create two primers (use a non conserved sequence!). BLAST the primers separated and analyse the result:
    i. Identify the same records
    ii. How many products would result during the PCR? (consider DNA strand!)
    iii. How many different species would be detected during the PCR? Would there be some false positive results?