Project 2

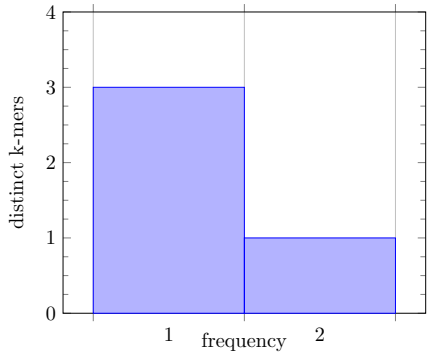
Deadline: Friday, 8 April 2022

Background information

In this project you will work with DNA sequences. Some definitions:

- A DNA sequence S of length n is an n-letter string made up of the letters `"A"`, `"C"`, `"G"`, `"T"`, representing a sequence of nucleotides.
- A k-mer K within S is a k-letter substring of S, i.e. a sequence of k consecutive nucleotides in S.
- The frequency of a k-mer K within S is the number of times the substring K can be found in S.
- A k-mer spectrum is a graphical representation of a DNA sequence S in the form of a histogram, showing how many unique k-mers appear a certain number of times in S. The frequency of occurrence is plotted on the x-axis and the number of unique k-mers with that frequency on the y-axis.

For example, the DNA sequence `"AACGACG"` contains the four unique 3-mers `"AAC"`, `"ACG"`, `"CGA"` and `"GAC"`, with all 3-mers appearing once, apart from `"ACG"`, which appears twice. Hence in this trivial example, the histogram representing the 3-mer spectrum would look like shown on the right.



Throughout this project you may assume that $n \leq 10^8$ and $k \leq 10^2$.

Task 1

Write a Python function that, given a DNA sequence S of length n and the number $k < n$ computes some characteristics of S, including the histogram data needed to produce the k-mer spectrum for S.
In particular:

- Your function should be defined as `kmer_hist(S, k)` and return two lists: `h, mfkmers`.
- The list `h` should contain at position ℓ the number of unique k-mers in S with frequency ℓ in S. The final entry in `h` should correspond to the frequency of the most frequent k-mer(s) in S.
- The list `mfkmers` should contain the most frequent k-mers in S. Hence every element of `mfkmers` should have frequency equal to `len(h)-1` in S. (Note that the length of `mfkmers` will often by 1.)

Your function `kmer_hist` may use all available standard types and methods in Python 3, but must work without importing any packages or modules. In particular, your function *should not* produce any graphical plots.

Together with your code you should submit a report with a very short description of your algorithm and an analysis of your algorithm's asymptotic complexity. Here you may for simplicity assume that *any* reading or writing access to a `dict`ionary in Python is $\mathcal{O}(k)$, when the key is a string of length k.

Task 2

Use your function `kmer_hist` from the previous task to compute and visualize some k-spectra for real-life DNA sequencing data. To this end, download the publicly available DNA sequencing data in FASTA format for

(a) the Escherichia coli bacteria:
`https://www.ncbi.nlm.nih.gov/nuccore/U00096.3?report=fasta`

(b) the human chromosome 21:
`https://www.ncbi.nlm.nih.gov/nuccore/CM000683.2?report=fasta`

You can find more details on the FASTA data format, and on the used notation at the links

- `https://en.wikipedia.org/wiki/FASTA_format`
- `https://en.wikipedia.org/wiki/Nucleic_acid_notation`

Note that before passing the data to your function `kmer_hist`, it needs to be "cleaned". For example, the FASTA data may contain comments, i.e. lines starting with the character `">"`, and the sequencing data may contain letters other than `"A"`, `"C"`, `"G"`, `"T"`. For the purpose of this task, you should remove any such letters before your analysis.
In your report, include the k-mer spectrum for the above e-coli and human chromosome 21 genomes for $k = 8$. In addition, for $k = 3, 8, 15, 25, 35$, report in a table on the most frequent k-mers in the two sets of sequencing data, stating their frequency and the k-mers themselves.

Task 3

Write a Python function that, given a DNA sequence S of length n and a list of k-mers L of length m, with $k < n$, finds the most frequent k-mer from the list L in S. You may assume that $m \leq 10^2$.
In particular:

- Your function should be defined as `kmer_search(S, L)` and return two integers: `pos, freq`.
- `pos` should be the first location in S of the most frequent k-mer listed in L. If there is more than one k-mer with the highest frequency, `pos` should refer to the k-mer that appears first (left-most) in S.
- `freq` should be the number of times that `S[pos:pos+k]` appears within S.
- If none of the k-mers listed in L can be found in S, simply return `None, 0`.

Your function `kmer_search` may use almost all available standard types and methods in Python 3, and must work without importing any packages or modules. However, in contrast to Task 1, your implementation should **not** use the Python types `dict`, `set`, or the Python function `hash()`.
Similarly to Task 1, in your report include a concise description of your algorithm and an analysis of your algorithm's asymptotic complexity.

Submission via Moodle

Prepare a single Python source file called `project2.py` that contains your functions `kmer_hist` and `kmer_search`, together with any routines or classes that you have written and that your functions depend on, but nothing else. Importing your source code via `import project2` should **not** execute any code. The docstring of the file `project2.py` must contain your full name. In addition, prepare a report in PDF format, called `project2.pdf`, that includes your answers for Tasks 1, 2 and 3.