Grundlagen der Bioinformatik
Assignment 2: Substring Search

SS 2016

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Vorstellung Lösungen Übung 1

Aufgetretene Probleme

- Sourcecode nicht mit abgegeben
- Verschicken der .jars
- Betreff in Mail: „[GdBioinfo] Abgabe Uebung X, Gruppe Y“

Assignment 2
Substring Search

Overview – Assignment 2 (20P)

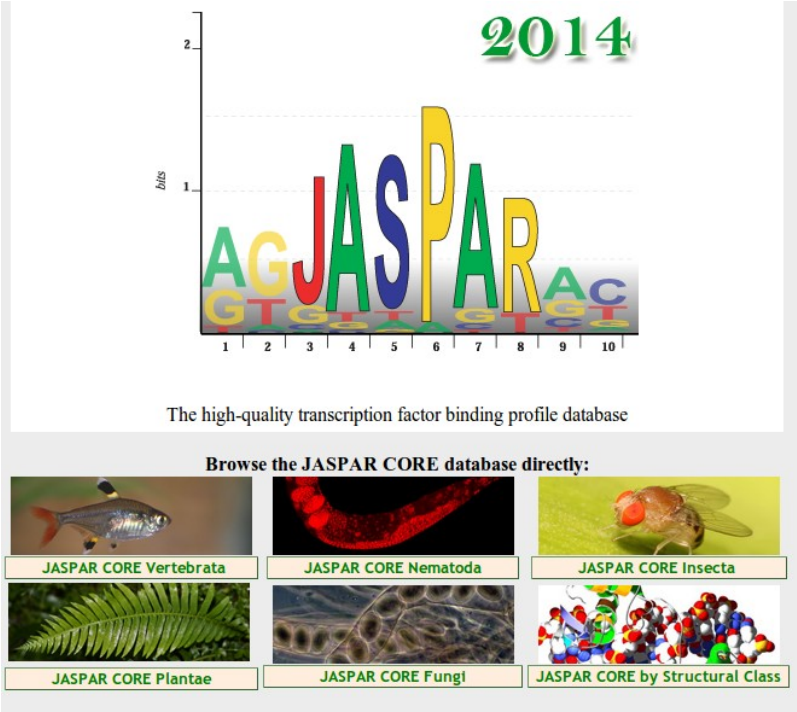
(1) Analyse transcription factor *GATA2* (4P)

(2) Substring search (10P)

(3) Properties of Boyer Moore Algorithm (6P)

(1) Transcription Factor *GATA2* (4P)

- *GATA2* is a transcription factor with established or assumed roles in a variety of different human cancers
- Seach *GATA2* in the JASPAR database



- JASPAR contains a set of transcription factor DNA-binding preferences, modeled as matrices
- Profiles derived from published collections of TF-binding sites
- Profile can be used to scan query sequences for presence of potential binding sites

(1) Transcription factor *GATA2* (4P)

- Search human *GATA2* in the JASPAR database
- Compute the information content of each position in the position specific weight matrix (PSWM, aka frequency matrix)
    - Find the exact formula on the web

- Submit
  - URL to the JASPAR information on *GATA2* (version .1, length 5)
  - Formula for information content used in sequence logos (1P)
  - Frequency matrix and IC of every position of the PSWM (2P)
    - Indicate process of calculation for at least one position
  - List of cancer types to which *GATA2* is associated and supporting papers from PubMed (1P)
  - http://www.ncbi.nlm.nih.gov/pubmed/
    - Useful databases: Uniprot (http://www.uniprot.org), OMIM (http://www.ncbi.nlm.nih.gov/omim/), NCBI (http://www.ncbi.nlm.nih.gov)

(2) Substring Search (10P)

(a) Load a template string (~60MB) into main memory (3P)
- File: sequence.fasta
- Don't use the concatenation parameter +

(b) Load a set of patterns (0P)
- File: patterns.fasta

(c) Search all exact occurrences of all patterns in the template and print first ten positions to STDOUT (7P)

(2.a) Load a sequence (3P)

- You need to load sequences in FASTA Format
  - „A sequence in FASTA format begins with a single-line description, followed by lines of sequence data. The description line is distinguished from the sequence by a greater-than symbol („>“) in the first column. … The sequence ends if another line starting with a „>“ appears; this indicatesthe start of another sequence“
  - Example:

```
> gi|5524211|gb|AAD44166.1| cytochrome b
LCLYTHIGRNIYYGSYLYSETWNTGIMLLLITMATAFMGYVLPWGQMS
EWIWGGFSVDKATLNRFFAFHFILPFTMVALAGVHLTFLHETGSNNPL
LLLLLALLSPDMLGDPDNHMPADPLNTPLHIKPEWYFLFAYAILRSVP
GLMPFLHTSKHRSMMLRPLSQALFWTLTMDLLTLTWIGSQP
>gi|5454351|gb| cytochrome x
LLLITMATAFMGYVLPWGQMSLCLYTHIGRNIYYGSYLYSETWNTGIM
LLLITMATAFMGYVLPWGQMS
```

  - File: sequence.fasta

(2.b) Load a Set of Patterns (0P)

- You will get another file which contains a set of sequences in FASTA format. These should be used as patterns.
- File: pattern.fasta
- Format as on previous slide

(2.c) Substring Search

- Implement an algorithm of your choice to search all occurrences of all patterns in the template

- Methods indexOf(„AT“), equals(„AT“), etc. are not accepted
  - Use charAt() (to access a string like an array)

- Submit:
  - A Java Archive including class files and source code
  - Commandline:

```
java -jar Assignment2_GrXY.jar pattern.fasta sequence.fasta
```

  - Print pattern, number of occurrences and first ten positions to STDOUT:

```
tccgga: 2506
[29562, 30667, 134810, 244142, 276754, 315062, 318466, 330540,
344995, 347336]
gctacc: 6799
...
```

  - Runtime of the algorithm and a sentence on the implementation (naive, Boyer Moore, ...)

For Orientation

Number of occurrences:

- tccgga: 2506
- gctacc: 6799
- taataa: 28279
- cctcagc: 17520
- cctgcagg: 2425
- ggcgcgcc: 141
- ccccccccccc: 140
- aaaaaaaaaaa: 52695
- aaaaaaaaaaaa: 44140
- aaaaaaaaaaaaaaa: 25063
- aaaaaaaaaaaaaaaaaaaa: 8571

(3) Properties of the Boyer Moore Algorithm (6P)

- Give a template and a pattern such that the BM algorithm, as presented in the lecture, needs to calculate in the order of |T| * |P| caracter comparisons and explain why (3P)

- Many implementations of the BM algorithm actually drop the good suffix rule, especially for larger alphabets. Give an argument why and when this can be useful (3P)

Abgabe

- Abgabe bis Mittwoch den 11.05.2016 um 23:59 Uhr

- Abgabe per Email an: yvonne.lichtblau@informatik.hu-berlin.de
  (gerne auch Fragen zur Übung per Email)
  - PDF mit Antworten zu 1, 2 und 3
  - Code als Jar Datei wie beschrieben (Übung 1)
  - Sourcecode
- .jar auf gruenau2 testen!

- Wir testen mit neuen Pattern
  (Länge: 4-50bp, Alphabet: E = {acgtn})