Assignment 1: Substring Search

SS 2018

Grundlagen der Bioinformatik

Überblick – Assignment 1 (20P)

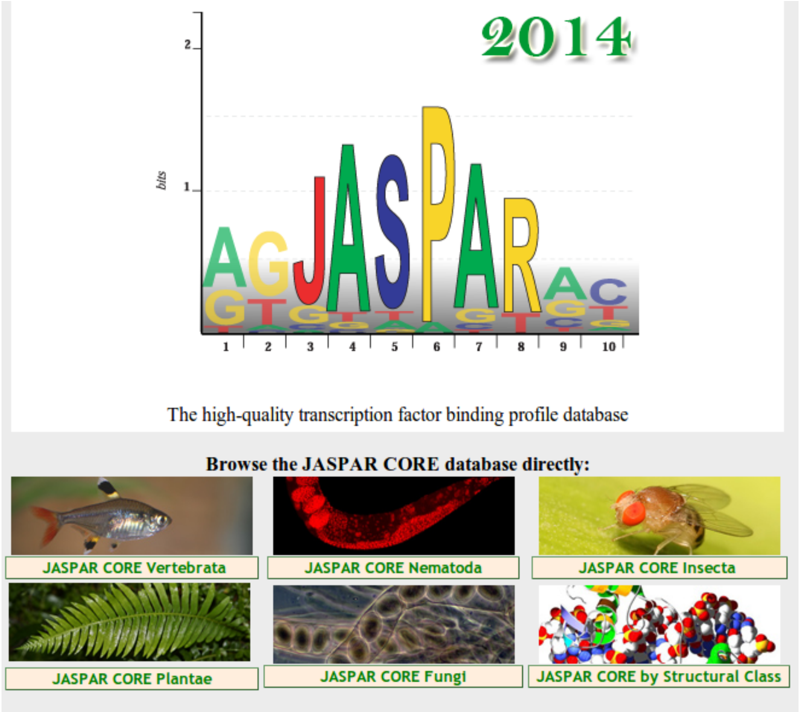
(1) Analyse transcription factor *GATA2* (4P)

(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



The high-quality transcription factor binding profile database

Browse the JASPAR CORE database directly:

- 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

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

Submit

- URL to the JASPAR information on *GATA2* (**Isoform .2**, length 5)
- Formula for information content used in sequence logos (1P)
- Frequency matrix and information content (IC) of every position of the PSWM (2P)
- Calculate IC for at least one position
- List of cancer types to which *GATA2* is associated and supporting papers from PubMed, 8x(Cancer, Title, PMID) (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 (7P)

- 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 GdBioinf1_[Gruppe].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)

1) 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)

2) 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)

Wichtig

- .py/.R/.jar auf gruenau2 testen!
- Wir testen mit neuem Pattern
  (Länge: 4-50bp, Alphabet: E = {acgtn})
- Bei Fragen: raik.otto@hu-berlin.de

Abgabe

- Abgabe bis 16.05.2018 um 23:59 Uhr

Upload **here**

https://box.hu-berlin.de/u/d/bdd2ffa6c66b4de5b2a6/

Dateiname: GdBioinf_[Assignmentnummer]_[Gruppennummer].zip
(z.B. GdBioinf_1_Gruppe_X.zip)

- Abgabe als .zip hochladen
- PDF mit Antworten zu 1, 2 und 3 zusammen abgeben
- Code als .Jar/.py/.R Dateiname: GdBioinf_[Assignmentnummer]_[Gruppennummer].jar
- Sourcecode