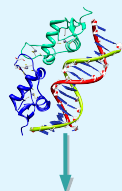


Introduction

D-Light on Promoters is a simple yet powerful client-server based system for calculating, querying and viewing transcription factor binding site (TFBS) annotation data on promoter sequences. The software provides scripts to set up an initial annotation dataset based on promoter sequences derived from the UCSC genome database[1] and position frequency matrices (PFMs) obtained from the JASPAR database[2]. Users can create personal accounts to add their own PFMs and/or promoter sequences for on-the-fly annotation.

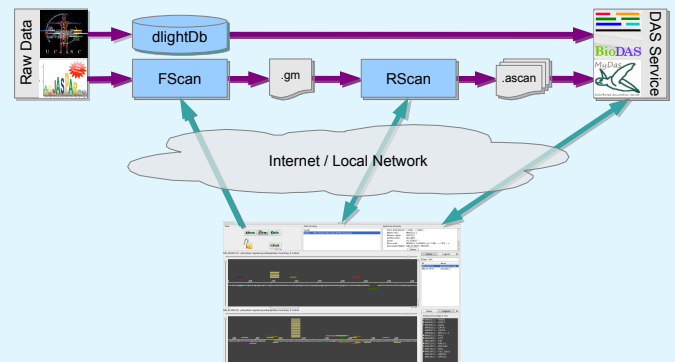
Background



The transcription of genes is controlled by the interplay of **transcription factors** (TFs) attached to their TFBSs on cis-regulatory elements. A **PFM** represents the binding site characteristic of a certain TF. PFMs are based on aligned binding site sequences derived by biological experiments. The frequency of occurrence for each base A,C,T or G is counted in each alignment column. The PFMs are subsequently used to predict potential binding sites for the corresponding TFs.

aaGTAACAATgc	A	[1	0	19	20	18	1	20	7]
agGTAACAATgc	C	[1	0	1	0	1	18	0	2]
gtGTAACAATgc	G	[17	0	0	0	1	0	0	3]
atGTAACAATgc	T	[1	20	0	0	0	1	0	8]
tGTAACAATgc											

Implementation



D-Light on Promoters consists of five main modules:

- **dlightDb**: MySQL database with annotations for PFMs and promoter sequences
- **FScan**: precalculates binding sites
- **RScan**: searches in FScan results
- **DAS server**: embeds scan results and annotations into a DAS[3] conform XML format (based on MyDas[4])
- **Client**: result visualization, data upload and annotation scans

User Interface

The **D-Light Client** is available as Java Applet or standalone Java application and provides views to (i) scan the annotation set, (ii) select scan results, (iii) search in the dlightDb database, and (iv) visualize the results. The visualization is based on the GenoViz SDK[5]. Results can be locally stored as text file or as image.

Scan Annotation

Matrix Selection: Matrix ACC(s) [FOK_Human_Rat.ascan]
Paired with ACC: MA0031
Gene Selection: Gene ACC(s) [FOK_Human_Rat.ascan]
Reference Genome: human
Save Result in: FOK_Human_Rat
Overwrite existing file: ☒

Constraints: Min. Distance: 10, Max. Distance: 100, Min. Score: 90
Exclude inordinately matching matrices: ☐ None, ☐ Top 5, ☐ Top 10
Omit hits in x-ref search: ☐ None, ☐ No-Match, ☐ No-Hom.

Add User Data: Matrix, Sequence

Start Scan

Select Ascan Result for Viewing

Results: FOK_Human_Rat.ascan, FOK_Rat.ascan, MA0002.ascan, arnt.ascan, arnt_arh.ascan, arnt_homodimer.ascan

Select File: Result File 1 [FOK_Human_Rat.ascan], Result File 2 [FOK_Rat.ascan]
Send to Viewer
Delete File, Refresh, Download

Search in Datasets

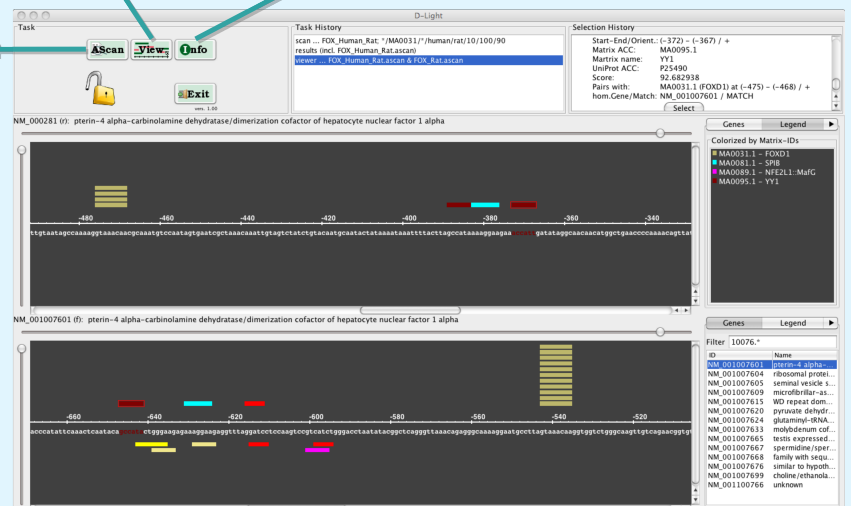
Search Criteria: Find: FOK*, Search in: ☒ Matrix ACC, ☒ Gene ACC, ☐ Result Files, ☒ Match Keywords, ☐ Gene Keywords, ☐ Sequence, ☐ Setup

Search Results: class: Winged Helix-Turn-Helix, comment: family: Forkhead, medline: 7957066, pvalue: 1e-10, tax_group: vertebrates, type: SELEX

MA0031 (CORE) vers. 1
name: FOKD1
protein: Q16676

Matrix:
A: 1 0 19 20 18 1 20 7
C: 1 0 1 0 1 18 0 2
G: 17 0 0 0 0 1 0 3
T: 1 20 0 0 0 1 0 8

Annotations: class: Winged Helix-Turn-Helix, comment: family: Forkhead, medline: 7957066, tax_group: vertebrates, type: SELEX



D-Light provides the opportunity to upload user-specified PFMs or DNA-sequences to extend the existing dataset. Unlike the initial dataset, all user-defined data are private and hidden from the other users.

Upload Matrix and Annotate

Matrix Selection: Matrix ACC(s) [FOK_Human_Rat.ascan]
Paired with ACC: MA0031
Gene Selection: Gene ACC(s) [FOK_Human_Rat.ascan]
Reference Genome: human
Save Result in: FOK_Human_Rat
Overwrite existing file: ☒

Constraints: Min. Distance: 10, Max. Distance: 100, Min. Score: 90
Exclude inordinately matching matrices: ☐ None, ☐ Top 5, ☐ Top 10
Omit hits in x-ref search: ☐ None, ☐ No-Match, ☐ No-Hom.

Add User Data: Matrix, Sequence

Start Scan

Conclusion

D-Light on Promoters is an easy to use client-server system for managing and querying TFBS annotation data. The client is written in Java to assure platform independency. The server only requires a Linux system. The built-in annotation method applies a simple scoring scheme. The modular setup allows the replacement of FScan by other scoring tools. D-Light is freely available and licensed under GNU General Public License, version 3.

References

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