

MEME-ChIP

Motif Analysis of Large Nucleotide Datasets

For further information on how to interpret these results please access <https://meme-suite.org/meme/doc/meme-chip-output-format.html>.
To get a copy of the MEME software please access <https://meme-suite.org>.

If you use MEME-ChIP in your research, please cite the following paper:

Philip Machanick and Timothy L. Bailey, "MEME-ChIP: motif analysis of large DNA datasets", *Bioinformatics* 27(12):1696-1697, 2011. [\[full text\]](#)

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DESCRIPTION



Hyperacetylated regions

MOTIFS

The significant motifs (E-value ≤ 0.05) found by the programs MEME, STREME and CentriMo; clustered by similarity and ordered by E-value.

Expand All Clusters Collapse All Clusters

Motif Found	Discovery/ Enrichment Program	E- value	Known or Similar Motifs	Distribution	SpaMo & FIMO
<p>Reverse Complement ⇌</p>	MEME	1.3e-068	CPEB1 HUMAN.H11MO.0.D PRDM6 HUMAN.H11MO.0.C FOXJ3 HUMAN.H11MO.0.A	Not Centrally Enriched	<ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3

Motif Found	Discovery/ Enrichment Program	E- value	Known or Similar Motifs	Distribution	SpaMo & FIMO
 <p>Reverse Complement ⇌</p>	MEME	3.1e-028	PITX2_HUMAN.H11MO.0.D	Not Centrally Enriched	<ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3
 <p>Reverse Complement ⇌</p>	MEME	2.2e-014	ZN770_HUMAN.H11MO.0.C PATZ1_HUMAN.H11MO.0.C ZN281_HUMAN.H11MO.0.A	Not Centrally Enriched	<ul style="list-style-type: none"> Motif Spacing Analysis Motif Sites in GFF3

PROGRAMS

Command	Running Time	Status	Outputs
getsize ./Galaxy8-hyperacetylation_fasta.fasta 1> \$metrics	0.05s	Success	
fasta-most -min 50 < ./Galaxy8-hyperacetylation_fasta.fasta 1> \$metrics	0.09s	Success	
fasta-center -dna -len 100 < ./Galaxy8-hyperacetylation_fasta.fasta 1> ./seqs-centered	0.13s	Success	<ul style="list-style-type: none"> seqs-centered
fasta-get-markov -nostatus -nosummary -dna -m 2 ./Galaxy8-hyperacetylation_fasta.fasta ./background	0.04s	Success	<ul style="list-style-type: none"> Background
meme ./seqs-centered -oc meme_out -mod zoops -nmotifs 3 -minw 6 -maxw 15 -bfile ./background -dna -searchsize 100000 -time 2919 -revcomp -nostatus	17m 44.08s	Success	<ul style="list-style-type: none"> MEME HTML MEME text MEME XML

Command	Running Time	Status	Outputs
streme --verbosity 1 --oc streme_out -dna --p ./seqs-centered --minw 6 --maxw 15 --time 5737 --order 2 --thresh 0.05 --totallength 4000000	20.31s	Success	<ul style="list-style-type: none"> STREME HTML STREME text STREME XML
centrimo -seqlen 2049 -verbosity 1 -oc centrimo_out -bfile ./background -score 5.0 -ethresh 10.0 ./Galaxy8-hyperacetylation_fasta.fasta meme_out/meme.xml streme_out/streme.xml db/motif_databases/HUMAN/HOCOMOCov11_full_HUMAN_mono_meme_format.meme	1.54s	Warnings	<ul style="list-style-type: none"> CentriMo HTML
tomtom -verbosity 1 -oc meme_tomtom_out -min-overlap 5 -dist pearson -evaluate -thresh 1 -no-ssc meme_out/meme.xml db/motif_databases/HUMAN/HOCOMOCov11_full_HUMAN_mono_meme_format.meme	4.53s	Success	<ul style="list-style-type: none"> Tomtom HTML Tomtom TSV Tomtom XML
tomtom -verbosity 1 -oc streme_tomtom_out -min-overlap 5 -dist pearson -evaluate -thresh 1 -no-ssc streme_out/streme.xml db/motif_databases/HUMAN/HOCOMOCov11_full_HUMAN_mono_meme_format.meme	2.93s	Success	<ul style="list-style-type: none"> Tomtom HTML Tomtom TSV Tomtom XML
tomtom -verbosity 1 -text -thresh 0.1 ./combined.meme ./combined.meme 1> ./motif_alignment.txt	0.04s	Success	<ul style="list-style-type: none"> Motif Alignment
spamo -verbosity 1 -oc spamo_out_1 -bgfile ./background -keepprimary -primary TTTTITKTTTTTTT ./Galaxy8-hyperacetylation_fasta.fasta meme_out/meme.xml meme_out/meme.xml streme_out/streme.xml	1.84s	Success	<ul style="list-style-type: none"> SpaMo HTML
spamo -verbosity 1 -oc spamo_out_2 -bgfile ./background -keepprimary -primary GCTGGGATTACAGGC ./Galaxy8-hyperacetylation_fasta.fasta meme_out/meme.xml meme_out/meme.xml streme_out/streme.xml	1.19s	Success	<ul style="list-style-type: none"> SpaMo HTML
spamo -verbosity 1 -oc spamo_out_3 -bgfile ./background -keepprimary -primary GGGHGGCSGMGGSGG ./Galaxy8-hyperacetylation_fasta.fasta meme_out/meme.xml meme_out/meme.xml streme_out/streme.xml	1.82s	Success	<ul style="list-style-type: none"> SpaMo HTML
fimo --parse-genomic-coord --verbosity 1 --oc fimo_out_1 --bgfile ./background --motif TTTTITKTTTTTTT meme_out/meme.xml ./Galaxy8-hyperacetylation_fasta.fasta	4.02s	Success	<ul style="list-style-type: none"> FIMO GFF FIMO HTML FIMO TSV
fimo --parse-genomic-coord --verbosity 1 --oc fimo_out_2 --bgfile ./background --motif GCTGGGATTACAGGC meme_out/meme.xml ./Galaxy8-hyperacetylation_fasta.fasta	3.90s	Success	<ul style="list-style-type: none"> FIMO GFF FIMO HTML FIMO TSV
fimo --parse-genomic-coord --verbosity 1 --oc fimo_out_3 --bgfile ./background --motif GGGHGGCSGMGGSGG meme_out/meme.xml ./Galaxy8-hyperacetylation_fasta.fasta	3.94s	Success	<ul style="list-style-type: none"> FIMO GFF FIMO HTML FIMO TSV

INPUT FILES

Alphabet

Background source: built from the (primary) sequences

Name	Bg.				Bg.	Name
Adenine	0.2666	A	~	T	0.2666	Thymine
Cytosine	0.2334	C	~	G	0.2334	Guanine

Primary Sequences

Database	Source	Sequence Count
Galaxy8-hyperacetylation_fasta	Galaxy8-hyperacetylation_fasta.fasta	958

Motifs

Database	Source	Motif Count
HOCOMOCov11 full HUMAN mono meme format	db/motif_databases/HUMAN/HOCOMOCov11_full_HUMAN_mono_meme_format.meme	769

MEME-ChIP version

5.5.1 (Release date: Sun Jan 29 10:33:12 2023 -0800)

Reference

Philip Machanick and Timothy L. Bailey, "MEME-ChIP: motif analysis of large DNA datasets", *Bioinformatics* **27**(12):1696-1697, 2011. [\[full text\]](#)

Command line summary

```
meme-chip -oc . -time 240 -ccut 100 -fdesc description -dna -order 2 -minw 6 -maxw 15 -db
db/motif_databases/HUMAN/HOCOMOCov11_full_HUMAN_mono_meme_format.meme -meme-mod zoops -meme-nmotifs 3 -meme-searchsize 100000 -streme-pvt
0.05 -streme-totallength 4000000 -centrimo-score 5.0 -centrimo-ethresh 10.0 Galaxy8-hyperacetylation_fasta.fasta
```