


```
-2823-09-10 04:28:13 -- https://jaspar.genereg.net/download/data/2822/CORE/JASPAR2822_CORE vertebrates_non-redundant_pfas_jaspar.txt
Resolving jaspar.genereg.net (jaspar.genereg.net)... 193.60.222.282
Connecting to jaspar.genereg.net (jaspar.genereg.net)|193.60.222.282|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 327864 (320K) [text/plain]
Saving to: 'Tutorial3/MotifFootprinting/JASPAR2822_CORE vertebrates_non-redundant_pfas_jaspar.txt'

JASPAR2822_CORE_ver 100%[=====] 320.18K  594KB/s   in 0.5s

2023-09-10 04:29:14 (594 KB/s) - 'Tutorial3/MotifFootprinting/JASPAR2822_CORE vertebrates_non-redundant_pfas_jaspar.txt' saved [327864/327864]

/opt/conda/lib/python3.10/site-packages/logomaker-0.8-py3.10.egg/logomaker/src/validate.py:98: SyntaxWarning:
"is" with a literal. Did you mean "=="?
  if matrix_type is 'information':
/opt/conda/lib/python3.10/site-packages/logomaker-0.8-py3.10.egg/logomaker/src/validate.py:184: SyntaxWarning:
"is" with a literal. Did you mean "=="?
  elif matrix_type is 'probability':
# TOBIAS 0.16.0 BINDetect (run started 2023-09-10 04:28:24.496648)
# Working directory: /home/jupyter
# Command line call: TOBIAS BINDetect --motifs Tutorial3/MotifFootprinting/JASPAR2822_CORE vertebrates_non-redundant_pfas_jaspar.txt --signals Tutorial3/MotifFootprinting/CTL_footprintscores.bw Tutorial3/MotifFootprinting/Mutant_footprintscores.bw --genome Tutorial3/InputFiles/chr4.fa --peaks Tutorial3/MotifFootprinting/MasterPeakList.bed --outdir Tutorial3/MotifFootprinting/DiffMotifs --cond_names CTL_Mutant --cores 7 --verbosity 1

# ----- Input parameters -----
# signals:      ['Tutorial3/MotifFootprinting/CTL_Footprintscores.bw', 'Tutorial3/MotifFootprinting/Mutant_Footprintscores.bw']
# peaks:      Tutorial3/MotifFootprinting/MasterPeakList.bed
# motifs:      ['Tutorial3/MotifFootprinting/JASPAR2822_CORE vertebrates_non-redundant_pfas_jaspar.txt']
# genomes:     Tutorial3/InputFiles/chr4.fa
# cond_names:  ['CTL', 'Mutant']
# peak_header: None
# naming:      name_id
# motif_pvalue: 0.0001
# bound_pvalue: 0.001
# pseudo:      None
# time_series: False
# skip_excel:  False
# output_peaks: None
# norm_off:     False
# prefix:       bindetect
# outdir:       /home/jupyter/Tutorial3/MotifFootprinting/DiffMotifs
# cores:        7
# split:        100
# debug:        False
# verbosity:    1

# ----- Output files -----
# /home/jupyter/Tutorial3/MotifFootprinting/DiffMotifs/'/beds/'_CTL_bound.bed
# /home/jupyter/Tutorial3/MotifFootprinting/DiffMotifs/'/beds/'_CTL_unbound.bed
# /home/jupyter/Tutorial3/MotifFootprinting/DiffMotifs/'/beds/'_Mutant_bound.bed
# /home/jupyter/Tutorial3/MotifFootprinting/DiffMotifs/'/beds/'_Mutant_unbound.bed
# /home/jupyter/Tutorial3/MotifFootprinting/DiffMotifs/'/beds/'_all.bed
# /home/jupyter/Tutorial3/MotifFootprinting/DiffMotifs/'/plots/'_log2fcs.pdf
# /home/jupyter/Tutorial3/MotifFootprinting/DiffMotifs/'/'_overview.txt
# /home/jupyter/Tutorial3/MotifFootprinting/DiffMotifs/'/'_overview.xlsx
# /home/jupyter/Tutorial3/MotifFootprinting/DiffMotifs/bindetect_distances.txt
# /home/jupyter/Tutorial3/MotifFootprinting/DiffMotifs/bindetect_results.txt
# /home/jupyter/Tutorial3/MotifFootprinting/DiffMotifs/bindetect_results.xlsx
# /home/jupyter/Tutorial3/MotifFootprinting/DiffMotifs/bindetect_figures.pdf
```

```
done


In [30]: #View the html results
Iframe(src="Tutorial3/MotifFootprinting/DiffMotifs/bindetect_CTL_Mutant.html", width=900, height=600)
```

Out[30]:



In the above html file you can hover over each point to see the motif name and the sequence. This type of plot is a volcano plot showing the differential signal on the x-axis and the significance values on the y-axis.

For example, the original paper focused on TP63, which is one of our differential dots in the html file.

 Drawing

Let's visualize the average footprint at TP63 motifs.

```
In [31]: #Iframe(src="Tutorial2/MotifFootprinting/MYBL1_MAO776.1/plots/MYBL1_MAO776.1_log2fcs.pdf", width=900, height=600)
```

#note change to Tutorial2

```
#TOBIAS PlotAggregate --TFBS Tutorial3/MotifFootprinting/DiffMotifs/TP63_MA0525.2/beds/TP63_MA0525.2_all.bed
#TOBIAS PlotAggregate --TFBS Tutorial3/MotifFootprinting/DiffMotifs/TP63_MA0525.2/beds/TP63_MA0525.2_all.bed
# TOBIAS 0.16.0 PlotAggregate (run started 2023-09-10 04:38:00.819069)
# Working directory: /home/jupyter
# Command line call: TOBIAS PlotAggregate --TFBS Tutorial3/MotifFootprinting/DiffMotifs/TP63_MA0525.2/beds/TP63_MA0525.2_all.bed --signals Tutorial3/MotifFootprinting/CTL_corrected.bw Tutorial3/MotifFootprinting/Mutant_corrected.bw --output Tutorial3/MotifFootprinting/TP63_footprint_compare.png --share_y both --verbosity 1 --plot_boundaries --flank 60 --smooth 2 --signal-on-x
```

```
# ----- Input parameters -----
# signals:      ['Tutorial3/MotifFootprinting/DiffMotifs/TP63_MA0525.2/beds/TP63_MA0525.2_all.bed']
# TFBS:         ['Tutorial3/MotifFootprinting/CTL_corrected.bw', 'Tutorial3/MotifFootprinting/Mutant_corrected.bw']
# regions:      []
# whitelist:    []
# blacklist:    []
# output:       Tutorial3/MotifFootprinting/TP63_footprint_compare.png
# output_txt:   None
# flank:        60
# title:        Aggregated signals
# TFBS_labels:  None
# signal_labels: None
# region_labels: None
# share_y:      both
# normalize:    False
# negate:       False
# smooth:       2
# log_transform: False
# plot_boundaries: True
# signal_on_x:  True
# remove_outliers: 1
# debug:        False
# verbosity:    1

# ----- Output files -----
# Tutorial3/MotifFootprinting/TP63_footprint_compare.png
```

```
In [32]: IFrame(src="Tutorial3/MotifFootprinting/TP63_footprint_compare.png", width=600, height=400)
```

Out[32]:



We can also get all the motifs that have differential footprints:

```
In [33]: #load the results as a pandas table Tutorial2/MotifFootprinting/bindetect_results.txt
dframe = pd.read_csv("Tutorial3/MotifFootprinting/DiffMotifs/bindetect_results.txt", sep='\t')
DiffMotifs = dframe[dframe['CTL_Mutant_pvalue'] < .05]
display(dframe)
write out to a tab separated file
DiffMotifs.to_csv('Tutorial3/MotifFootprinting/DiffMotifs_p05.txt')
```

	output_prefix	name	motif_id	cluster	total_tfbs	CTL_mean_score	CTL_bound	Mutant_mean_score	Mutant_b
0	Amr1_MAO004.1	Amr1	MA0004.1	C_MYC	38	85.97575	16	108.49061	
1	AhrAm1_MAO006.1	Ahr-Amr1	MA0006.1	C_Ahr-Amr1	48	122.76975	24	115.50042	
2	Ddl3Cclpba_MAO019.1	Ddl3-Cclpba	MA0019.1	C_Ddl3-Cclpba	62	80.02321	24	80.35243	
3	Mecom_MAO029.1	Mecom	MA0029.1	C_Mecom	74	61.72563	20	58.21735	
4	FOXF2_MAO030.1	FOXF2	MA0030.1	C_FOXD1	70	54.90034	16	57.53936	
...
836	ZNF281_MAI630.2	ZNF281	MA1630.2	C_ZNF281	442	87.47115	177	93.39986	
837	BACH1_MAI633.2	BACH1	MA1633.2	C_JUNB	292	107.33995	180	93.78144	
838	Ptdm4_MAI647.2	Ptdm4	MA1647.2	C_Ptdm4	90	65.86800	28	60.37410	
839	THAP1_MAO597.2	THAP1	MA0597.2	C_THAP1	236	90.57476	101	82.80139	
840	NR5A1_MAI540.2	NR5A1	MA1540.2	C_NR5A1	88	60.86295	20	63.31876	

841 rows × 12 columns

Great job!

Thank you for completing these tutorials. Feel free to download these notebooks, customize, and use them to process your own data.

```
In [ ]:
```