Motif Export

Yichen Han

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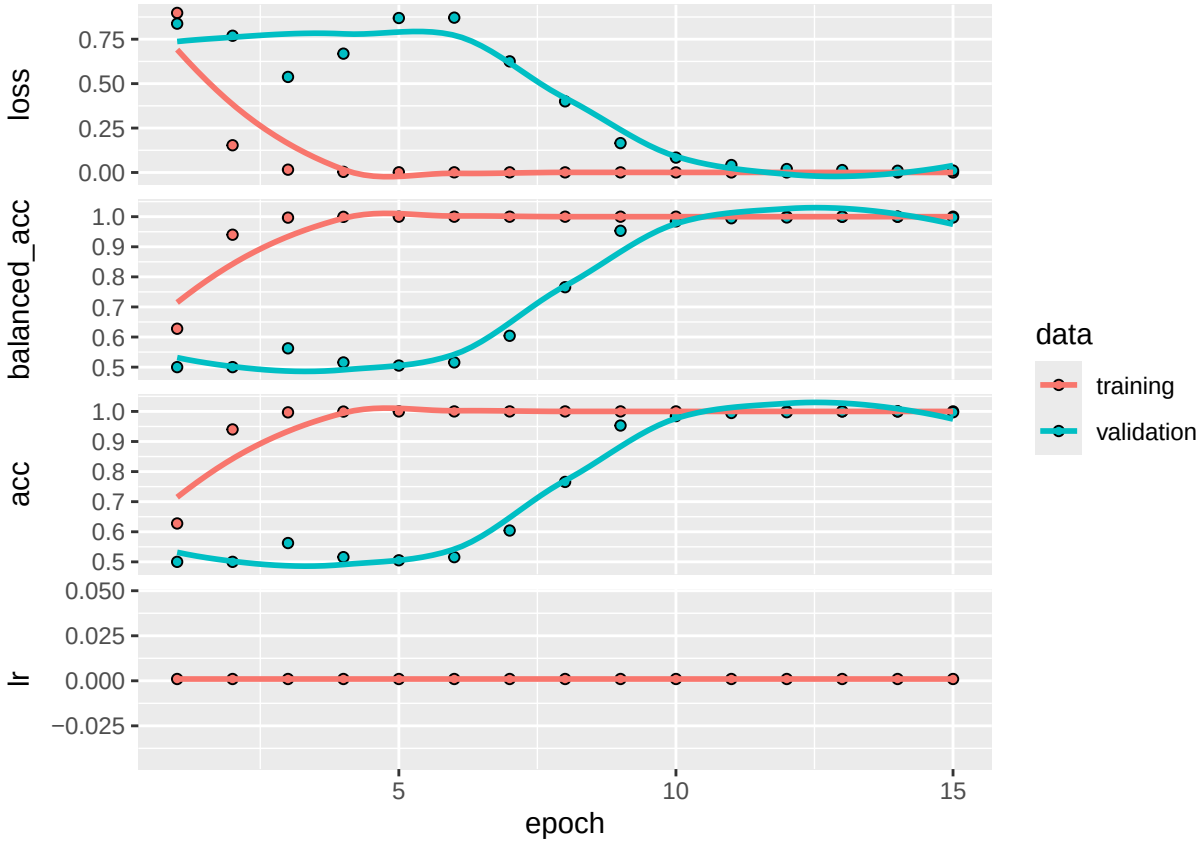
Motif detection

Based on randomly generated sequence with length 450 bp, ACGT are drawn with equal probs, and then insert a motif `TATAGCGCAGCTGTCAGCATGAGTCCATGA` at a random starting point. Data 10000.

Model: LSTM-CNN, learning rate 0.001, batch size 32, accuracy 100%.




```
## Using checkpoint checkpoints/motifeq-both_2/Ep.015-val_loss0.00-val_acc1.000.hdf5
```

Model Evaluation

```
## [[1]]
## [[1]]$confusion_matrix
```

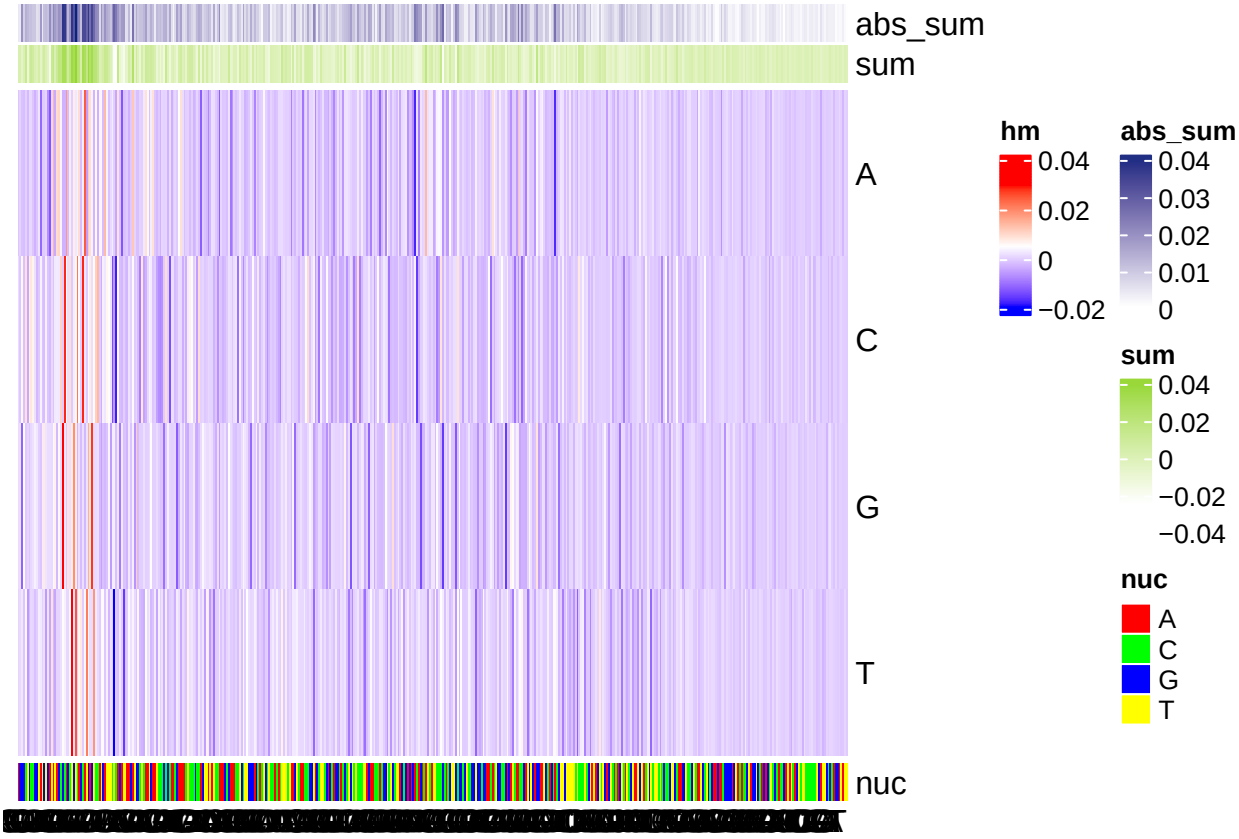
```
##           Truth
## Prediction normal motif
##     normal    640     0
##     motif       0   640
##
## [[1]]$accuracy
## [1] 1
##
## [[1]]$categorical_crossentropy_loss
## [1] 0.002400922
##
## [[1]]$AUC
## NULL
##
## [[1]]$AUPRC
## NULL
```

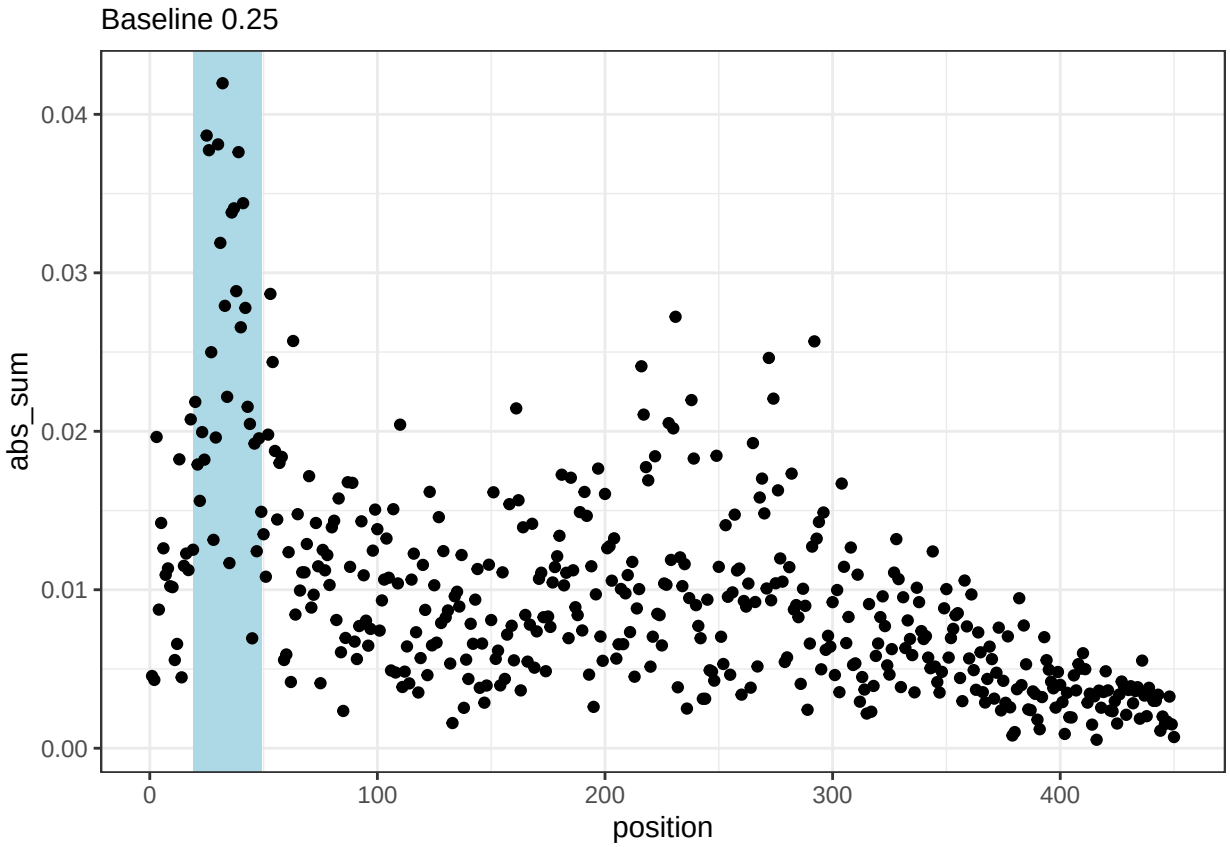
IG

Baseline: 0.25

```
##              [,1]     [,2]
## [1,] 0.0002209859 0.999779
```

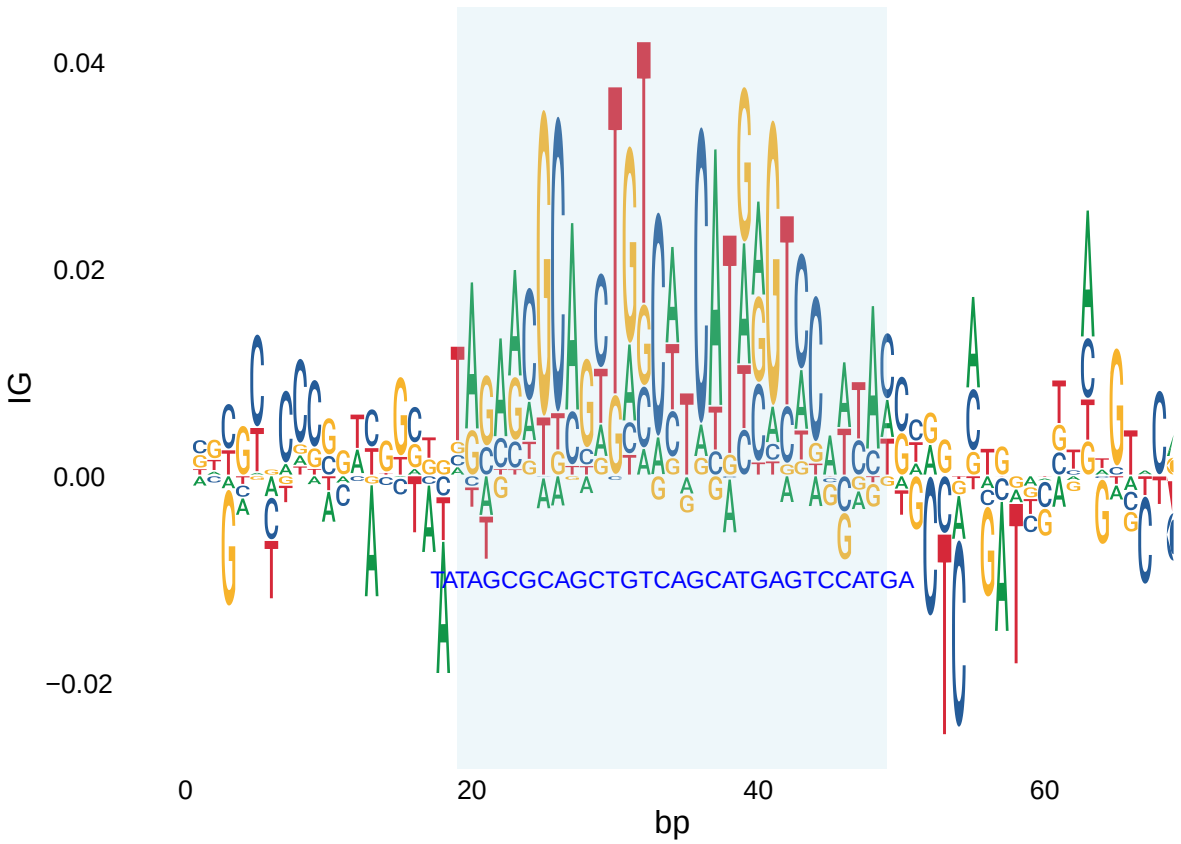
```
## [[1]]
```






```
## Warning: The ‘<scale>‘ argument of ‘guides()‘ cannot be ‘FALSE‘. Use "none" instead as
## of ggplot2 3.3.4.
## i The deprecated feature was likely used in the ggseqlogo package.
##   Please report the issue at <https://github.com/omarwagih/ggseqlogo/issues>.
## This warning is displayed once every 8 hours.
## Call ‘lifecycle::last_lifecycle_warnings()‘ to see where this warning was
## generated.

## Scale for x is already present.
## Adding another scale for x, which will replace the existing scale.
```


0.04
0.02
0.00
−0.02
IG
TATAGCGCAGCTGTCAGCATGAGTCCATGA
0
20
40
60
bp