RSDexport

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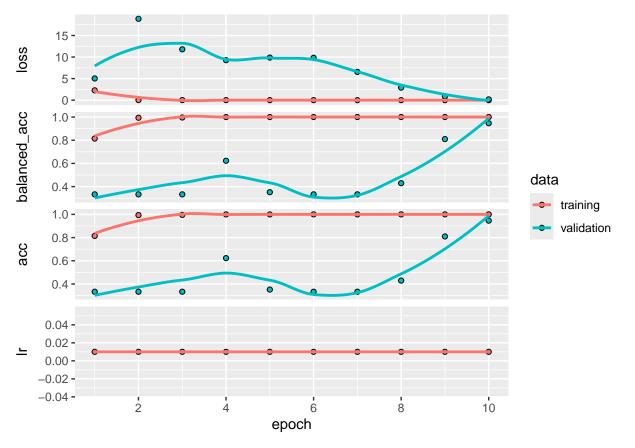
Experiment 39

Spec.region excluded for "abnormal". Functional change not guaranteed.

Call: GenePermutation(triplets, keyed, num.perm=15000, min.subs=10, max.subs=30, spec.region=30:60)

Model: maxlen = 477, batch_size = 64, steps_per_epoch = 45, epochs = 10, step = c(1, 1, 1)

```
# load outputs/hist39.rds
hist39 <- readRDS(file="outputs/hist39.rds")
plot(hist39)</pre>
```



```
checkpoint_path <- file.path("checkpoints")
dir_path <- file.path("outputs")</pre>
```

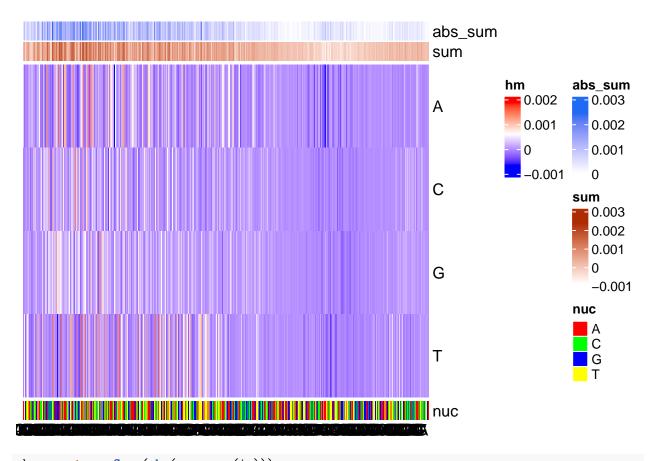
Using checkpoint checkpoints/rsd-permutation_39/Ep.010-val_loss0.18-val_acc0.946.hdf5

Model at last Epoch

```
path_special_test <- file.path("special/test")</pre>
path_normal_test <- file.path("normal/test")</pre>
path_abnormal_test <- file.path("abnormal/test")</pre>
eval_model <- evaluate_model(path_input = c(path_normal_test,</pre>
  path_abnormal_test, path_special_test),
  model = model,
 batch_size = 64,
  step = 5,
 vocabulary_label = list(c("normal", "abnormal", "special")),
 number_batches = 10,
 mode = "label_folder",
  verbose = FALSE
)
eval_model
## [[1]]
## [[1]]$confusion_matrix
             Truth
## Prediction normal abnormal special
## normal 254
                          26
    abnormal
                  0
                           213
                                     0
##
    special
                          17
                                   256
##
##
## [[1]]$accuracy
## [1] 0.9414062
## [[1]]$categorical_crossentropy_loss
## [1] 0.1702538
## [[1]]$AUC
## NULL
##
## [[1]]$AUPRC
## NULL
special_seq <- permute_sequence(triplets, keyed, type="ok", min.subs=5, max.subs=30,</pre>
                                 dict=codon.dict, spec.cond=FALSE, spec.region=NULL)
special_seq <- permute_sequence(special_seq, keyed, type="func", min.subs=5, max.subs=30,</pre>
                                 dict=codon.dict, spec.cond=TRUE, spec.region=30:60)
special_seq <- paste(special_seq, collapse = "")</pre>
onehot_instance <- seq_encoding_label(char_sequence = special_seq,</pre>
```

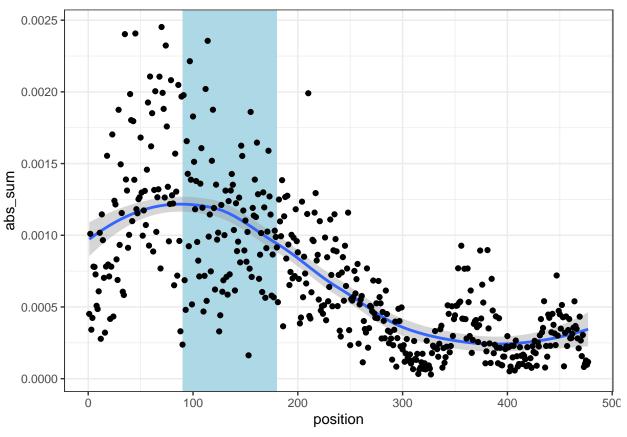
```
maxlen = 477,
                                          start_ind = 1,
                                          vocabulary = c("A", "C", "G", "T"))
head(onehot_instance[1,,])
        [,1] [,2] [,3] [,4]
## [1,]
              0
          1
                    0
## [2,]
          0
               0
                     0
                         1
## [3,]
        0
              0
                  1
                         0
## [4,]
        0
## [5,]
        0
              0
                     0
                         1
## [6,]
                     0
pred <- predict(model, onehot_instance, verbose = 0)</pre>
pred
##
                [,1]
                             [,2] [,3]
## [1,] 2.989441e-09 3.559504e-18
ig <- integrated_gradients(</pre>
 input_seq = onehot_instance,
 baseline_type = "shuffle",
 target_class_idx = 3,
 model = model,
 num_baseline_repeats = 50)
heatmaps_integrated_grad(integrated_grads = ig,
                        input_seq = onehot_instance)
```

[[1]]



```
abs_sum <- rowSums(abs(as.array(ig)))
df <- data.frame(abs_sum = abs_sum, position = 1 : 477)
ggplot(df, aes(x = position, y = abs_sum)) + geom_rect(aes(xmin = 90, xmax = 180, ymin = -Inf, ymax = Inf, ymax
```

'geom_smooth()' using method = 'loess' and formula = 'y ~ x'



```
# abs_sum <- rowSums(abs(as.array(ig)))</pre>
#df <- data.frame(abs_sum = abs_sum, position = 1 : 477)
\#ggplot(df, aes(x = position, y = abs_sum)) + geom_rect(aes(xmin = 90, xmax = 180, ymin = -Inf, ymax = -Inf
# modification: df should be summed every 3 rows, position reassigned accordingly.
df_mod <- df %>%
      mutate(group = rep(1:(nrow(df) / 3), each = 3)) %>%
      group_by(group) %>%
      summarise(
             abs_sum_sum = sum(abs_sum),
             abs_sum_median = median(abs_sum),
             abs_sum_mean = mean(abs_sum),
             abs_sum_max = max(abs_sum)
# Split special_seq (a string) into triplets (every third character)
chars <- strsplit(special_seq, "")[[1]]</pre>
# Create triplets
trip_spec <- sapply(seq(1, length(chars), by = 3), function(i) {</pre>
      paste(chars[i:min(i+2, length(chars))], collapse = "")
})
# Get the index of sequences at which trip_spec != triplets
index <- which(trip_spec != triplets)</pre>
```

```
# Plot the results with different smooth lines for sum, median, mean, and max
ggplot(df_mod, aes(x = group)) +
    geom_rect(aes(xmin = 30, xmax = 60, ymin = -Inf, ymax = Inf), fill = "lightblue", alpha = 0.2) +
# draw points of max
geom_point(aes(x = group, y = abs_sum_max), color = "purple") +
geom_smooth(aes(y = abs_sum_sum, color = "Sum"), method = "auto", se = FALSE) +
geom_smooth(aes(y = abs_sum_median, color = "Median"), method = "auto", se = FALSE) +
geom_smooth(aes(y = abs_sum_mean, color = "Mean"), method = "auto", se = FALSE) +
geom_smooth(aes(y = abs_sum_max, color = "Max"), method = "auto", se = FALSE) +
scale_color_manual(values = c("Sum" = "blue", "Median" = "green", "Mean" = "orange", "Max" = "purple"
geom_point(data = data.frame(group = index), aes(x = group, y = 0), shape = 4, size = 3, color = "red
theme_bw() +
labs(y = "Absolute Sum of IG", color = "Statistic", x = "AA Index")
```

```
## 'geom_smooth()' using method = 'loess' and formula = 'y ~ x'
## 'geom_smooth()' using method = 'loess' and formula = 'y ~ x'
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```

