Outputs inspection half CIFAR10

```
library(ggplot2)
## Warning: package 'ggplot2' was built under R version 4.0.5
library(dplyr)
## Warning: package 'dplyr' was built under R version 4.0.5
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
       filter, lag
##
## The following objects are masked from 'package:base':
##
       intersect, setdiff, setequal, union
library(tidyr)
## Warning: package 'tidyr' was built under R version 4.0.5
library("ggpubr")
## Warning: package 'ggpubr' was built under R version 4.0.5
library(LDATS)
## Warning: package 'LDATS' was built under R version 4.0.5
library(stringr)
source("utils.R")
## Warning: package 'hash' was built under R version 4.0.5
## hash-2.2.6.1 provided by Decision Patterns
## Warning: package 'reticulate' was built under R version 4.0.5
```

```
## Warning: package 'berryFunctions' was built under R version 4.0.5
##
## Attaching package: 'berryFunctions'
## The following object is masked from 'package:dplyr':
##
between
```

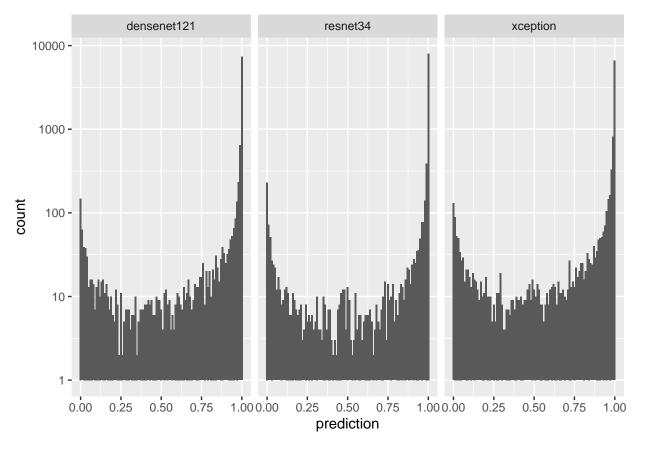
Visualization on CIFAR10. We are using data of three neural networks trained on reduced CIFAR10 training set. Half of the CIFAR10 training set was extracted as a validation set. We then divided both the reduced training set and validation set into 50 disjoint subsets and trained an ensemble on each of them. In this visualization, we are trying to inspect the outputs deeper, mainly to make sense of strange behavior of nll metric for ensemble outputs.

```
base_dir <- "../data/data_train_val_half_c10"
repls <- 0:0
folds <- 0:49

nets_outputs <- load_network_outputs(base_dir, repls)
ens_outputs <- load_ensemble_outputs(base_dir, repls, folds)
net_results <- read.csv(file.path(base_dir, "net_accuracies.csv"))
ens_results <- read.csv(file.path(base_dir, "ensemble_accuracies.csv"))</pre>
```

```
classes <- dim(nets_outputs[["test_outputs"]])[4]</pre>
nets_num <- length(nets_outputs[["networks"]])</pre>
preds <- nets_outputs[["test_outputs"]]</pre>
labs <- nets_outputs[["test_labels"]]</pre>
network <- c()
prediction <- c()</pre>
replication <- c()
for (ri in repls + 1)
  for (net_i in seq_along(nets_outputs[["networks"]]))
    net_outputs_prob <- softmax(preds[ri, net_i, , ])</pre>
    cur_pred <- c()</pre>
    for (class in 1:classes)
      class_probs <- net_outputs_prob[labs[ri, ] == (class - 1), class]</pre>
      cur_pred <- c(cur_pred, class_probs)</pre>
    network <- c(network, rep(nets_outputs[["networks"]][net_i], length(cur_pred)))</pre>
    prediction <- c(prediction, cur_pred)</pre>
  }
  replication <- c(replication, rep(ri, length(prediction) - length(replication)))
networks_predictions <- data.frame(network, replication, prediction)</pre>
```

nets_cor_preds_histo <- ggplot(data=networks_predictions) + geom_histogram(mapping=aes(x=prediction), b
nets_cor_preds_histo</pre>

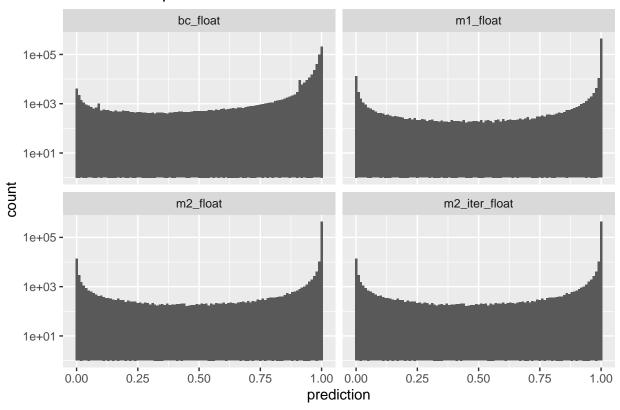


```
classes <- dim(nets_outputs[["test_outputs"]])[4]</pre>
labs <- nets_outputs[["test_labels"]]</pre>
method <- c()
prediction <- c()</pre>
replication <- c()
fold <- c()
for (ri in repls + 1)
{
  for (m_i in seq_along(ens_outputs$methods))
    for (f_i in folds + 1)
      cur_pred <- c()</pre>
      for (class in 1:classes)
        class_probs <- ens_outputs$val_training[ri, m_i, f_i, labs[ri, ] == (class - 1), class]</pre>
         cur_pred <- c(cur_pred, class_probs)</pre>
      method <- c(method, rep(ens_outputs$methods[m_i], length(cur_pred)))</pre>
      prediction <- c(prediction, cur_pred)</pre>
      fold <- c(fold, rep(f_i - 1, length(cur_pred)))</pre>
    }
  }
  replication <- c(replication, rep(ri - 1, length(cur_pred) - length(replication)))</pre>
}
```

val_ens_predictions <- data.frame(method, replication, fold, prediction)</pre>

val_ens_cor_preds_histo <- ggplot(data=val_ens_predictions) + geom_histogram(mapping=aes(x=prediction),
val_ens_cor_preds_histo</pre>

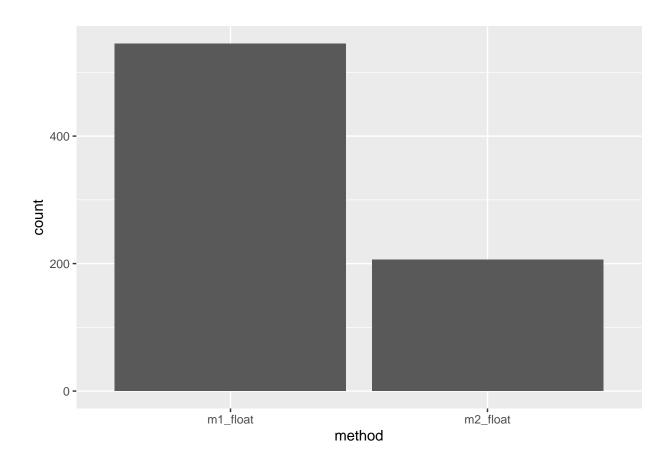
Probabilities predicted for the correct class - ens trained on val



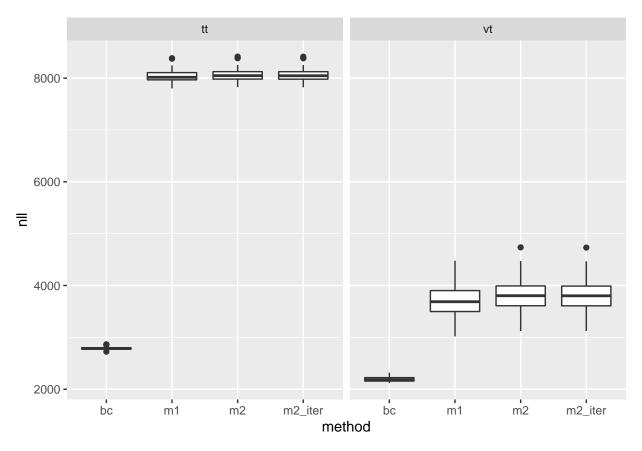
val_ens_zero_counts <- ggplot(data=val_ens_predictions[val_ens_predictions\$prediction == 0,]) + geom_h</pre>

Warning: Ignoring unknown parameters: binwidth, bins, pad

val_ens_zero_counts



val_ens_nll <- ggplot(data=ens_results) + geom_boxplot(mapping=aes(x=method, y=nll)) + facet_wrap(~train
val_ens_nll</pre>

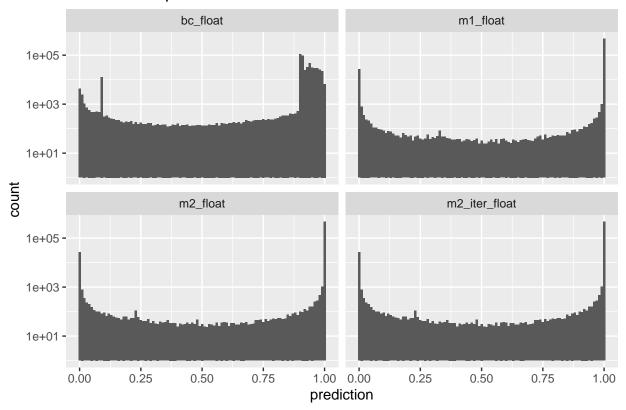


```
classes <- dim(nets_outputs[["test_outputs"]])[4]</pre>
labs <- nets_outputs[["test_labels"]]</pre>
method <- c()
prediction <- c()</pre>
replication <- c()
fold <- c()
for (ri in repls + 1)
  for (m_i in seq_along(ens_outputs$methods))
    for (f_i in folds + 1)
      cur_pred <- c()</pre>
      for (class in 1:classes)
        class_probs <- ens_outputs$train_training[ri, m_i, f_i, labs[ri, ] == (class - 1), class]</pre>
        cur_pred <- c(cur_pred, class_probs)</pre>
      method <- c(method, rep(ens_outputs$methods[m_i], length(cur_pred)))</pre>
      prediction <- c(prediction, cur_pred)</pre>
      fold <- c(fold, rep(f_i - 1, length(cur_pred)))</pre>
    }
  }
  replication <- c(replication, rep(ri - 1, length(cur_pred) - length(replication)))</pre>
}
```

train_ens_predictions <- data.frame(method, replication, fold, prediction)</pre>

train_ens_cor_preds_histo <- ggplot(data=train_ens_predictions) + geom_histogram(mapping=aes(x=predicti
train_ens_cor_preds_histo</pre>

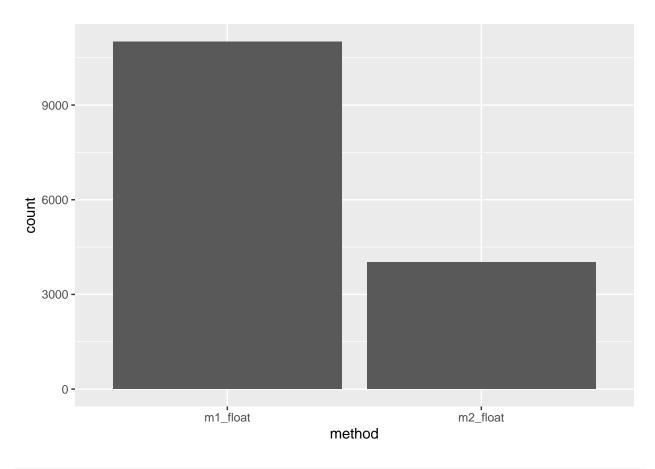
Probabilities predicted for the correct class - ens trained on train



train_ens_zero_counts <- ggplot(data=train_ens_predictions[train_ens_predictions\$prediction == 0,]) + ;</pre>

Warning: Ignoring unknown parameters: binwidth, bins, pad

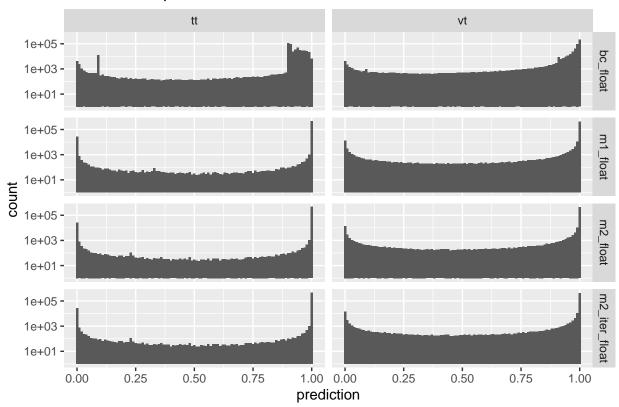
train_ens_zero_counts



```
val_ens_predictions$train_type <- "vt"
train_ens_predictions$train_type <- "tt"
ens_predictions <- rbind(val_ens_predictions, train_ens_predictions)</pre>
```

ens_cor_preds_histo <- ggplot(data=ens_predictions) + geom_histogram(mapping=aes(x=prediction), binwidtens_cor_preds_histo</pre>

Probabilities predicted for the correct class



Here we observe similar results to those in vasualizations_ensemble_outputs_CIF10.