Outputs inspection 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)
library(reshape2)
## Warning: package 'reshape2' was built under R version 4.0.3
## Attaching package: 'reshape2'
## The following object is masked from 'package:tidyr':
##
       smiths
```

library(reticulate) ## Warning: package 'reticulate' was built under R version 4.0.5 np <- import("numpy") 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 'berryFunctions' was built under R version 4.0.5 ## ## Attaching package: 'berryFunctions' ## The following object is masked from 'package:dplyr': ##</pre>

Visualization on CIFAR10. We are using data of three neural networks trained on reduced CIFAR10 training set. These networks were trained in 30 replications. In each replication, 500 samples from the training set were randomly extracted and formed validation set. In each replication, we trained two ensembles on the outputs of neural networks. First one was trained on randomly chosen subset, of size 500, of nn training set, second on the extracted validation set. In this visualization, we are trying to inspect the outputs deeper, mainly to make sense of strange behavior of nll metric for ensemble outputs.

Warning: package 'purrr' was built under R version 4.0.3

##

between

```
base_dir <- "../data/data_train_val_c10"
repls <- 0:29
classes <- 10

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

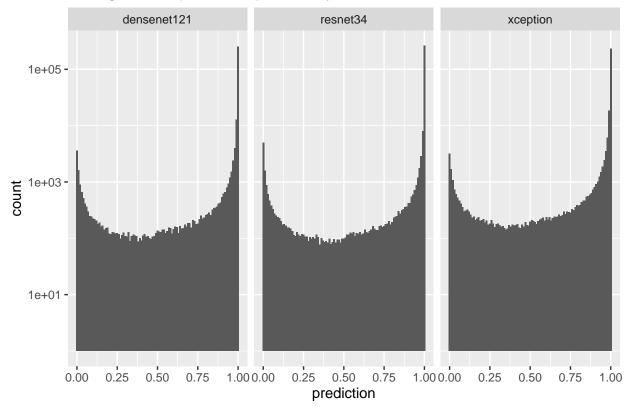
For clearer visualization, we will plot just the predicted probability of the correct class for all the methods.

```
preds <- nets_outputs$test_outputs
for (ri in repls + 1)
{
    for (net_i in seq_along(nets_outputs[["networks"]]))
    {
        preds[ri, net_i, ,] <- softmax(preds[ri, net_i, ,])
    }
}
nets_test_cor_probs <- gather(preds, 1 + nets_outputs$test_labels[1, ], 3, 4)</pre>
```

```
nets_test_cor_probs <- melt(nets_test_cor_probs)
nets_test_cor_probs <- nets_test_cor_probs[, c(-3, -4)]
names(nets_test_cor_probs) <- c("replication", "network", "prediction")
nets_test_cor_probs$network <- as.factor(nets_test_cor_probs$network)
levels(nets_test_cor_probs$network) <- nets_outputs$networks</pre>
```

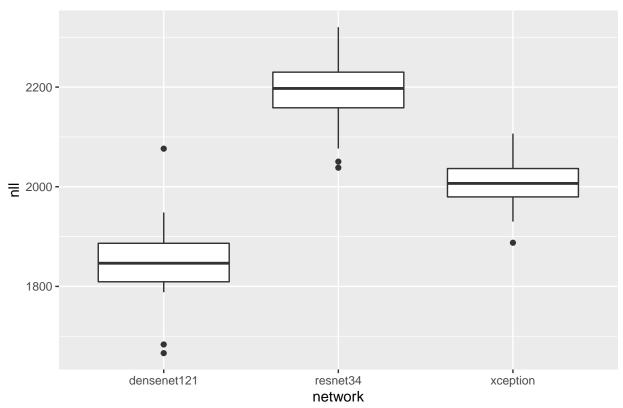
nets_cor_preds_histo <- ggplot(data=nets_test_cor_probs) + geom_histogram(mapping=aes(x=prediction), bi
ggtitle("Histograms of predicted probability for the correct class") + facet_wrap(~network) + scale_y
nets_cor_preds_histo</pre>

Histograms of predicted probability for the correct class



networks_nll <- ggplot(data=net_results) + geom_boxplot(mapping=aes(x=network, y=nll)) + ggtitle("NLL or networks_nll</pre>

NLL of networks

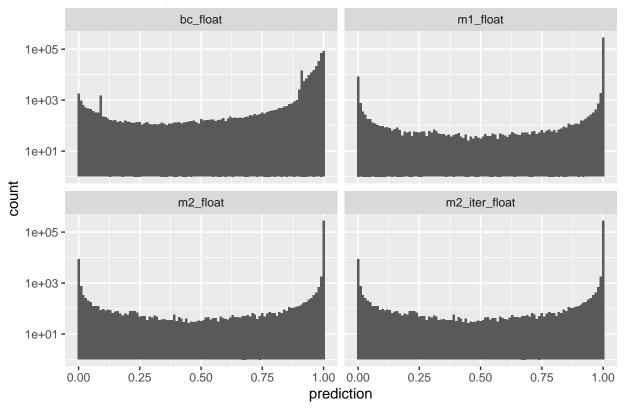


Networks nll seems to have good correspondence with lowest prediction probability column in the previous histograms.

```
val_ens_cor_probs <- gather(ens_outputs$val_training, 1 + nets_outputs$test_labels[1, ], 3, 4)
val_ens_cor_probs <- melt(val_ens_cor_probs)
val_ens_cor_probs <- val_ens_cor_probs[, c(-3, -4)]
names(val_ens_cor_probs) <- c("replication", "method", "prediction")
val_ens_cor_probs$method <- as.factor(val_ens_cor_probs$method)
levels(val_ens_cor_probs$method) <- ens_outputs$methods</pre>
```

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

Probabilities predicted for the correct class - ens trained on val



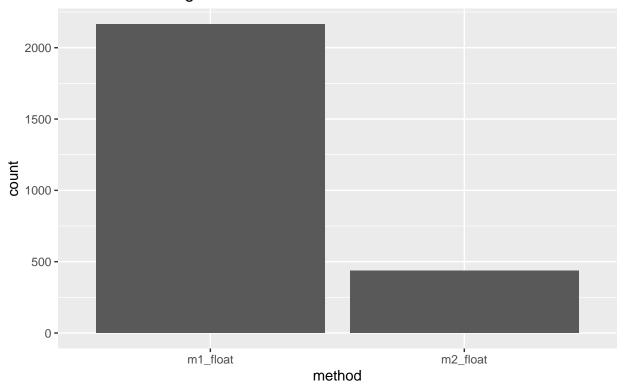
Coupling method be produces far fewer probabilities falling into the lowest bin for the correct class than m1 and m2.

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

Warning: Ignoring unknown parameters: binwidth, bins, pad

val_ens_zero_counts

Counts of zero or lower probabilities predicted for the correct class by coup Validation training

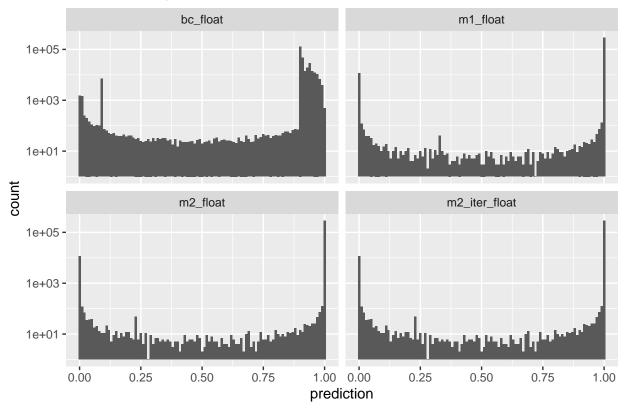


m2_iter and bc didn't produce any zero probability outputs in this replication.

```
train_ens_cor_probs <- gather(ens_outputs$train_training, 1 + nets_outputs$test_labels[1, ], 3, 4)
train_ens_cor_probs <- melt(train_ens_cor_probs)
train_ens_cor_probs <- train_ens_cor_probs[, c(-3, -4)]
names(train_ens_cor_probs) <- c("replication", "method", "prediction")
train_ens_cor_probs$method <- as.factor(train_ens_cor_probs$method)
levels(train_ens_cor_probs$method) <- ens_outputs$methods</pre>
```

```
train_ens_cor_preds_histo <- ggplot(data=train_ens_cor_probs) + geom_histogram(mapping=aes(x=prediction
train_ens_cor_preds_histo</pre>
```

Probabilities predicted for the correct class - ens trained on train



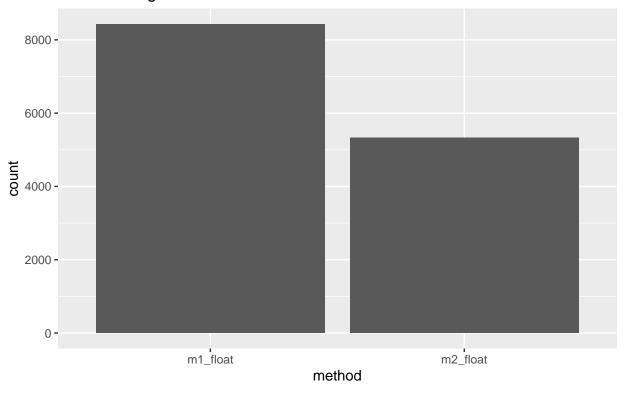
Also in this case, coupling method bc produces far fewer probabilities falling into the lowest bin for the correct class than m1 and m2.

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

Warning: Ignoring unknown parameters: binwidth, bins, pad

train_ens_zero_counts

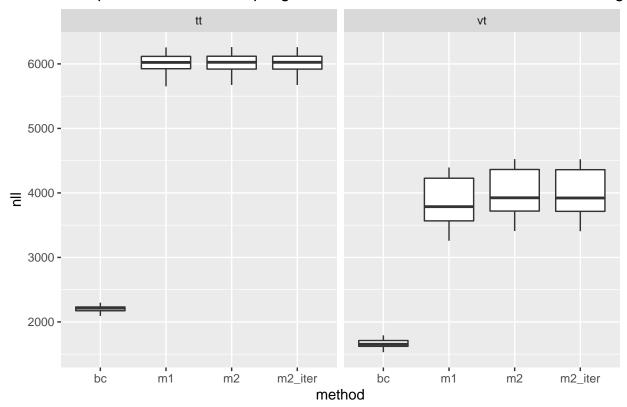
Counts of zero or lower probabilities predicted for the correct class by cour Train training



m2_iter and bc didn't produce any zero probability outputs in this replication.

val_ens_nll <- ggplot(data=ens_results) + geom_boxplot(mapping=aes(x=method, y=nll)) + facet_wrap(~training ggtitle("Comparison of nll for coupling methods for different LDA train methodologies")
val_ens_nll</pre>

Comparison of nll for coupling methods for different LDA train methodologi

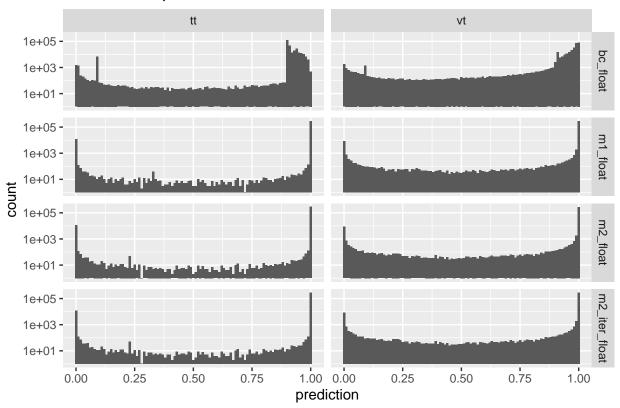


When LDA is trained on training data, be method has clearly superior nll, however in the case of training LDA on validation data, other coupling methods perform similarly, or better.

```
val_ens_cor_probs$train_type <- "vt"
train_ens_cor_probs$train_type <- "tt"
ens_cor_probs <- rbind(val_ens_cor_probs, train_ens_cor_probs)</pre>
```

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

Probabilities predicted for the correct class



Bayes covariant coupling method produces more uniformly distributed predictions than methods m1 and m2. Also, there is a big difference in each method between ensemble trained on validation and ensemble trained on train set. Ensembles trained on validation set produce generally more uniformly distributed predictions. However, ensembles trained on training set attain statistically significantly higher accuracy.

```
ens_Rs <- load_R_matrices(base_dir, repls)</pre>
```

```
df_val_Rs <- melt(ens_Rs$val_training)
names(df_val_Rs) <- c("replication", "precision", "sample", "class1", "class2", "prob")
class <- nets_outputs$test_labels[1, df_val_Rs$sample] + 1
df_val_Rs$class <- as.factor(class)
df_val_Rs[,c("class1", "class2")] <- lapply(df_val_Rs[,c("class1", "class2")], factor)
val_class_mean_Rs <- df_val_Rs %>% group_by(precision, class1, class2, class) %>% summarise(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(prob=mean(
```

'summarise()' has grouped output by 'precision', 'class1', 'class2'. You can override using the '.gr

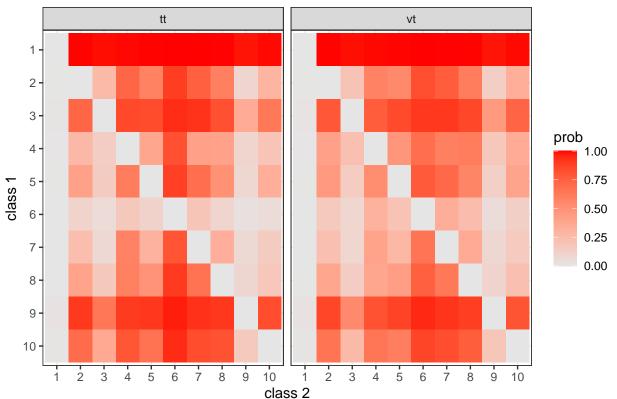
```
df_train_Rs <- melt(ens_Rs$train_training)
names(df_train_Rs) <- c("replication", "precision", "sample", "class1", "class2", "prob")
class <- nets_outputs$test_labels[1, df_train_Rs$sample] + 1
df_train_Rs$class <- as.factor(class)
df_train_Rs[,c("class1", "class2")] <- lapply(df_train_Rs[,c("class1", "class2")], factor)
train_class_mean_Rs <- df_train_Rs %>% group_by(precision, class1, class2, class) %>% summarise(prob=me
```

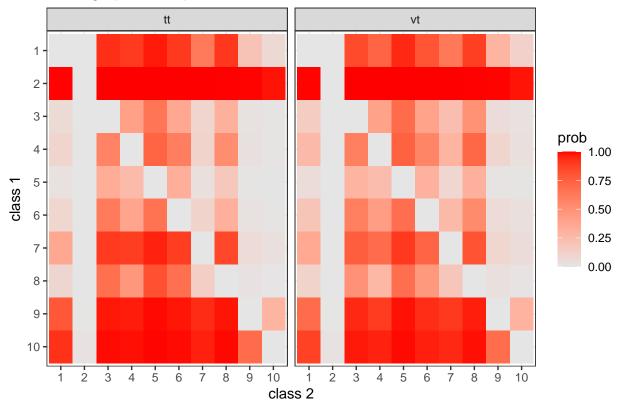
'summarise()' has grouped output by 'precision', 'class1', 'class2'. You can override using the '.gr

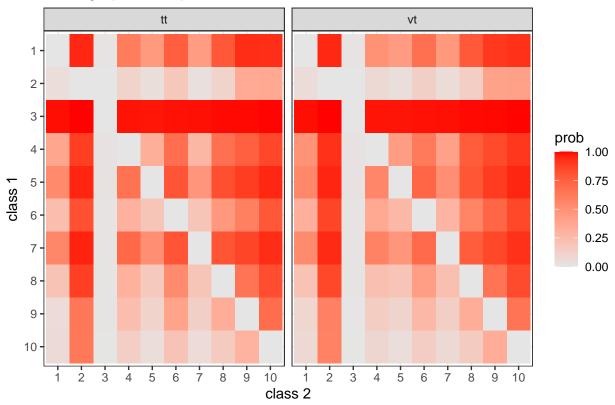
```
val_class_mean_Rs$train_type <- "vt"
train_class_mean_Rs$train_type <- "tt"
class_mean_Rs <- rbind(val_class_mean_Rs, train_class_mean_Rs)

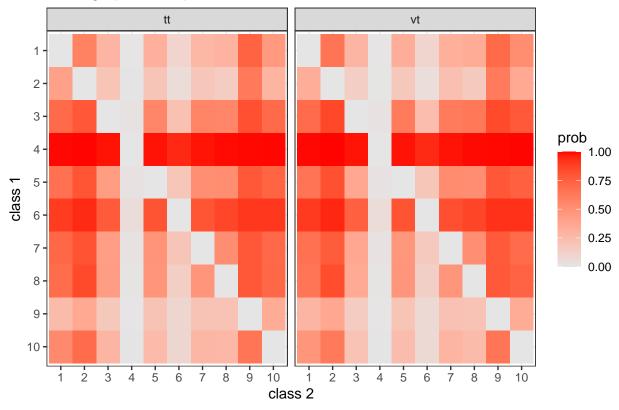
df_aggr_Rs_diff <- class_mean_Rs %>% pivot_wider(names_from = train_type, values_from = prob) %>% mutat

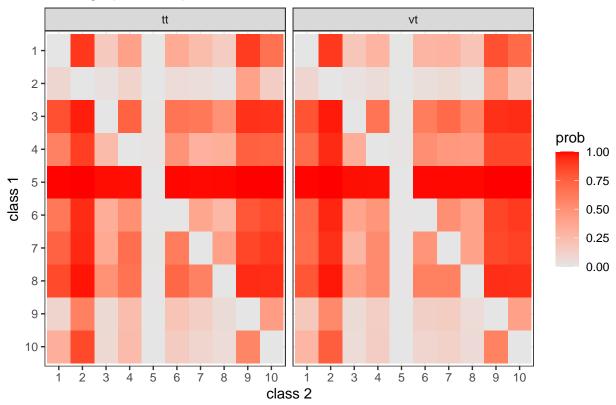
for (cls in 1:classes)
{
    cur_class_Rs <- class_mean_Rs %>% filter(class == cls)
    plot_cls <- ggplot(cur_class_Rs, aes(x = class2, y = class1)) +
        geom_raster(aes(fill=prob)) +
        facet_wrap(~train_type) +
        scale_fill_gradient(low="grey90", high="red", limits=c(0, 1)) +
        scale_y_discrete(limits=rev) +
        labs(x="class 2", y="class 1", title=paste("Average pairwise probabilities - class ", cls)) +
        theme_bw()
    print(plot_cls)
}</pre>
```

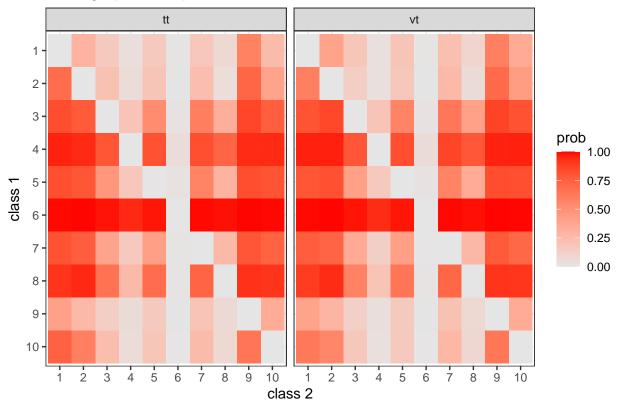


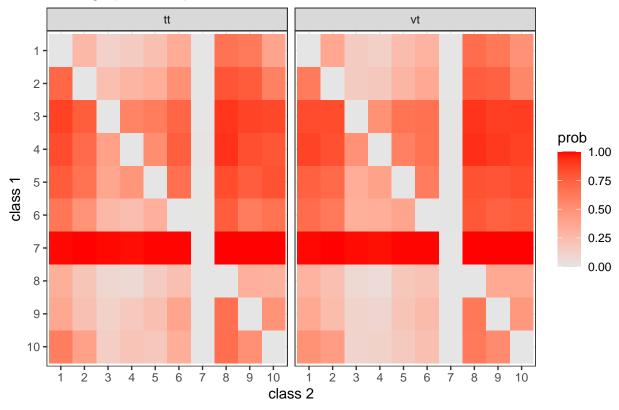


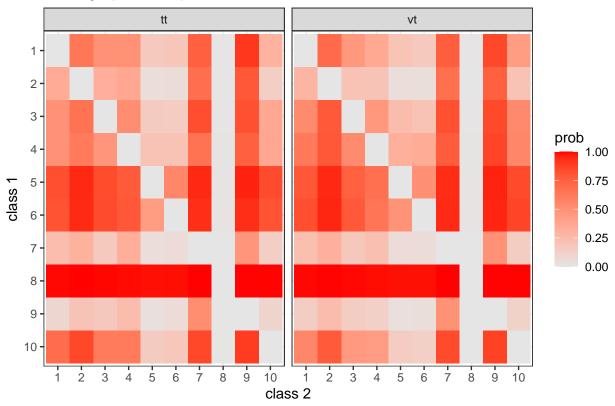


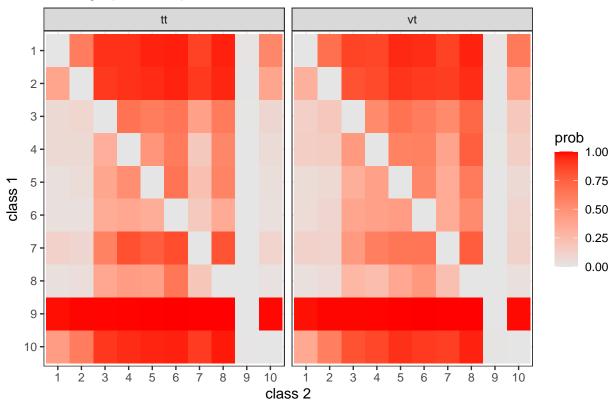


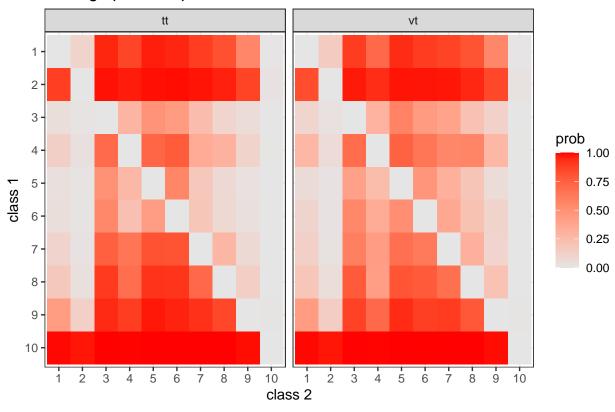






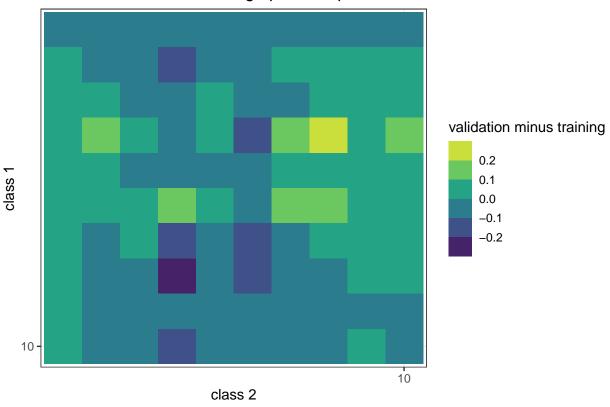


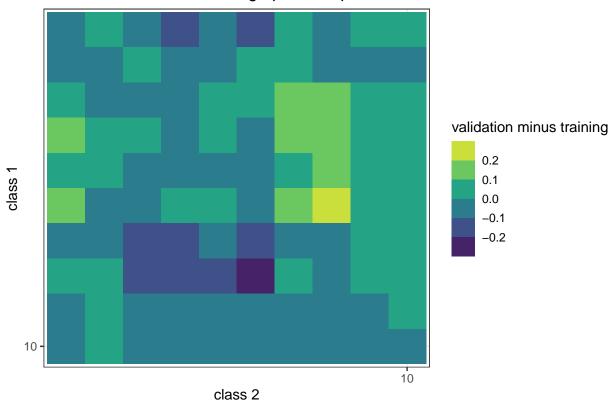


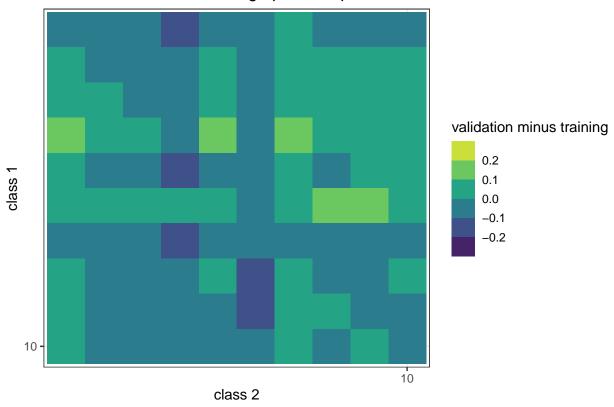


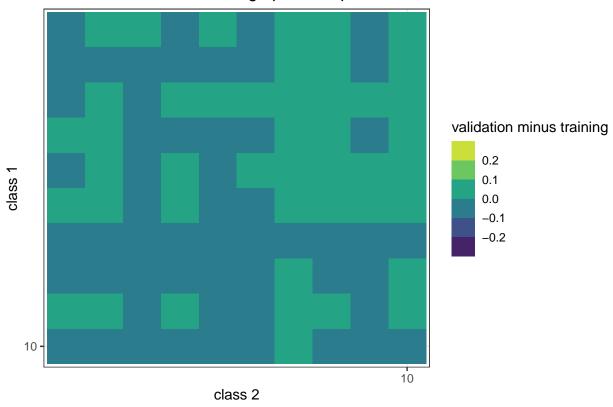
```
for (cls in 1:classes)
{
    cur_class_Rs <- df_aggr_Rs_diff %>% filter(class == cls)
    plot_cls <- ggplot(cur_class_Rs, aes(x = class2, y = class1)) +
        geom_raster(aes(fill=val_min_train)) +
        scale_fill_binned(type="viridis", limits=c(-0.3, 0.3), name="validation minus training") +
        scale_y_discrete(limits=rev, breaks=seq(0, classes, 10)) +
        scale_x_discrete(breaks=seq(0, classes, 10)) +
        labs(x="class 2", y="class 1", title=paste("Differences between average pairwise probabilities - cl
        theme_bw()

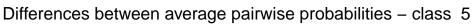
    print(plot_cls)
}</pre>
```

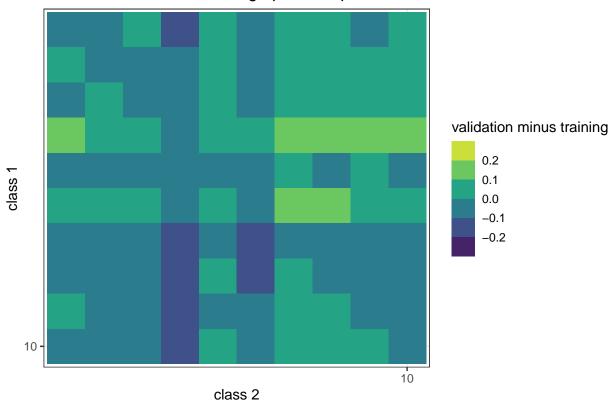


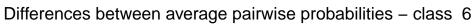


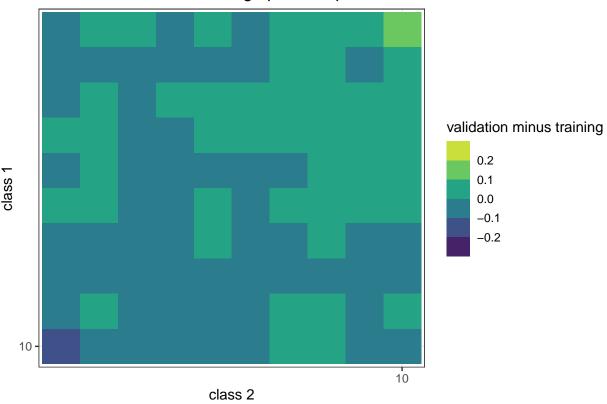


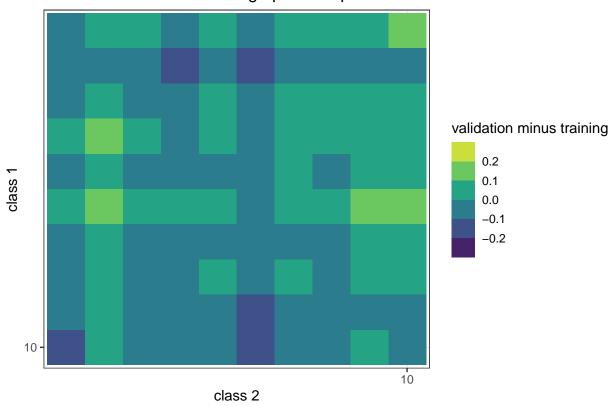


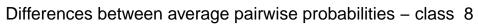


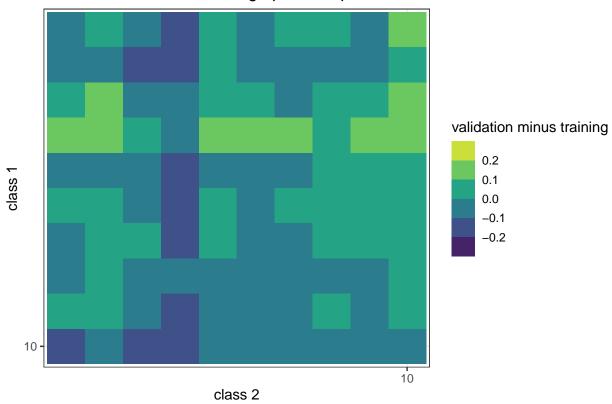


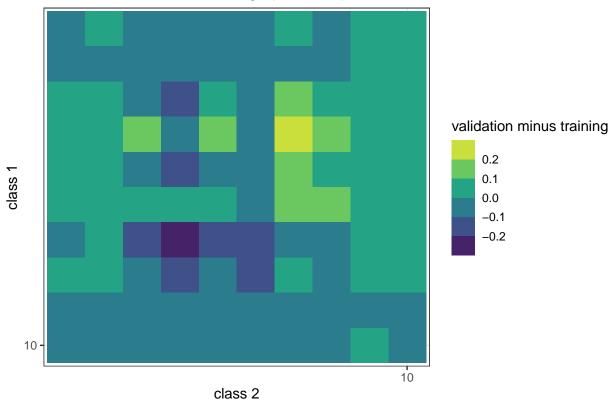


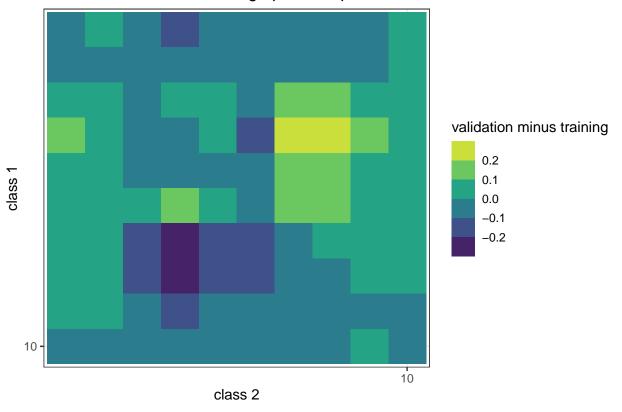






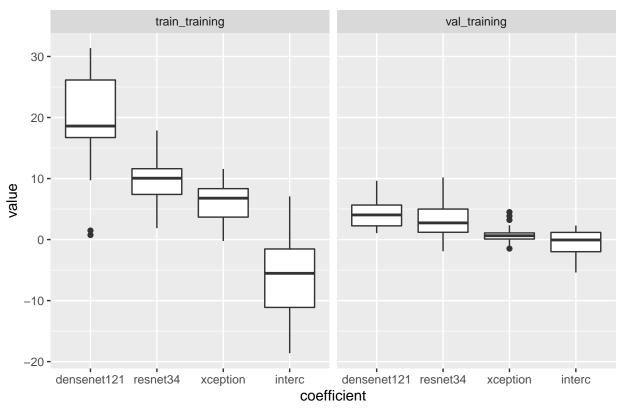


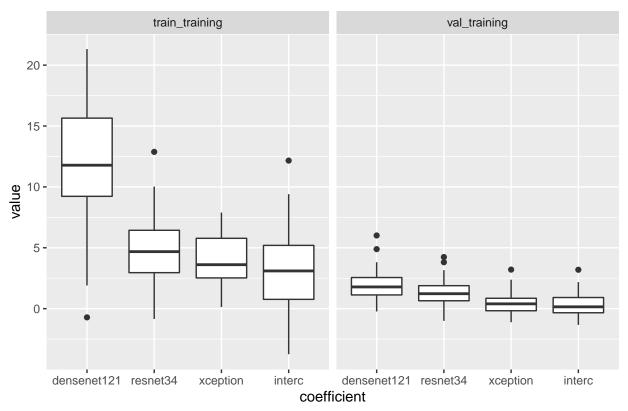


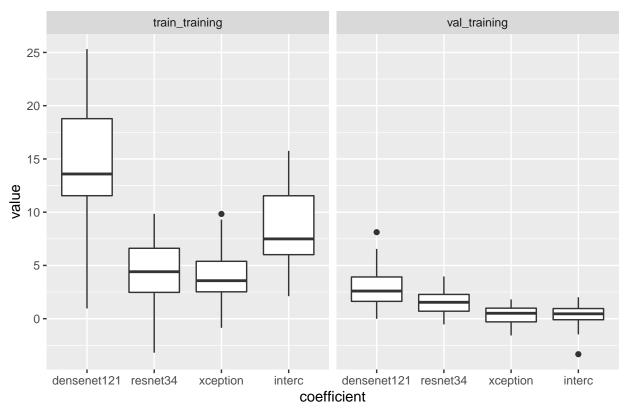


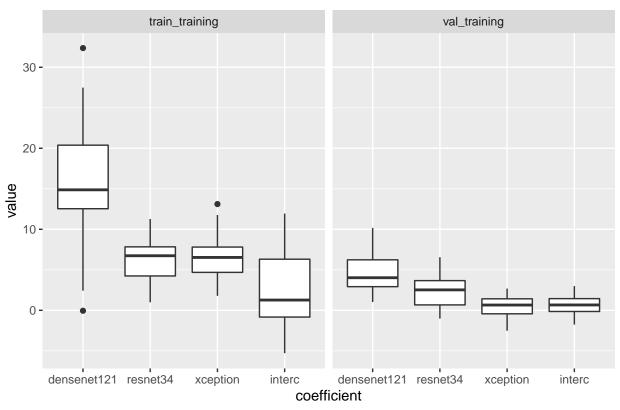
lda_coefs <- load_lda_coefs(base_dir, repls)</pre>

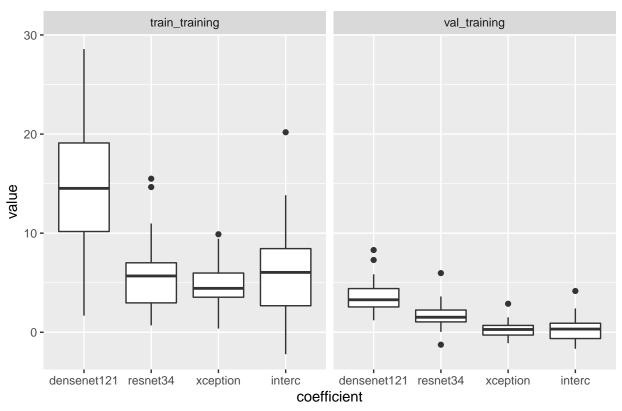
```
for (cl1 in 1:(classes - 1))
{
   for (cl2 in (cl1 + 1):classes)
   {
      cur_plt <- lda_coefs %>% filter(class1 == cl1 & class2 == cl2) %>% ggplot() + geom_boxplot(aes(x=coefficients for class", cl1, "vs", cl2))
      print(cur_plt)
   }
}
```

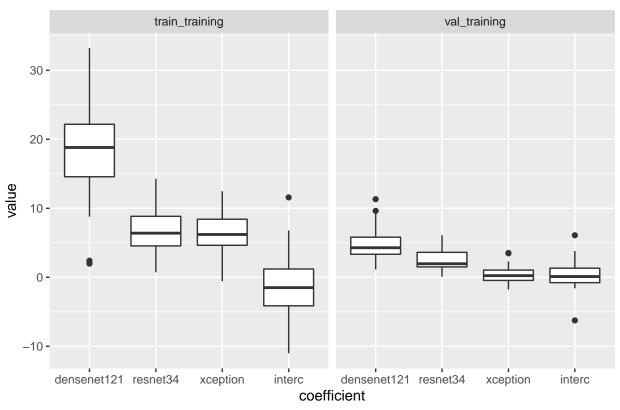


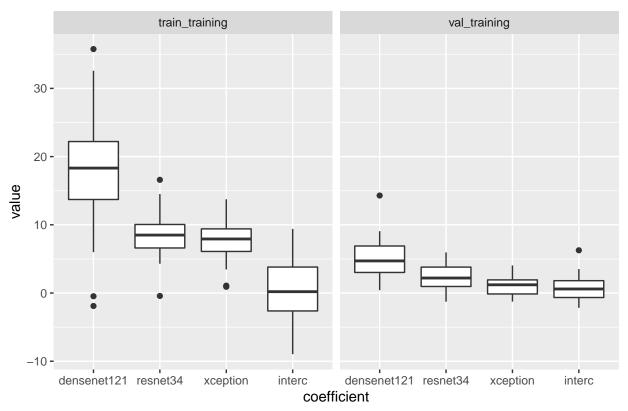


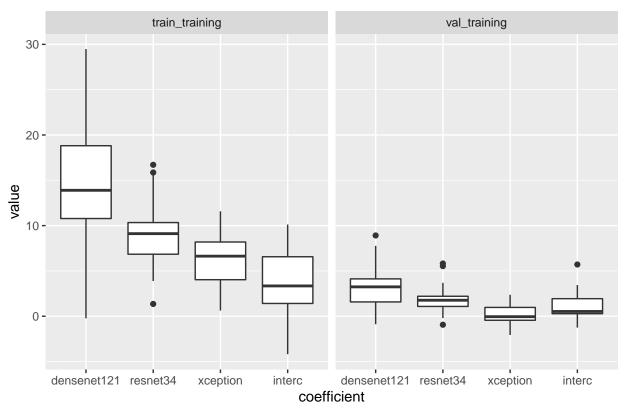


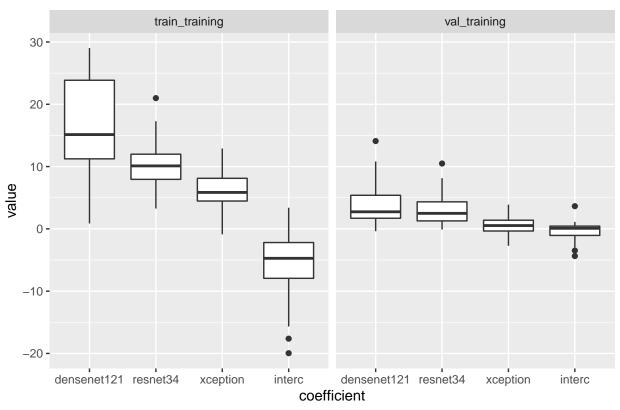


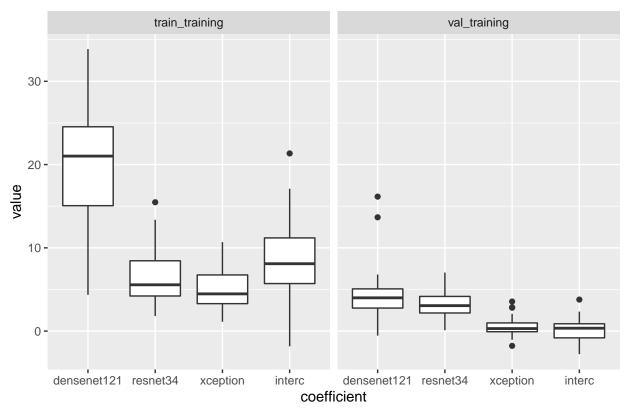


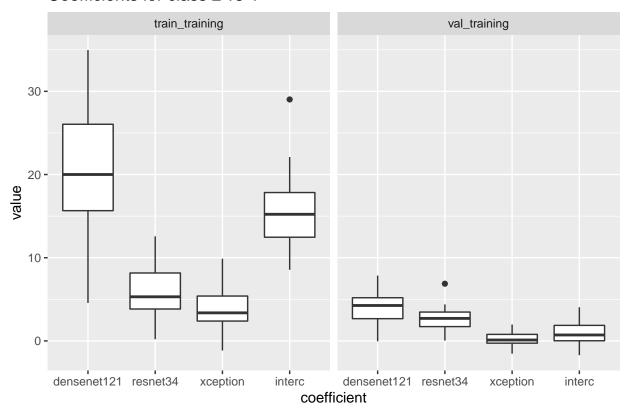


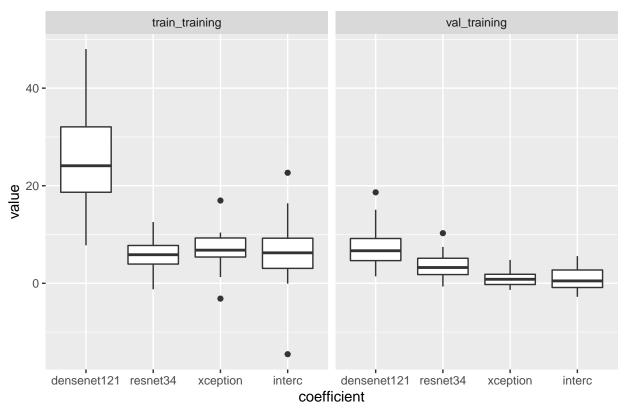


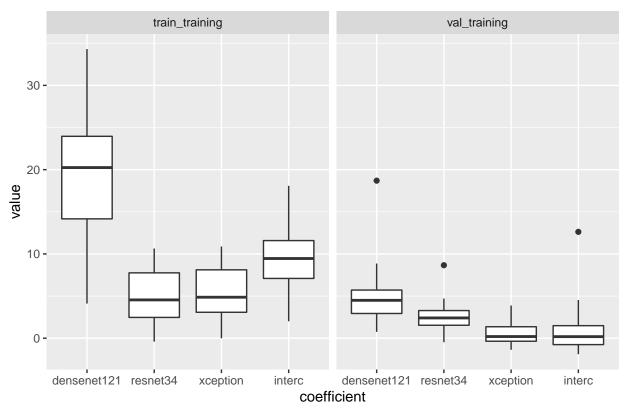


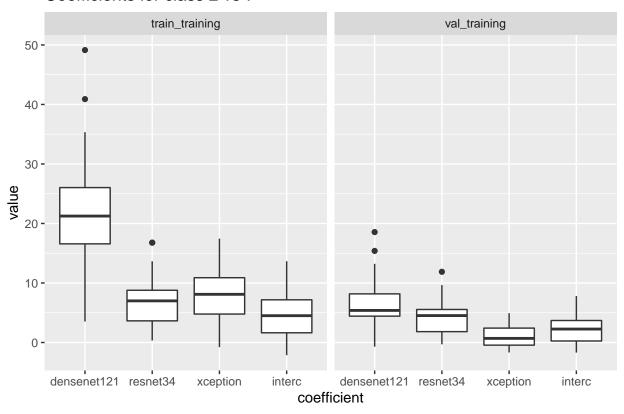


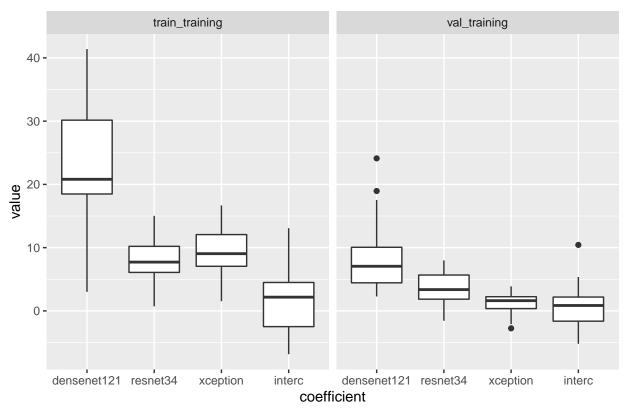


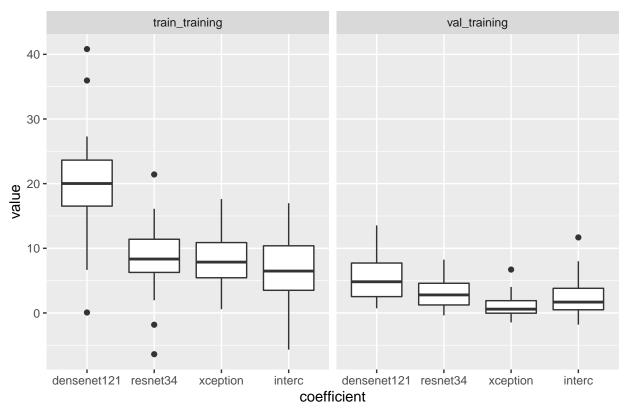


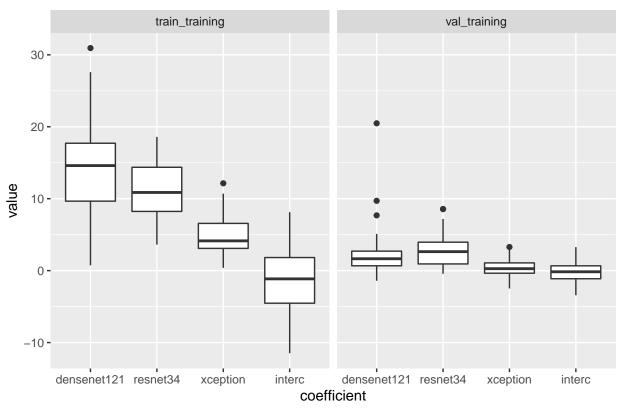


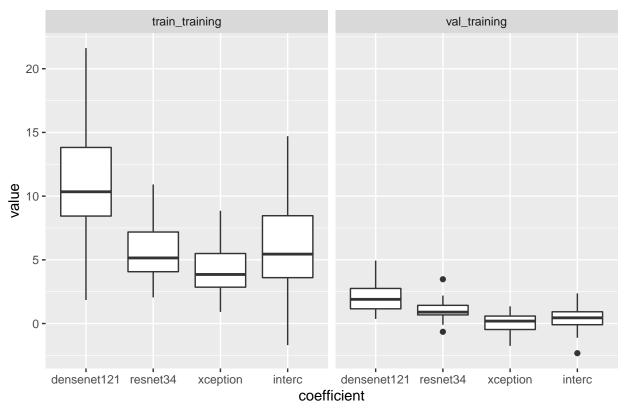


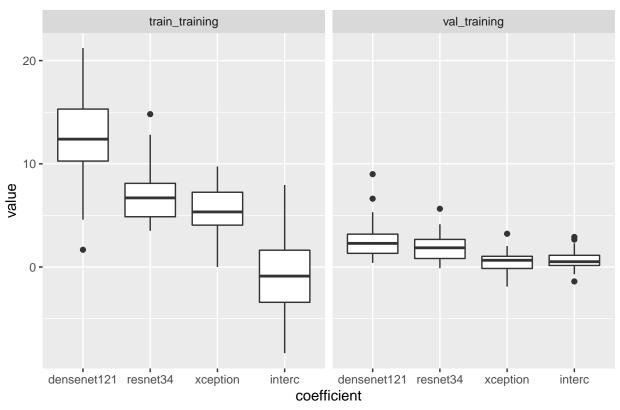


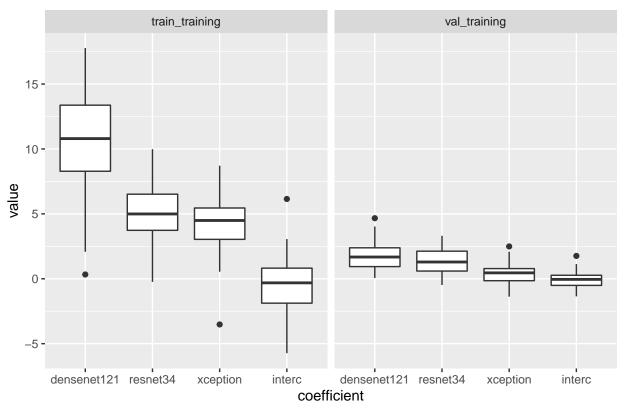


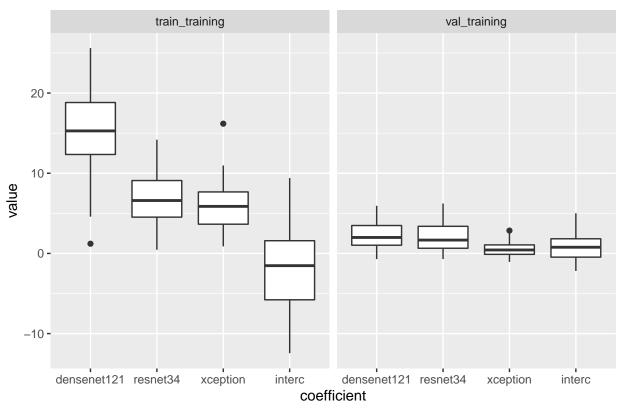


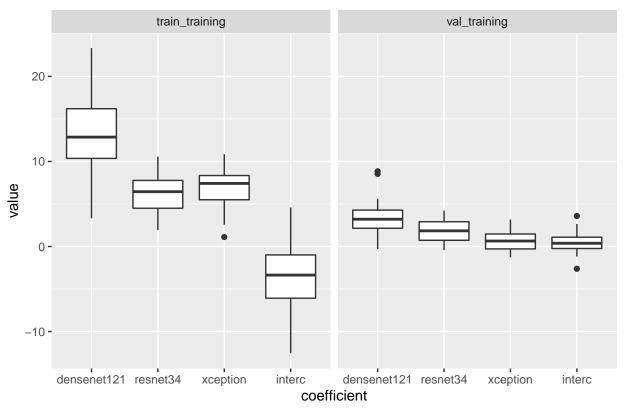


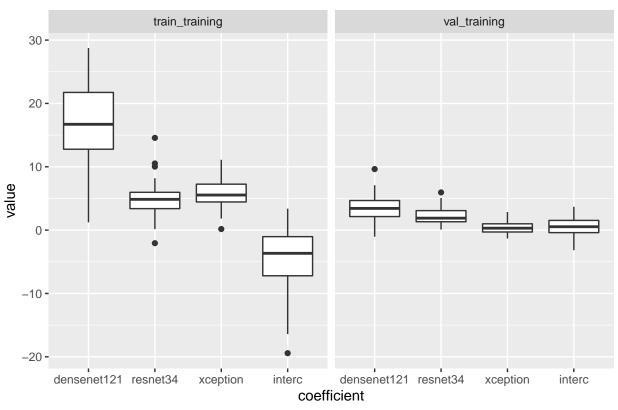


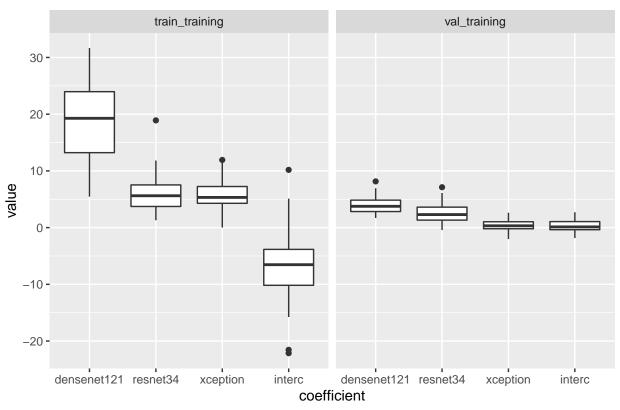


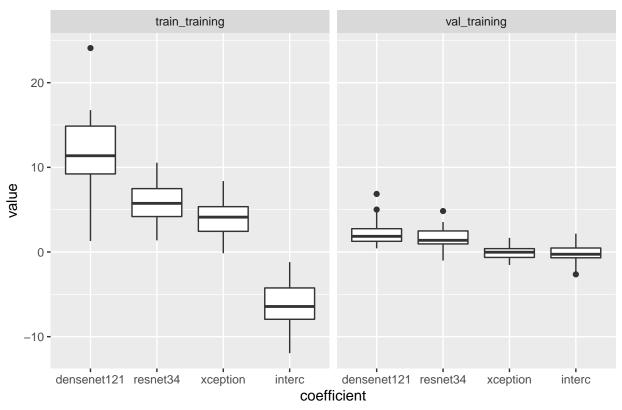


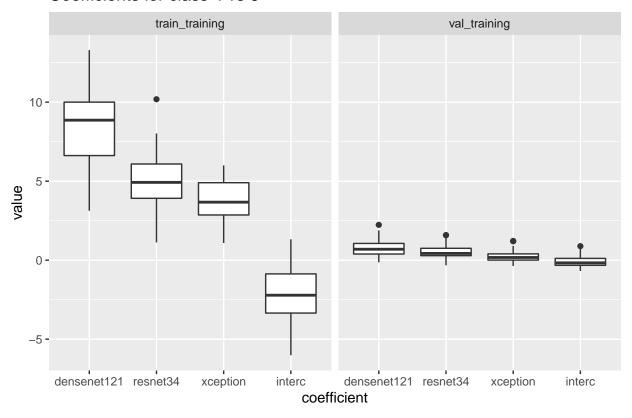


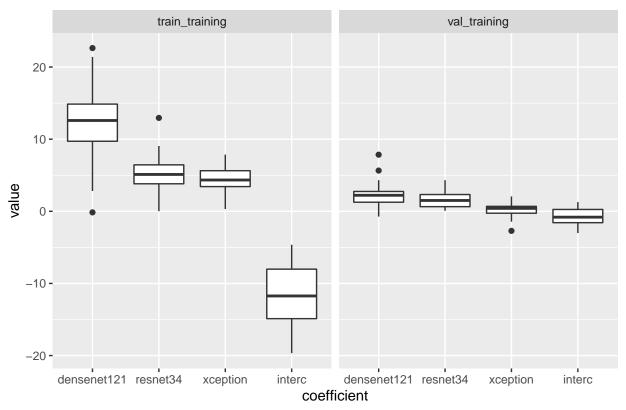


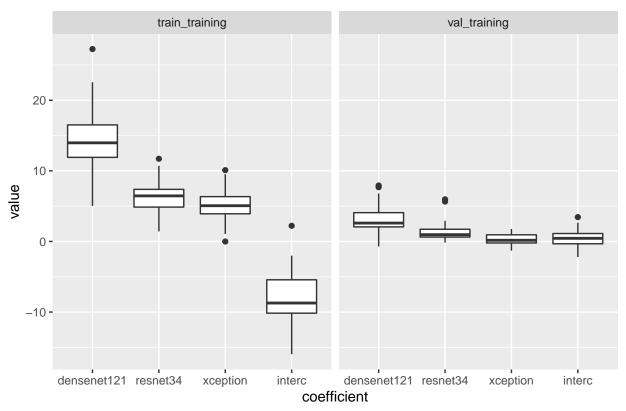


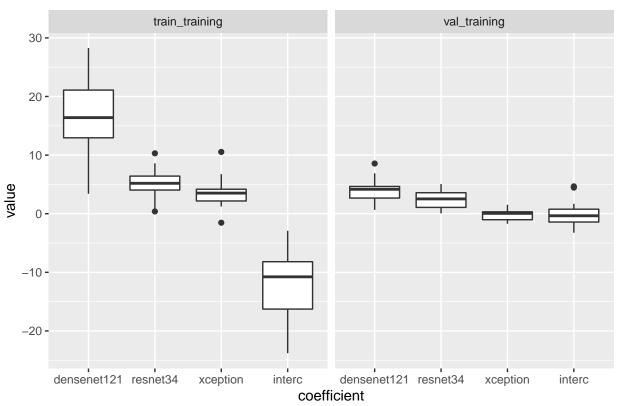


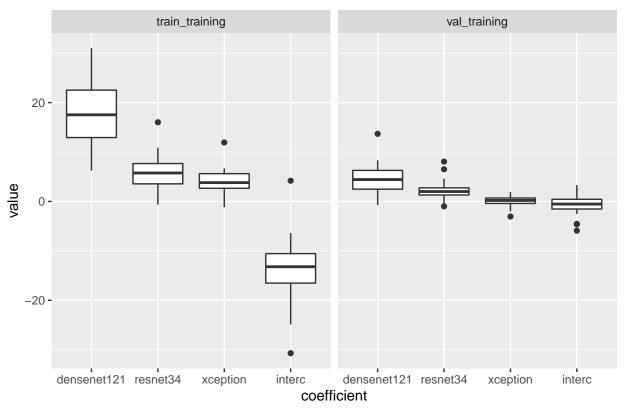


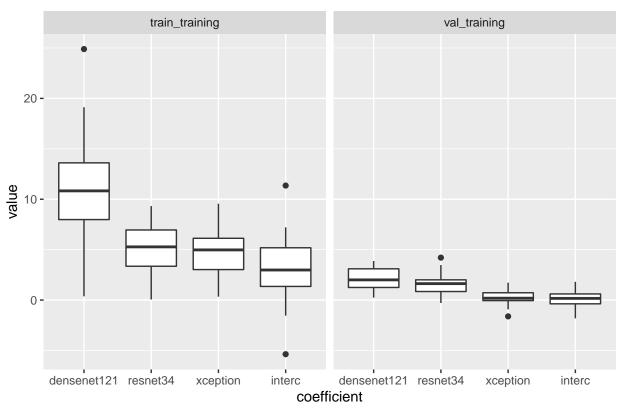


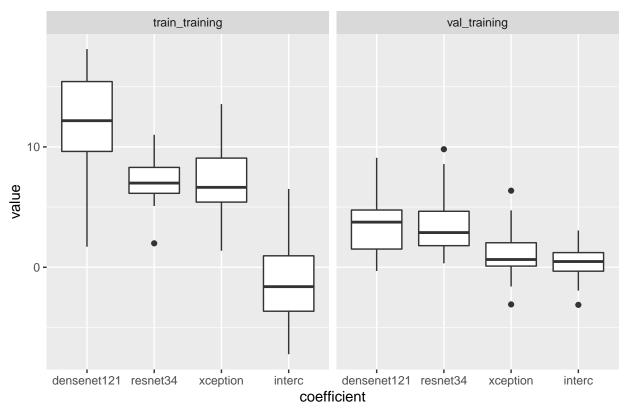


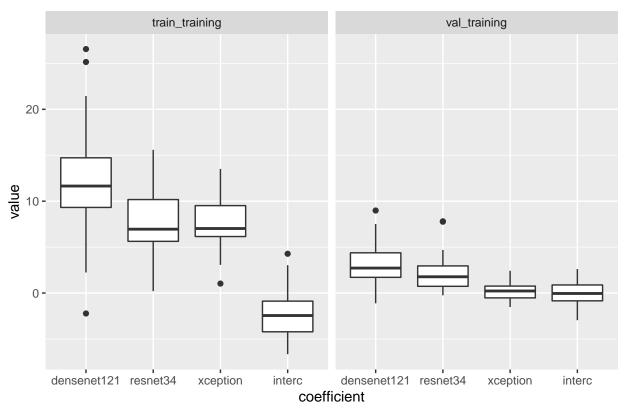


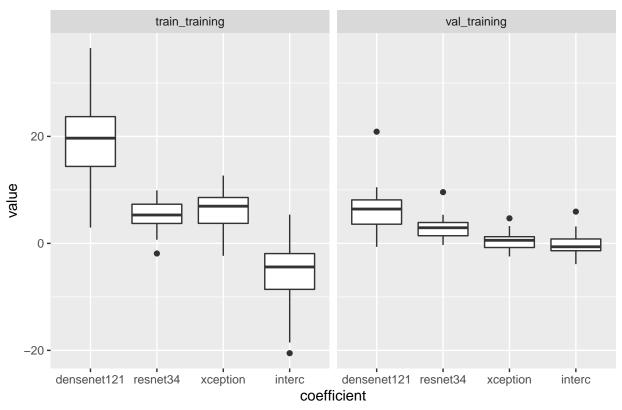


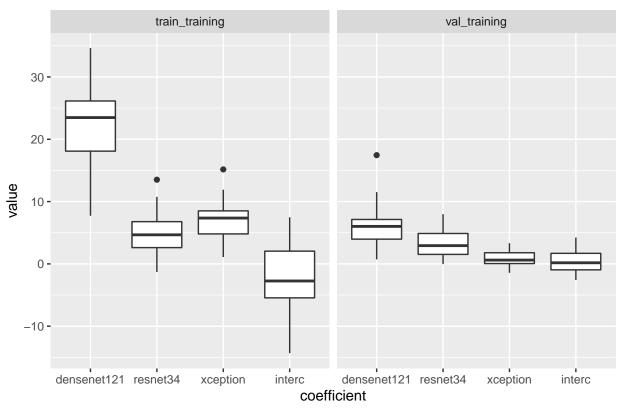


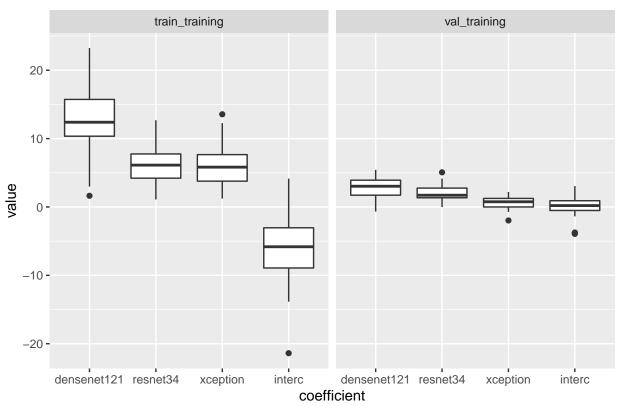


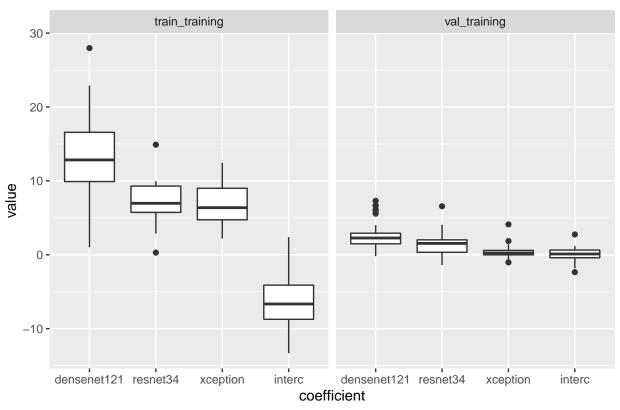


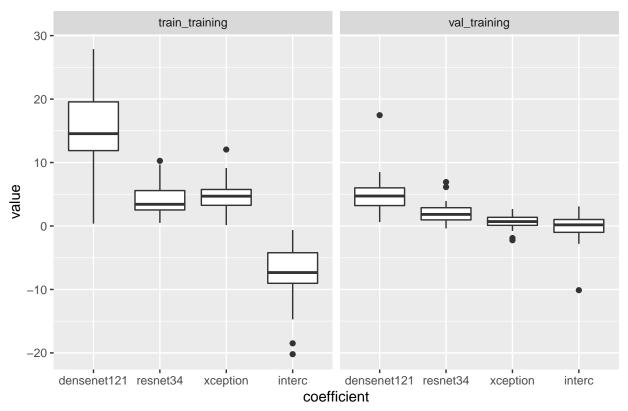


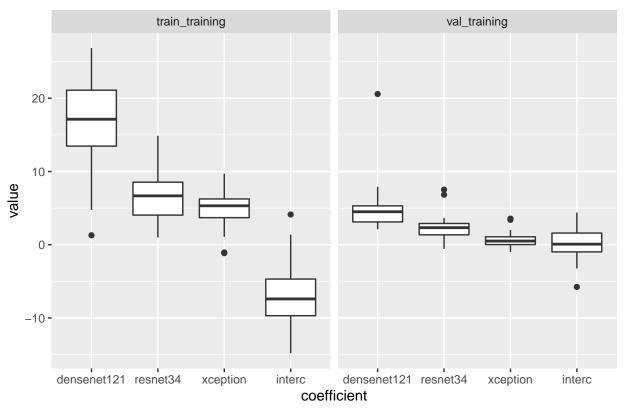


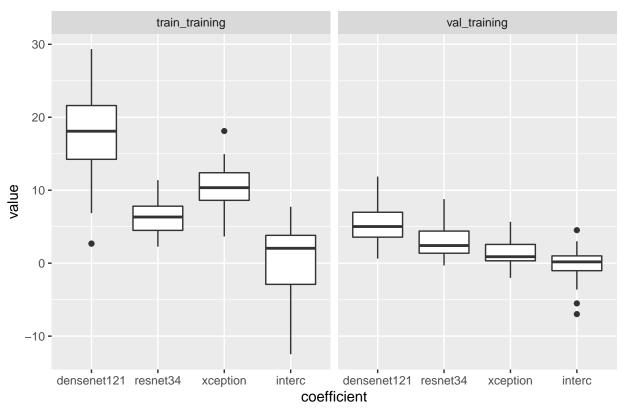


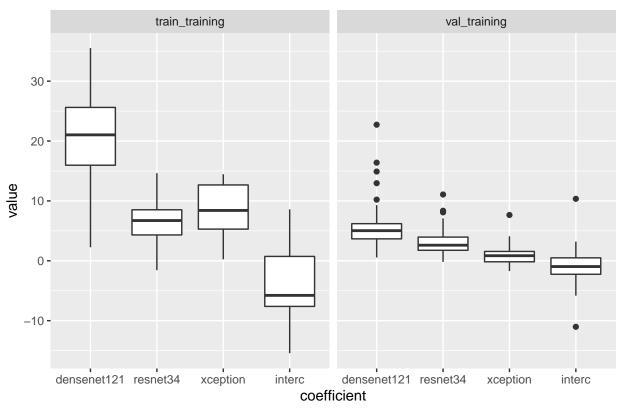


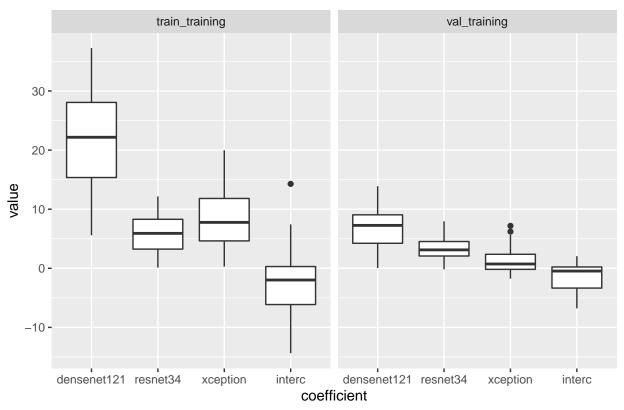


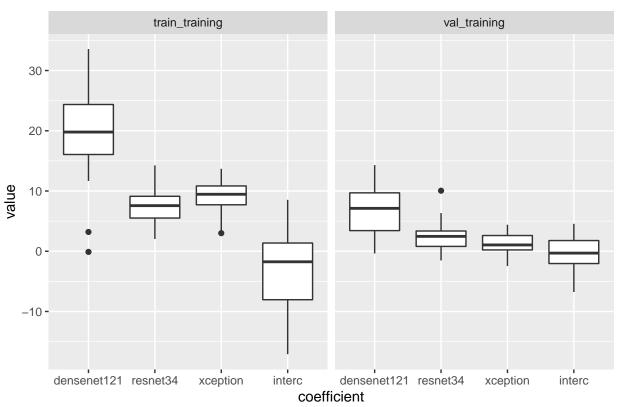


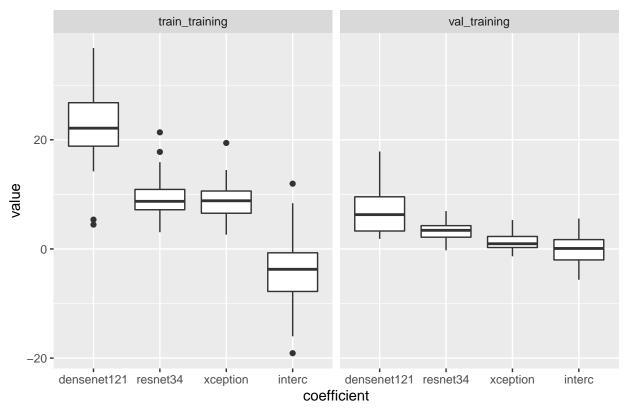


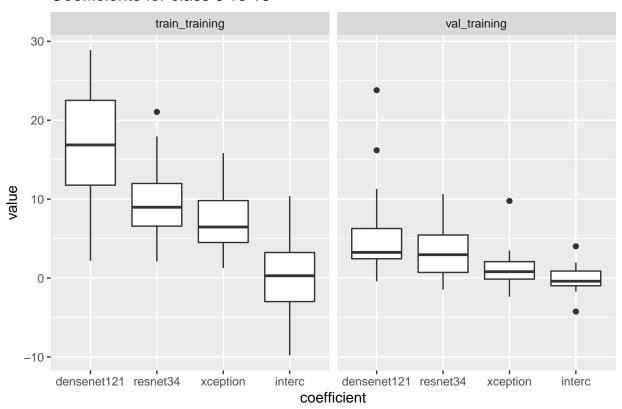










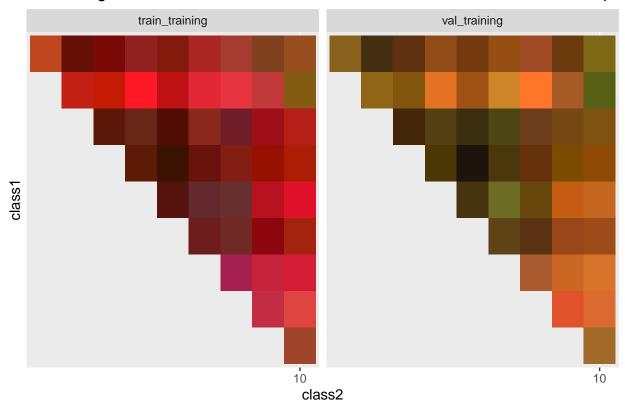


avg_lda_coefs <- lda_coefs %>% filter(coefficient != "interc") %>% group_by(class1, class2, precision,

'summarise()' has grouped output by 'class1', 'class2', 'precision', 'train_type'. You can override

```
raster_plot <- ggplot(avg_lda_c_w) +
  geom_tile(aes(x=class2, y=class1, fill=rgb(densenet121, resnet34, xception))) +
  scale_y_discrete(limits=rev, breaks=seq(0,classes, 10)) + scale_x_discrete(breaks=seq(0,classes, 10))
raster_plot</pre>
```

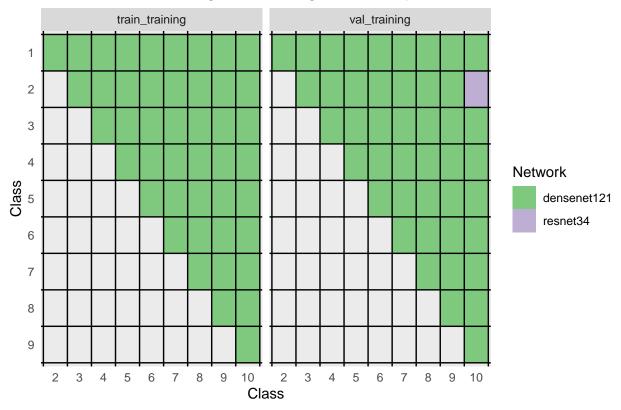
RGB image formed from Ida coefficients for networks densenet, resnet, xceptic



Correspondence between colors and networks is red - densenet, green - resnet, blue - xception.

```
coefs_grid <- ggplot(avg_lda_c_w, aes(x=class2, y=class1, fill=top_net)) +</pre>
 geom_raster() +
  scale_fill_brewer(type="qual") +
  facet_wrap(~train_type) +
  scale_y_discrete(limits=rev) +
  geom_vline(xintercept=seq(-0.5, 9.5, 1.0)) +
  geom_hline(yintercept=seq(-0.5, 9.5, 1.0)) +
  guides(fill=guide_legend(title="Network")) +
 xlab("Class") +
 ylab("Class") +
  ggtitle("Network with highest lda weight for class pairs") +
  theme(plot.title = element_text(hjust = 0.5),
       axis.ticks = element_blank(),
       panel.grid.major = element_blank(),
       panel.grid.minor = element_blank())
coefs_grid
```

Network with highest Ida weight for class pairs



Densenet is clearly dominant for both LDA training methodologies.