

Outputs inspection half CIFAR100

```
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(ggVennDiagram)
```

```
## Warning: package 'ggVennDiagram' was built under R version 4.0.5
```

```
library(stringr)
```

```
library(abind)
```

```
## Warning: package 'abind' was built under R version 4.0.3
```

```
library(patchwork)
```

```
## Warning: package 'patchwork' was built under R version 4.0.3
```

```
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:ggVennDiagram':
```

```
##
```

```
## circle
```

```
## The following object is masked from 'package:dplyr':
```

```
##
```

```
## between
```

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

```
## Warning: package 'reshape2' was built under R version 4.0.3
```

```
##
```

```
## Attaching package: 'reshape2'
```

```
## The following object is masked from 'package:tidyr':
```

```
##
```

```
## smiths
```

Visualization on both CIFAR 10 and 100. To better understand the differences between `train_training` and `val_training` LDA training methodologies, we focus on pairwise predictions. This allows us to observe the outputs of LDA models without interference from the coupling methods.

CIFAR 10 - validation set of size 500

```
base_dir <- "../data/data_train_val_c10"
```

```
repls <- 0:29
```

```
folds <- 0:0
```

```
classes <- 10
```

```
net_pw_results <- read.csv(file.path(base_dir, "net_pw_accuracies.csv"))
```

```
ens_pw_results <- read.csv(file.path(base_dir, "ensemble_pw_accuracies.csv"))
```

```
net_pw_results[, c("class1", "class2")] <- lapply(net_pw_results[, c("class1", "class2")], as.factor)
```

```
ens_pw_results[, c("class1", "class2")] <- lapply(ens_pw_results[, c("class1", "class2")], as.factor)
```

```

for (ri in repls)
{
  net_plot <- net_pw_results %>% filter(repli == ri) %>%
    ggplot(mapping=aes(x=class2, y=class1, fill=accuracy)) + geom_raster() + facet_wrap(~network) +
    xlab("Class") +
    ylab("Class") +
    scale_y_discrete(limits=rev) +
    scale_fill_binned(type="viridis", limits=c(0.92, 1), name="accuracy") +
    coord_fixed() +
    ggtitle("Pairwise accuracies networks") +
    theme(plot.title = element_text(hjust = 0.5),
          axis.ticks = element_blank(),
          panel.grid.major = element_blank(),
          panel.grid.minor = element_blank())

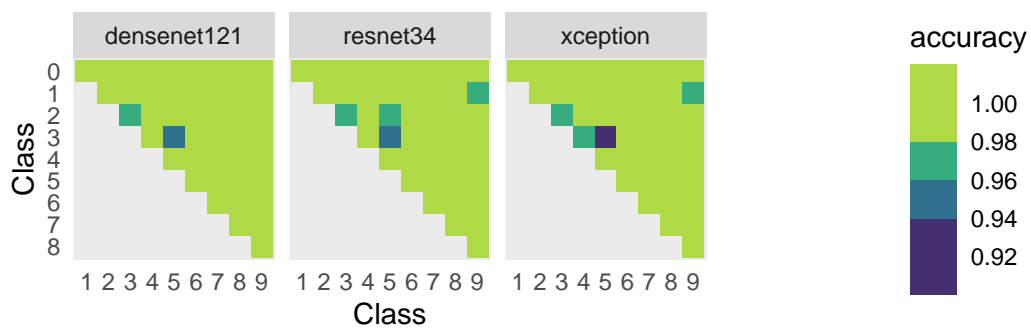
  ens_plot <- ens_pw_results %>% filter(repli == ri & fold == 1) %>%
    ggplot(mapping=aes(x=class2, y=class1, fill=accuracy)) + geom_raster() + facet_wrap(~train_set) +
    xlab("Class") +
    ylab("Class") +
    scale_y_discrete(limits=rev) +
    coord_fixed() +
    ggtitle("Pairwise accuracies ensembles") +
    scale_fill_binned(type="viridis", limits=c(0.92, 1), name="accuracy") +
    theme(plot.title = element_text(hjust = 0.5),
          axis.ticks = element_blank(),
          panel.grid.major = element_blank(),
          panel.grid.minor = element_blank())

  print((net_plot/ens_plot) + plot_annotation(title=paste("Replication ", ri)))
}

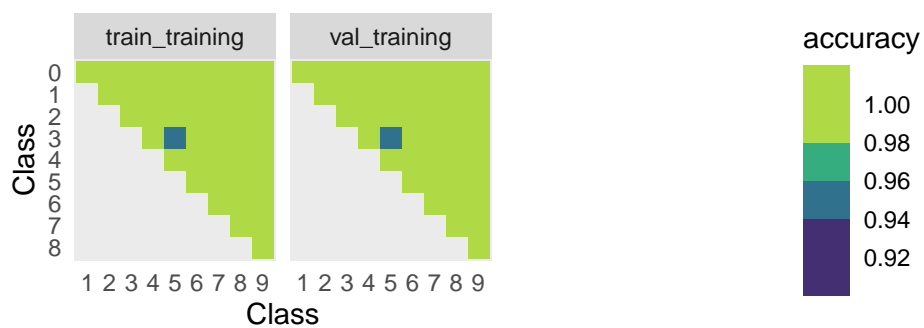
```

Replication 0

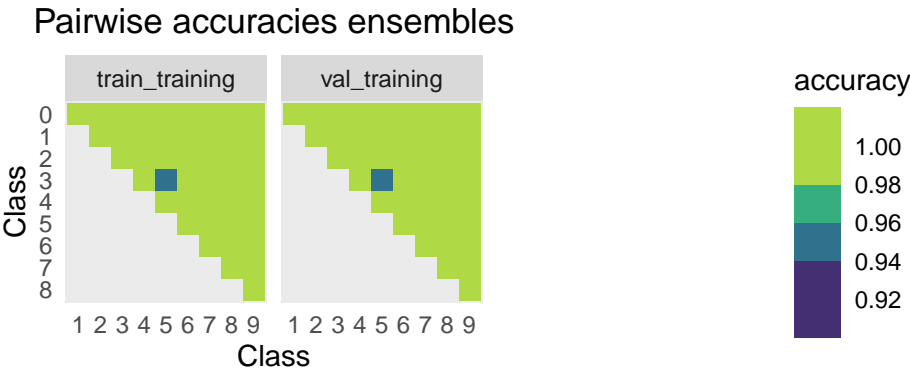
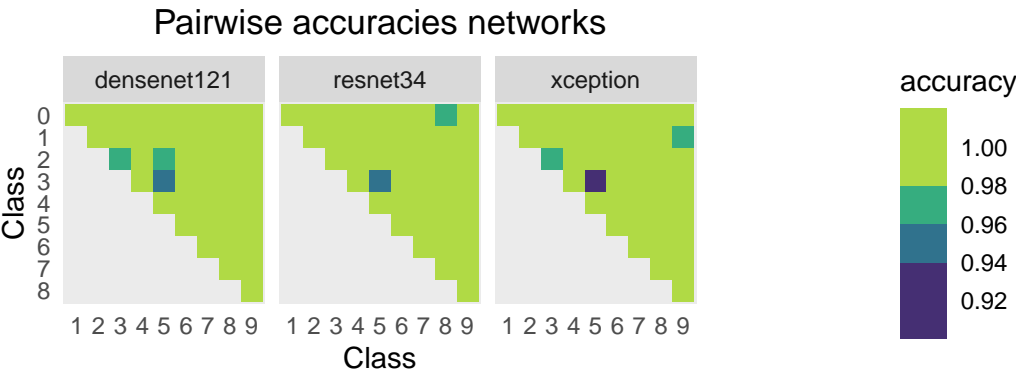
Pairwise accuracies networks



Pairwise accuracies ensembles

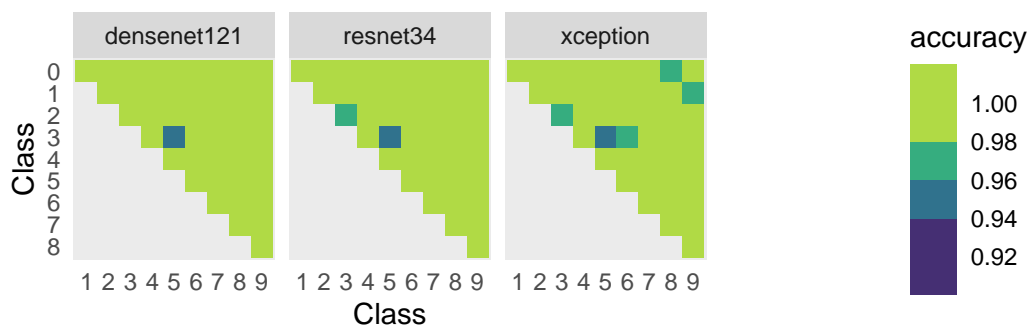


Replication 1



Replication 2

Pairwise accuracies networks

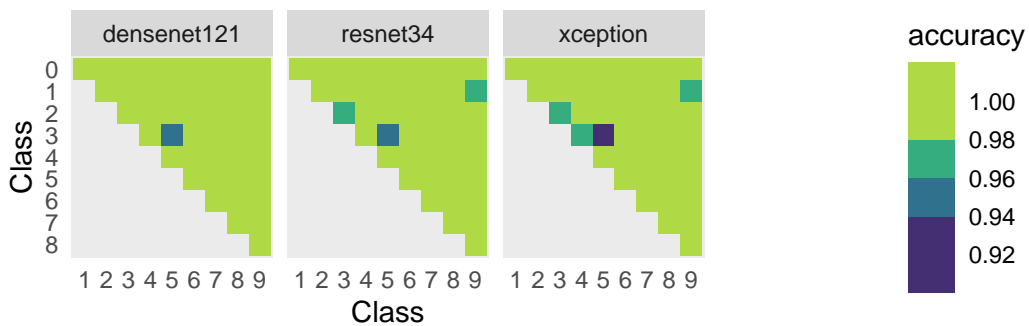


Pairwise accuracies ensembles

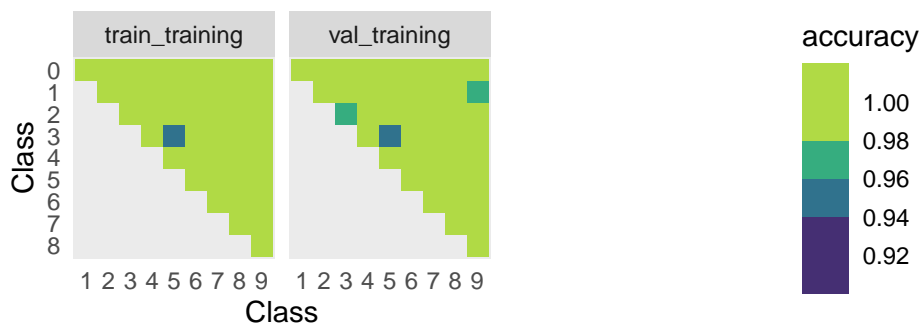


Replication 3

Pairwise accuracies networks

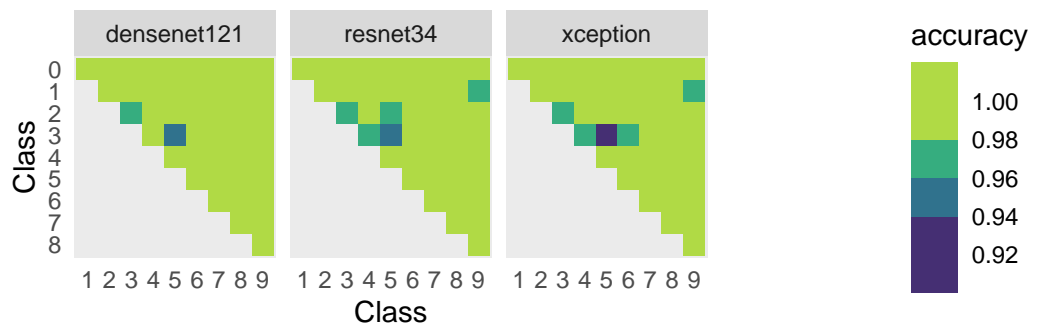


Pairwise accuracies ensembles

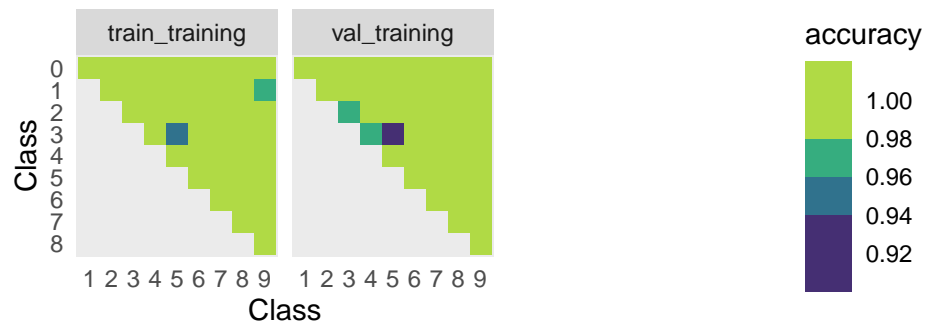


Replication 4

Pairwise accuracies networks

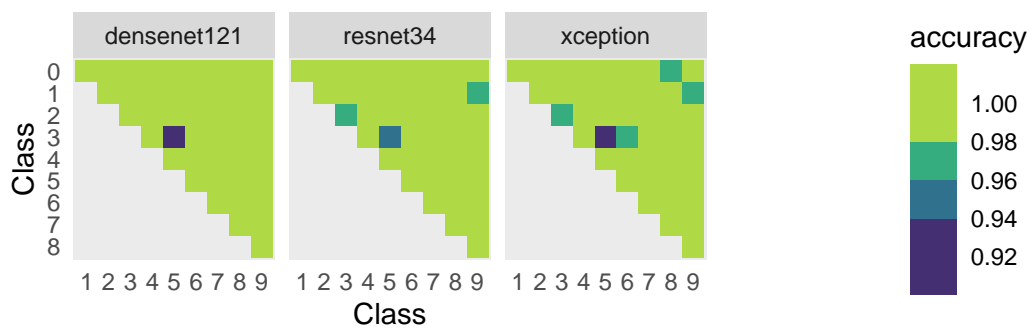


Pairwise accuracies ensembles

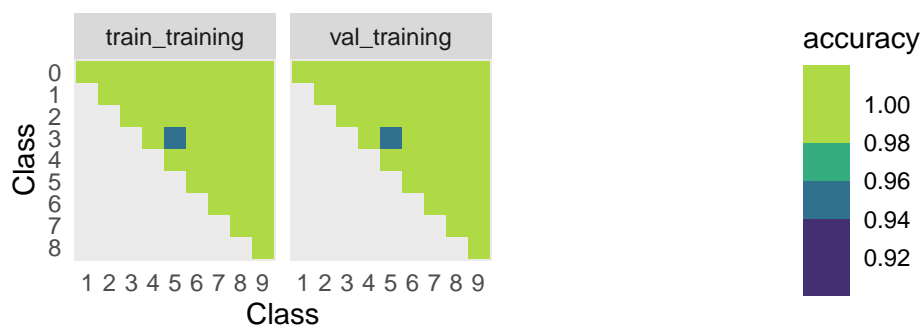


Replication 5

Pairwise accuracies networks

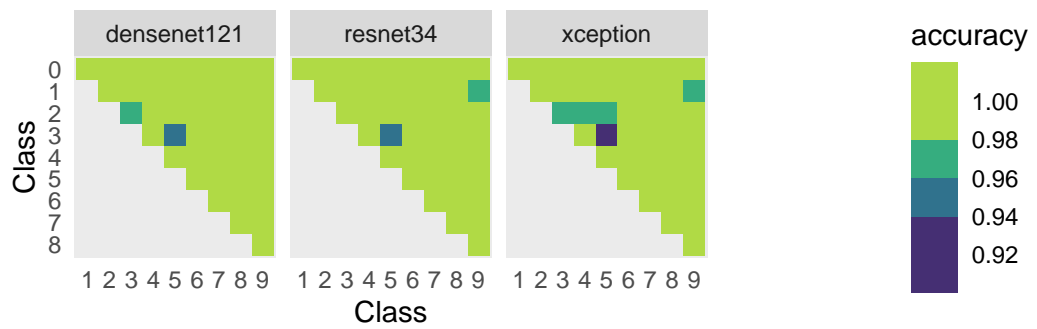


Pairwise accuracies ensembles

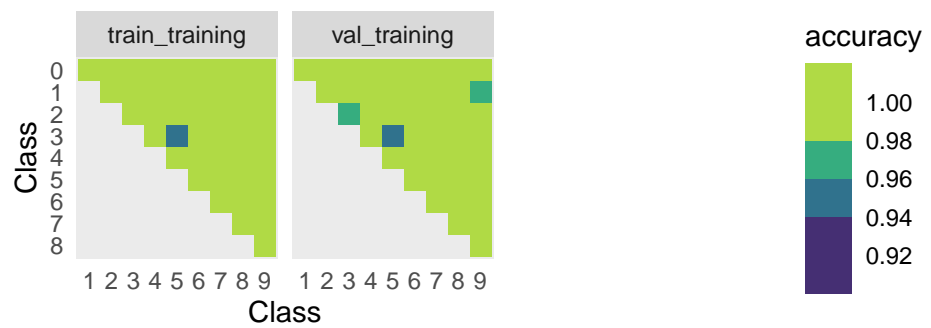


Replication 6

Pairwise accuracies networks

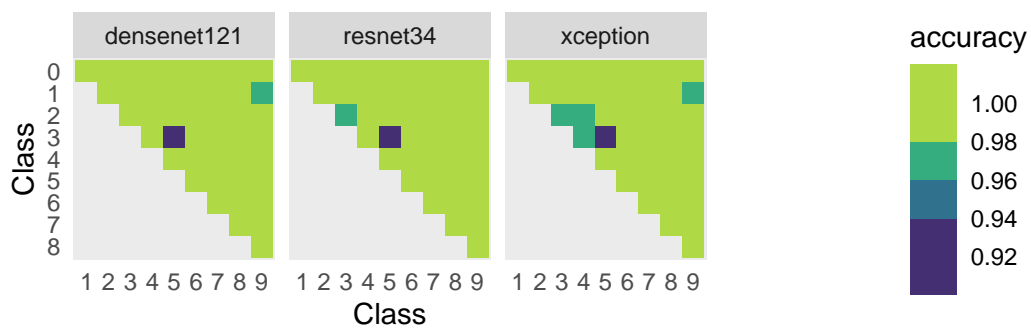


Pairwise accuracies ensembles

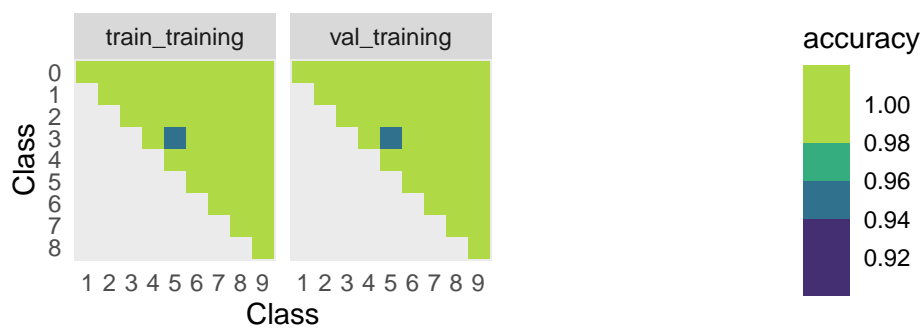


Replication 7

Pairwise accuracies networks

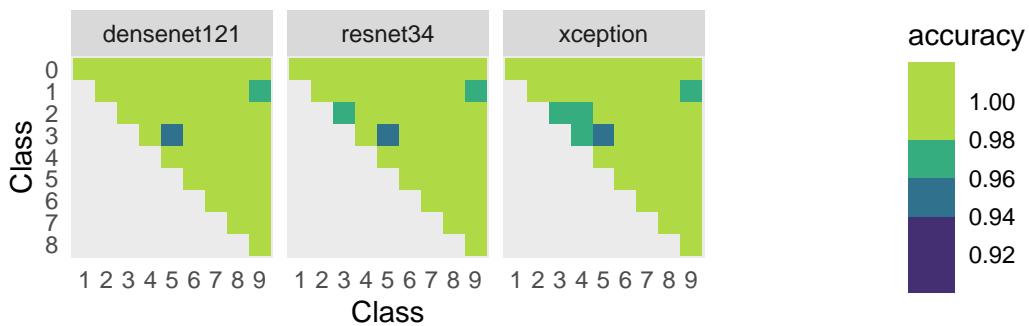


Pairwise accuracies ensembles

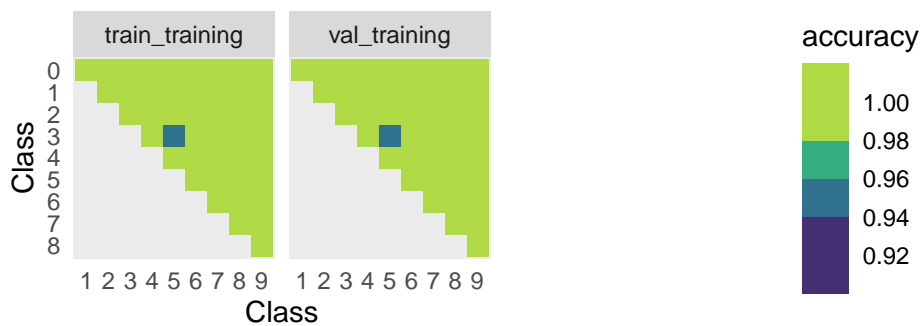


Replication 8

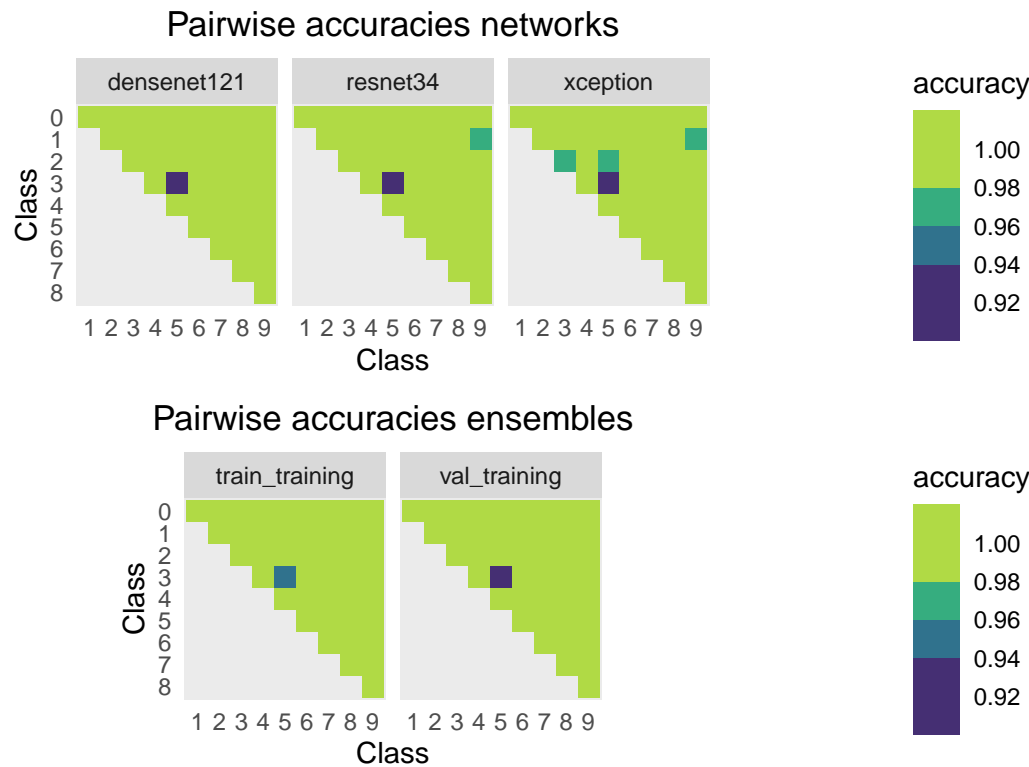
Pairwise accuracies networks



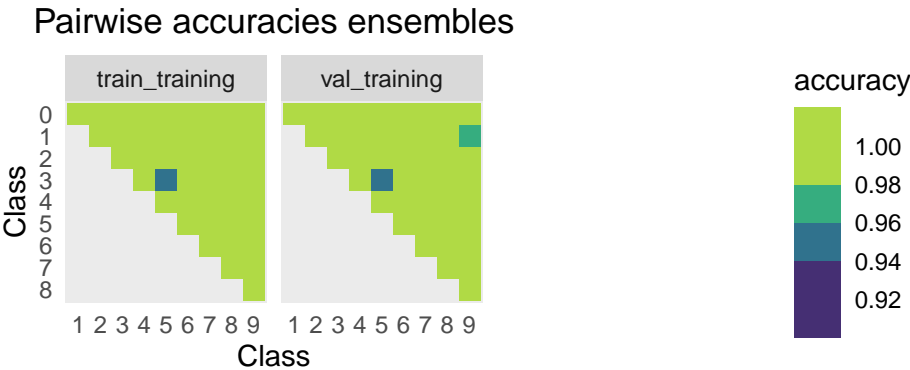
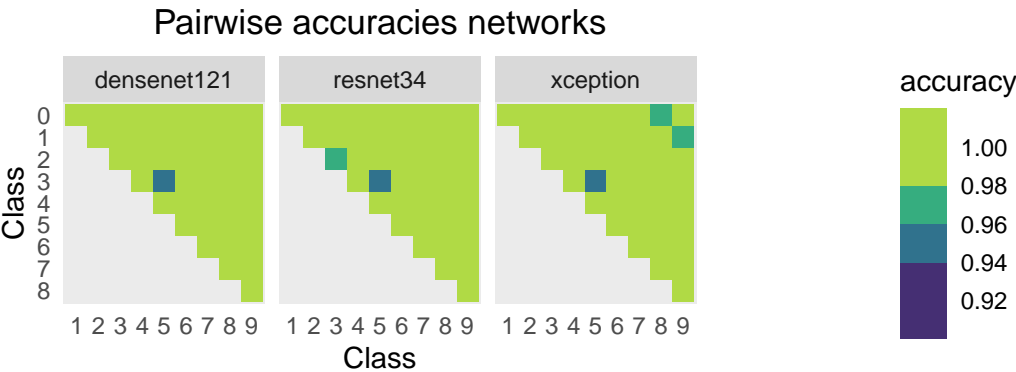
Pairwise accuracies ensembles



Replication 9

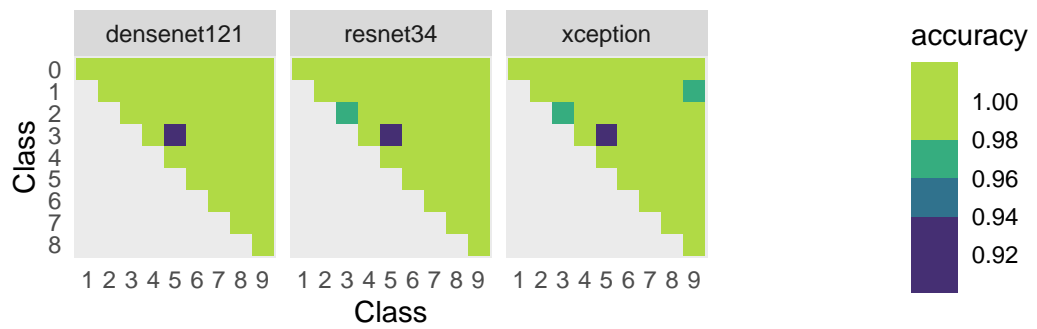


Replication 10

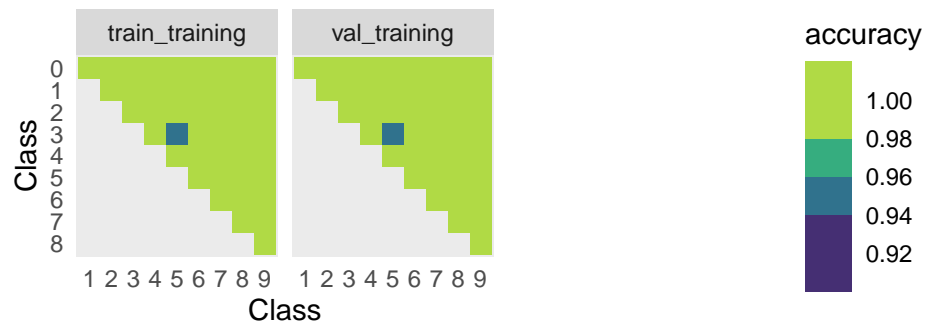


Replication 11

Pairwise accuracies networks

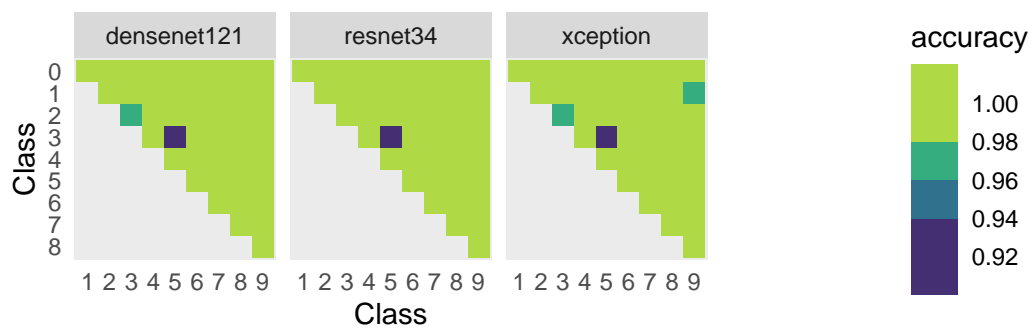


Pairwise accuracies ensembles

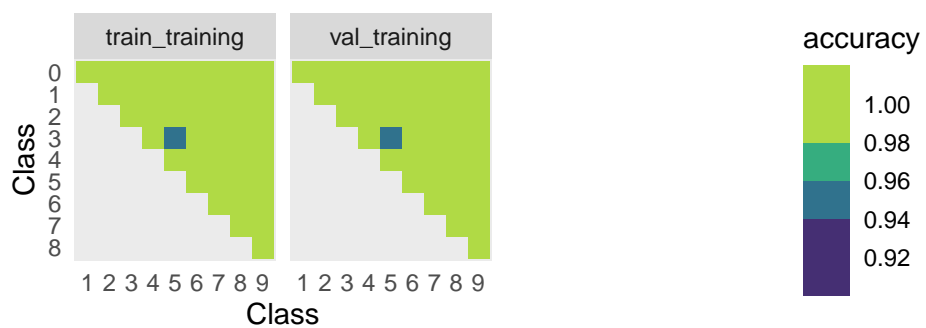


Replication 12

Pairwise accuracies networks

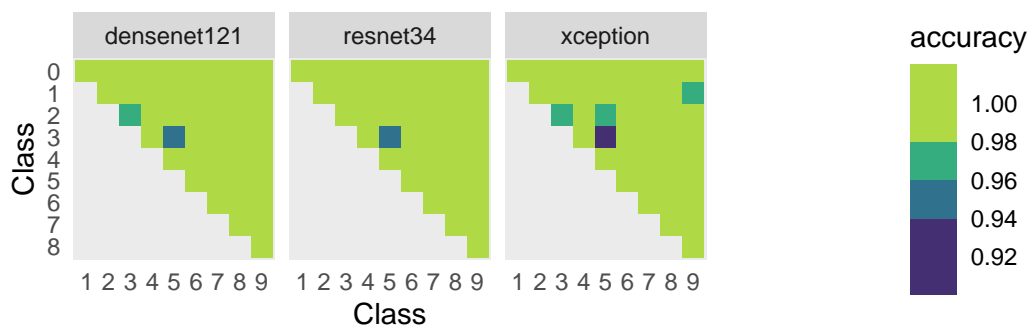


Pairwise accuracies ensembles

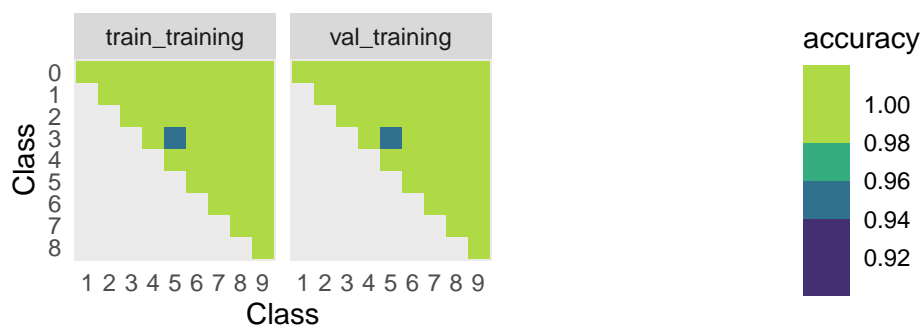


Replication 13

Pairwise accuracies networks

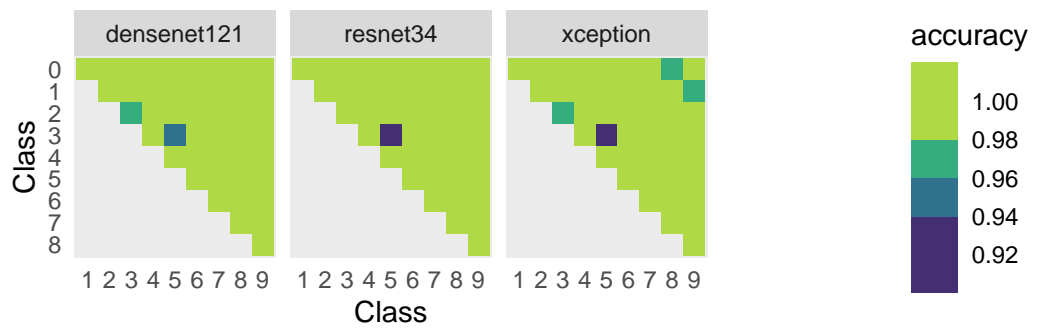


Pairwise accuracies ensembles

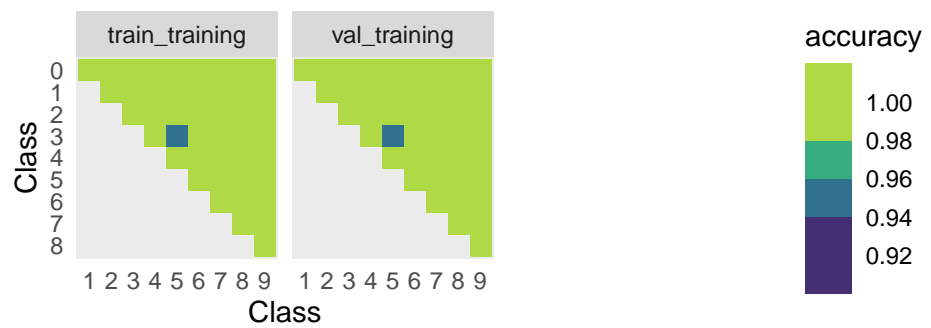


Replication 14

Pairwise accuracies networks

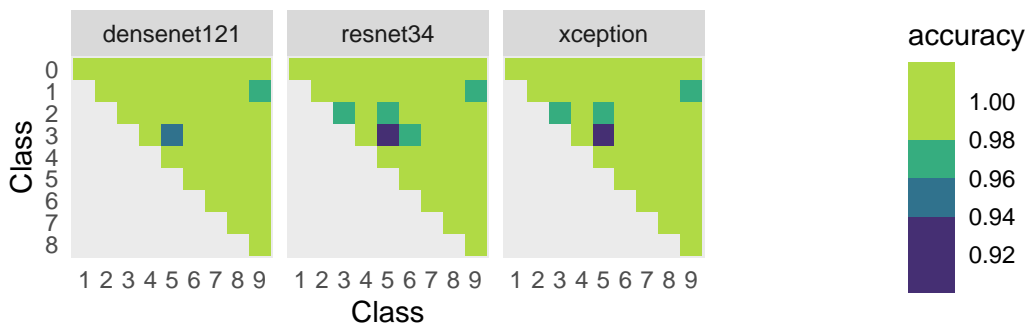


Pairwise accuracies ensembles



Replication 15

Pairwise accuracies networks

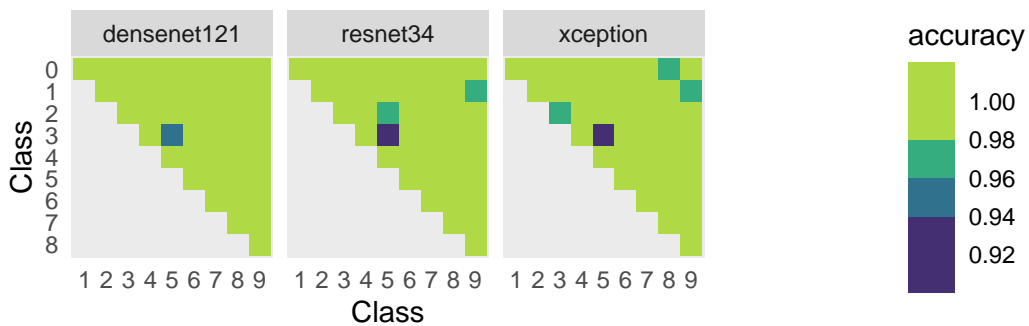


Pairwise accuracies ensembles

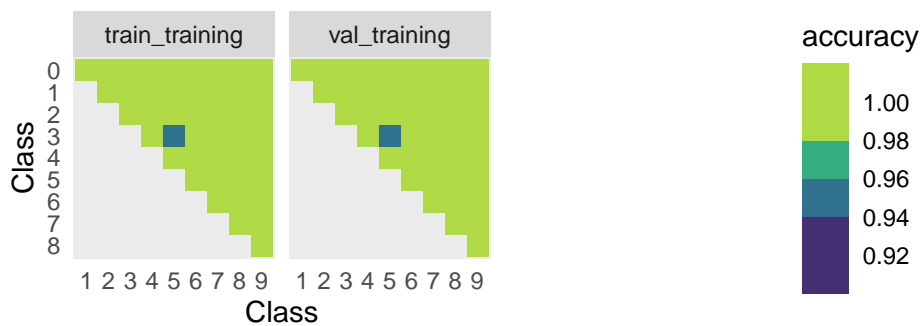


Replication 16

Pairwise accuracies networks

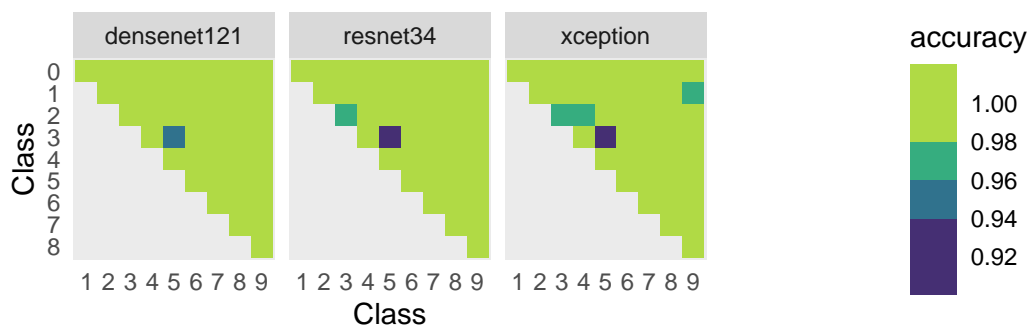


Pairwise accuracies ensembles

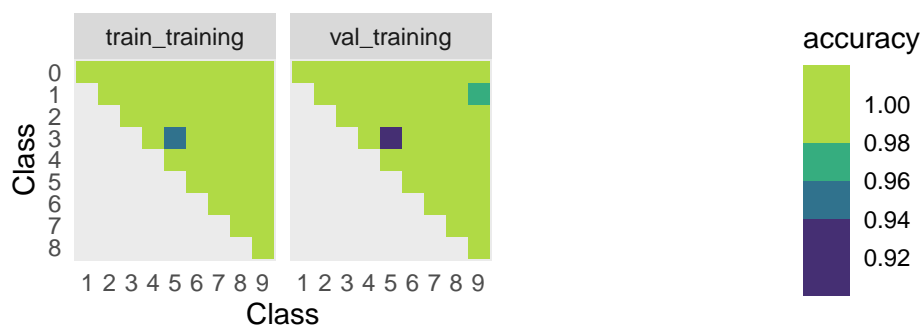


Replication 17

Pairwise accuracies networks

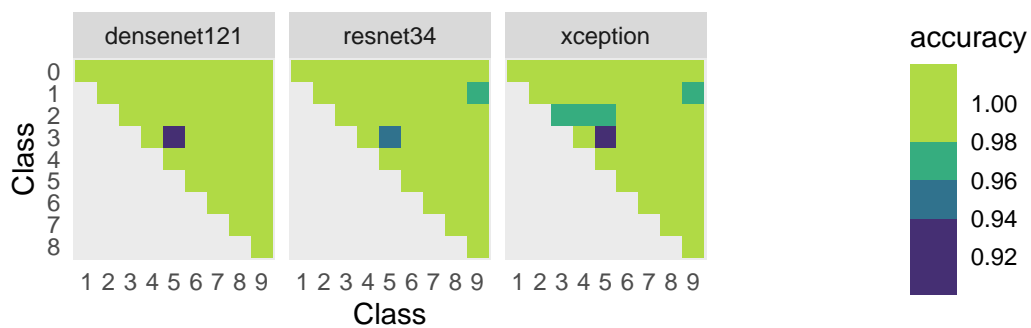


Pairwise accuracies ensembles

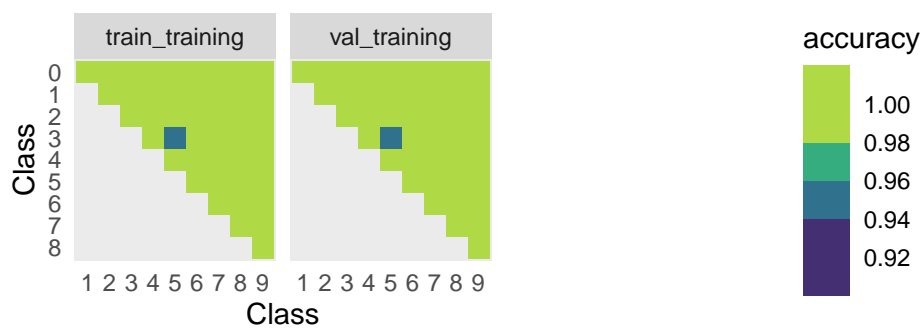


Replication 18

Pairwise accuracies networks

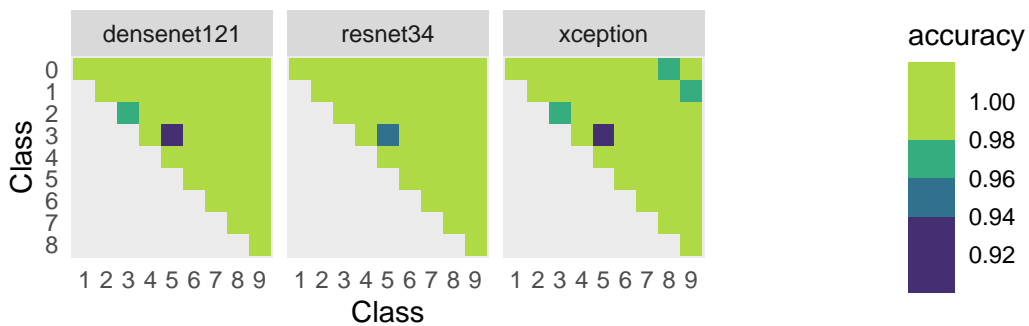


Pairwise accuracies ensembles

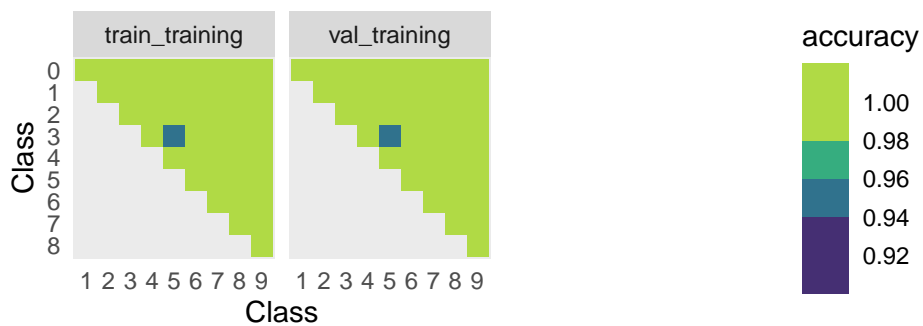


Replication 19

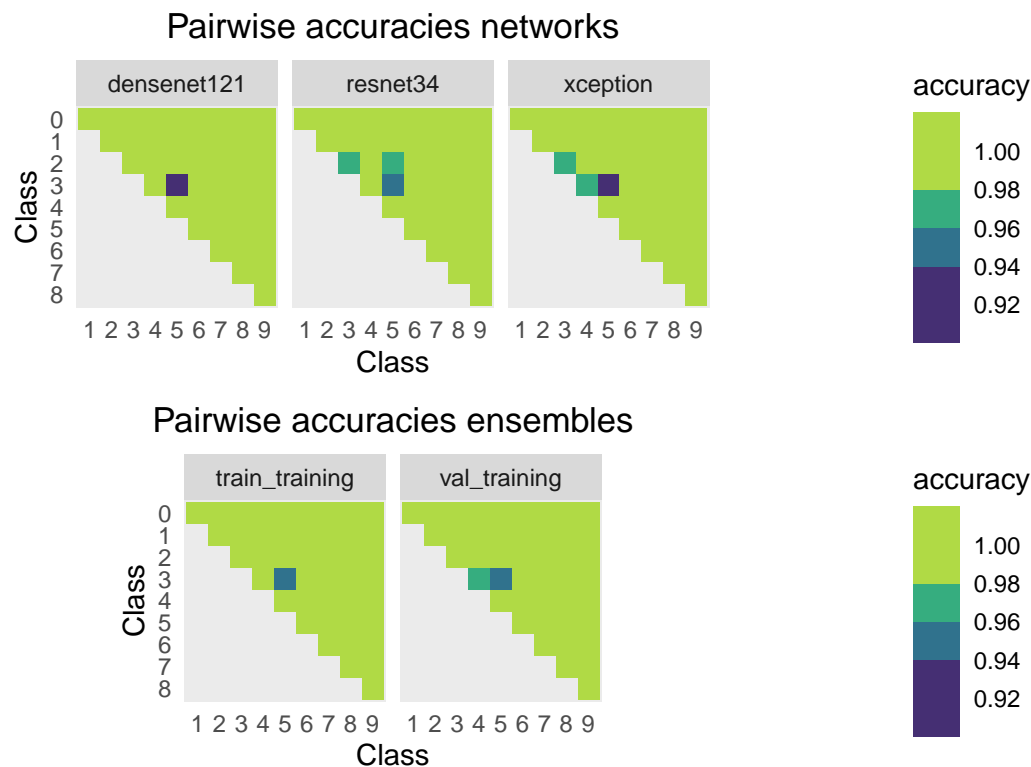
Pairwise accuracies networks



Pairwise accuracies ensembles

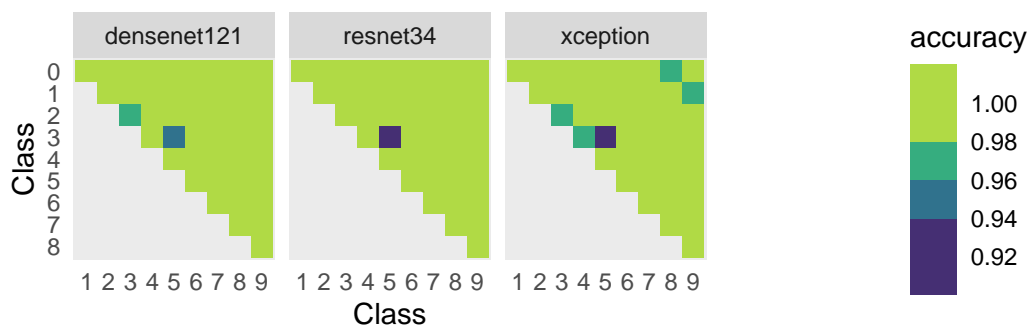


Replication 20



Replication 21

Pairwise accuracies networks

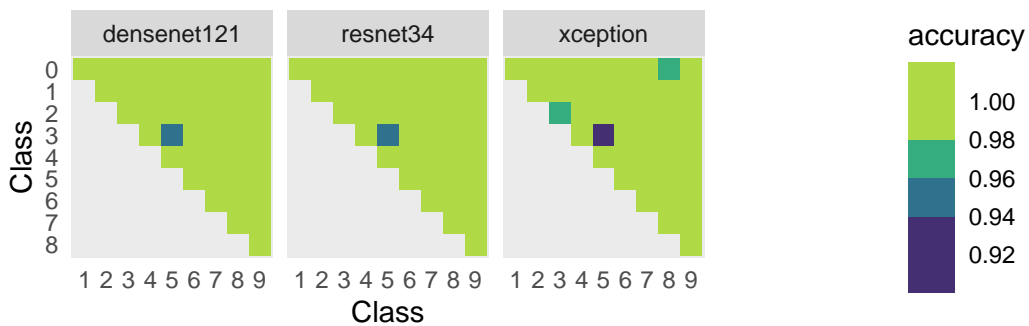


Pairwise accuracies ensembles

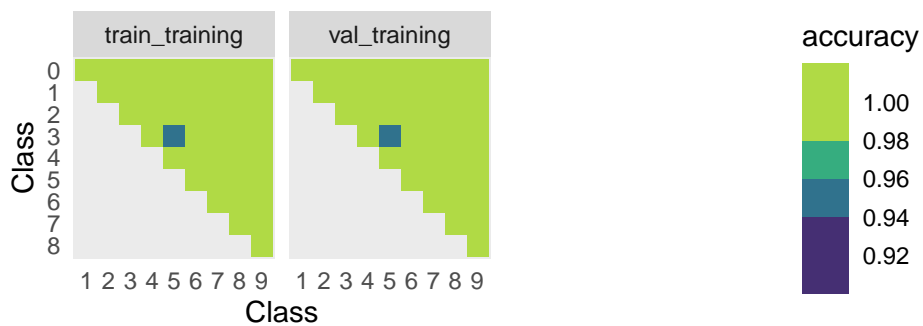


Replication 22

Pairwise accuracies networks

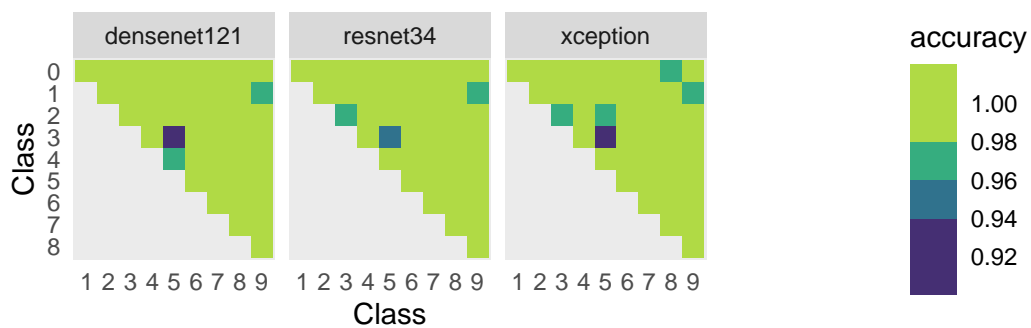


Pairwise accuracies ensembles

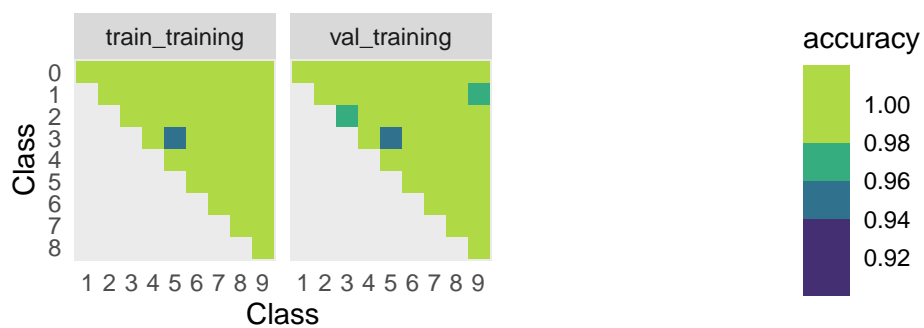


Replication 23

Pairwise accuracies networks

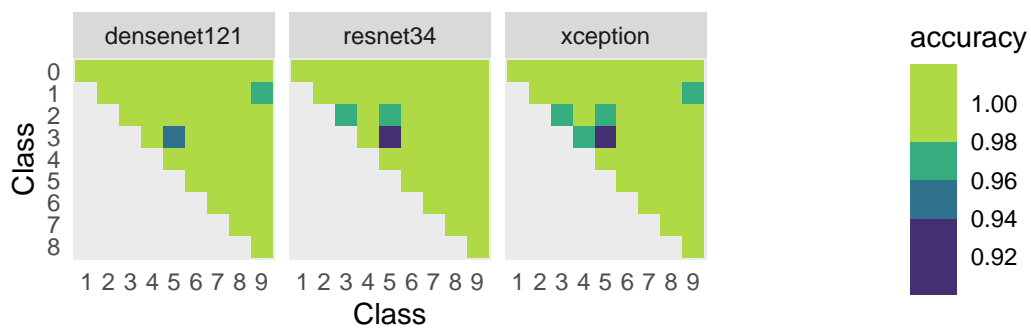


Pairwise accuracies ensembles

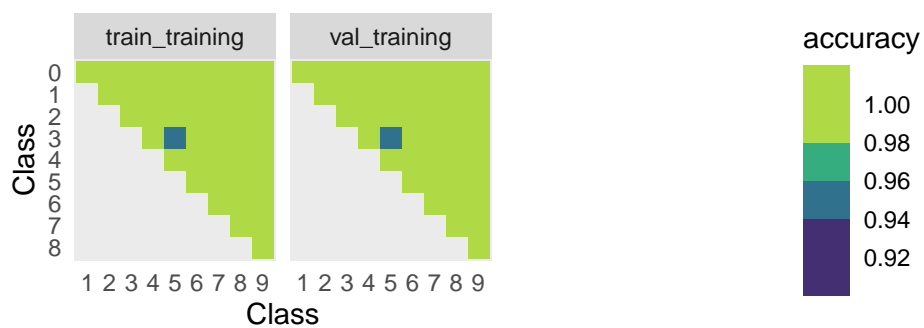


Replication 24

Pairwise accuracies networks

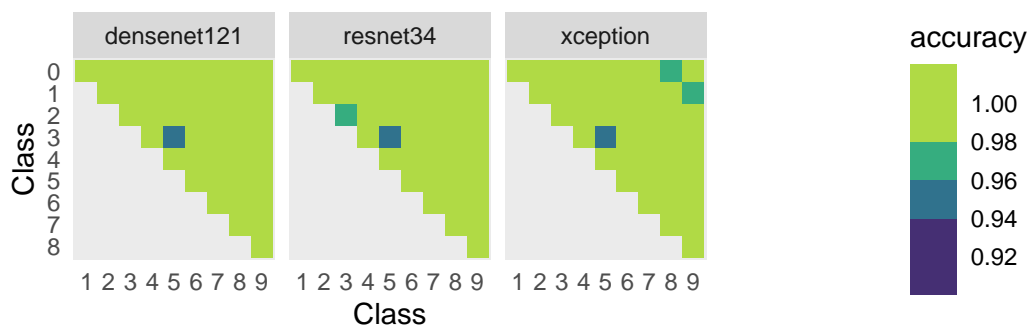


Pairwise accuracies ensembles

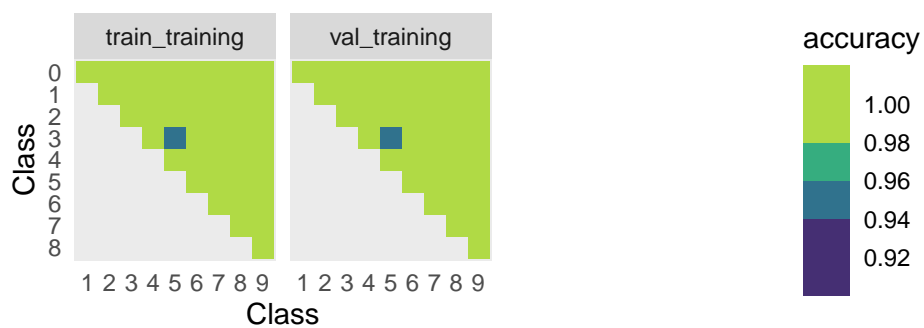


Replication 25

Pairwise accuracies networks

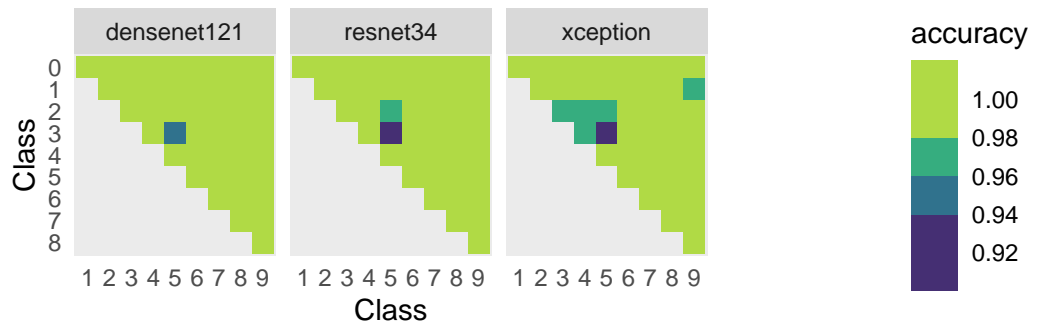


Pairwise accuracies ensembles

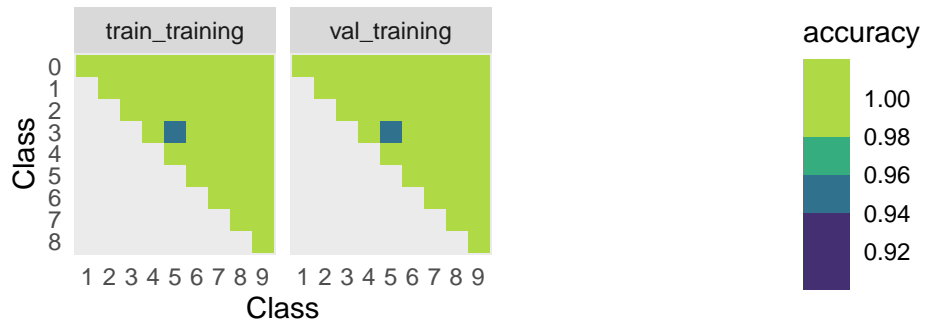


Replication 26

Pairwise accuracies networks

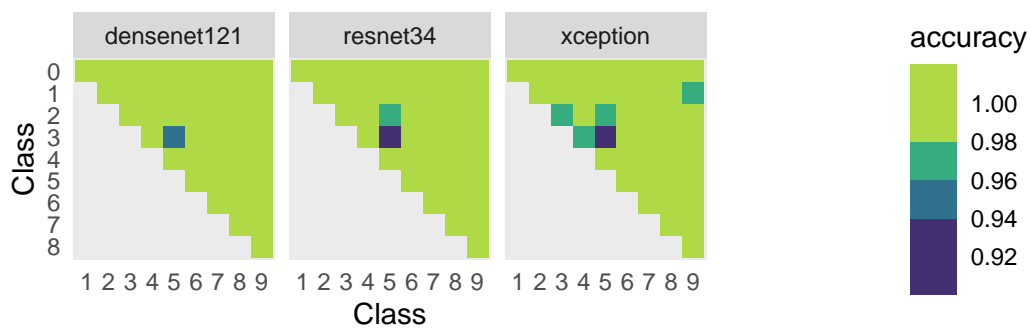


Pairwise accuracies ensembles

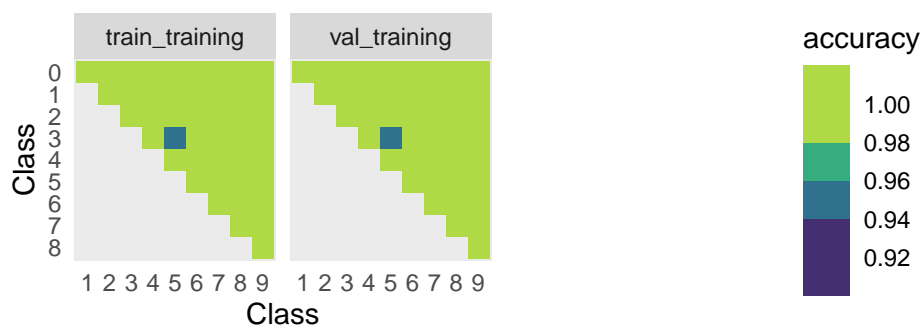


Replication 27

Pairwise accuracies networks

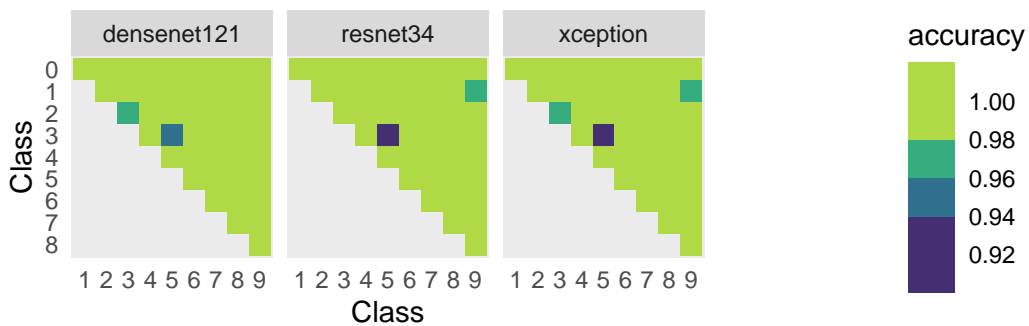


Pairwise accuracies ensembles

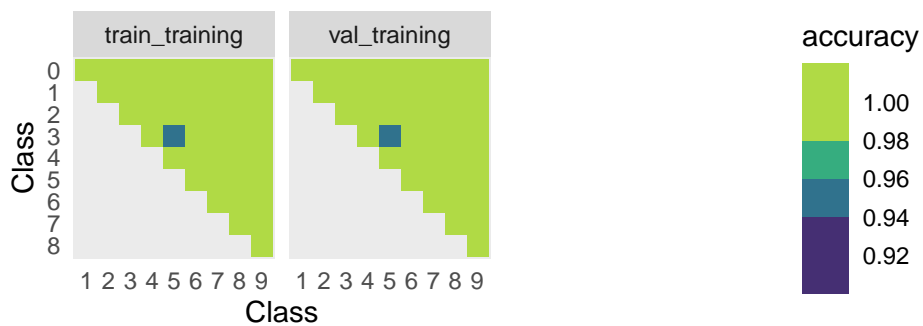


Replication 28

Pairwise accuracies networks

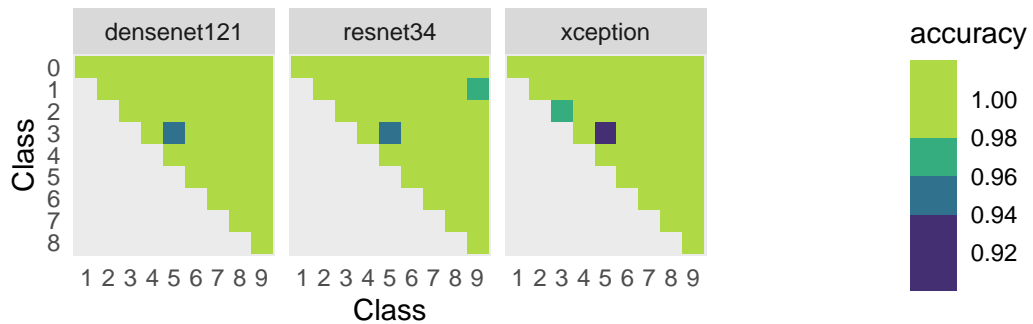


Pairwise accuracies ensembles

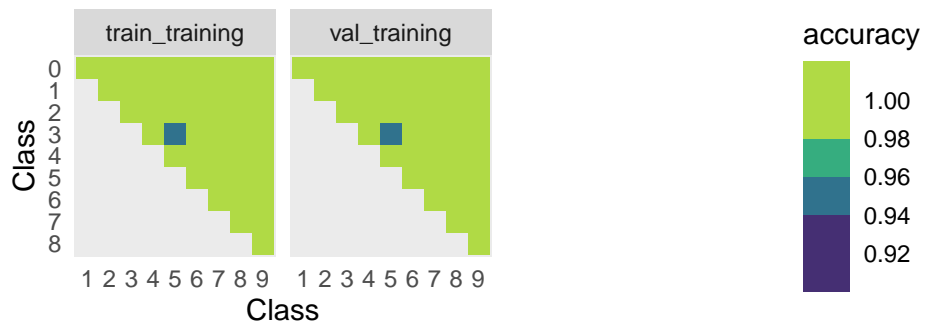


Replication 29

Pairwise accuracies networks



Pairwise accuracies ensembles



LDA combination is able to improve pairwise probabilities in almost all examples. It seems to be a little bit more successful than vt. Especially problematic seem classes 3 and 5 - cat and dog.

CIFAR 10 - validation set of size 25000

```
base_dir <- "../data/data_train_val_half_c10"
repls <- 0:0
folds <- 0:49
classes <- 10

net_pw_results <- read.csv(file.path(base_dir, "net_pw_accuracies.csv"))
ens_pw_results <- read.csv(file.path(base_dir, "ensemble_pw_accuracies.csv"))
net_pw_results[, c("class1", "class2")] <- lapply(net_pw_results[, c("class1", "class2")], as.factor)
ens_pw_results[, c("class1", "class2")] <- lapply(ens_pw_results[, c("class1", "class2")], as.factor)

for (ri in repls)
{
  net_plot <- net_pw_results %>% filter(repli == ri) %>%
    ggplot(mapping=aes(x=class2, y=class1, fill=accuracy)) + geom_raster() + facet_wrap(~network) +
    xlab("Class") +
    ylab("Class") +
    scale_y_discrete(limits=rev) +
    scale_fill_binned(type="viridis", limits=c(0.92, 1), name="accuracy") +
    coord_fixed() +
```

```

ggtitle("Pairwise accuracies networks") +
theme(plot.title = element_text(hjust = 0.5),
      axis.ticks = element_blank(),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank())

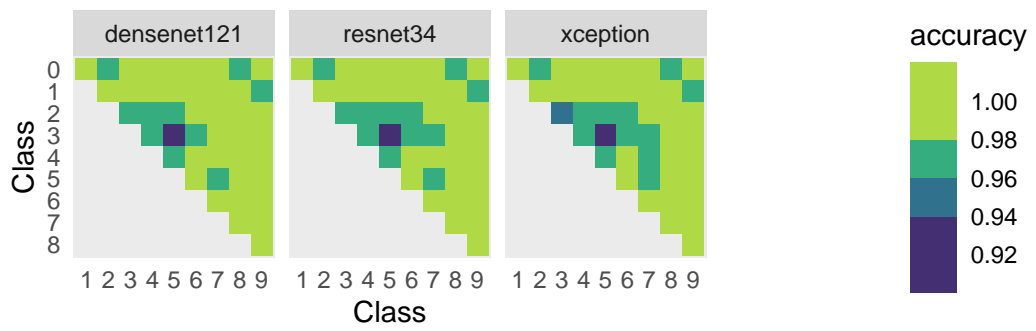
for (fi in folds)
{
  ens_plot <- ens_pw_results %>% filter(repli == ri & fold == fi) %>%
    ggplot(mapping=aes(x=class2, y=class1, fill=accuracy)) + geom_raster() + facet_wrap(~train_set) +
    xlab("Class") +
    ylab("Class") +
    scale_y_discrete(limits=rev) +
    coord_fixed() +
    ggtitle("Pairwise accuracies ensembles") +
    scale_fill_binned(type="viridis", limits=c(0.92, 1), name="accuracy") +
    theme(plot.title = element_text(hjust = 0.5),
          axis.ticks = element_blank(),
          panel.grid.major = element_blank(),
          panel.grid.minor = element_blank())

  print((net_plot/ens_plot) + plot_annotation(title=paste("Replication ", ri, ", fold ", fi)))
}
}

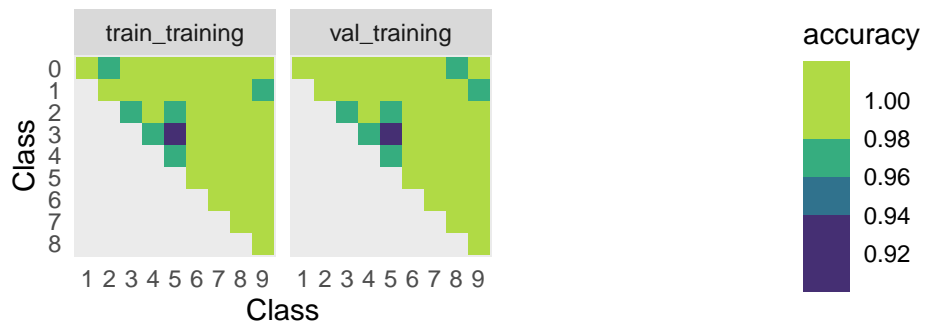
```

Replication 0 , fold 0

Pairwise accuracies networks

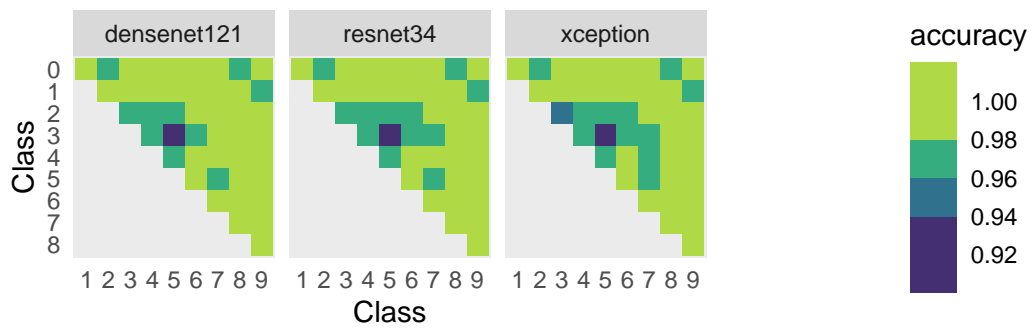


Pairwise accuracies ensembles

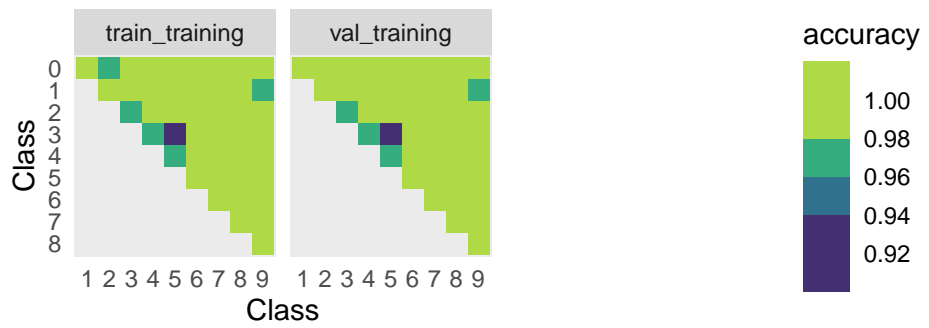


Replication 0 , fold 1

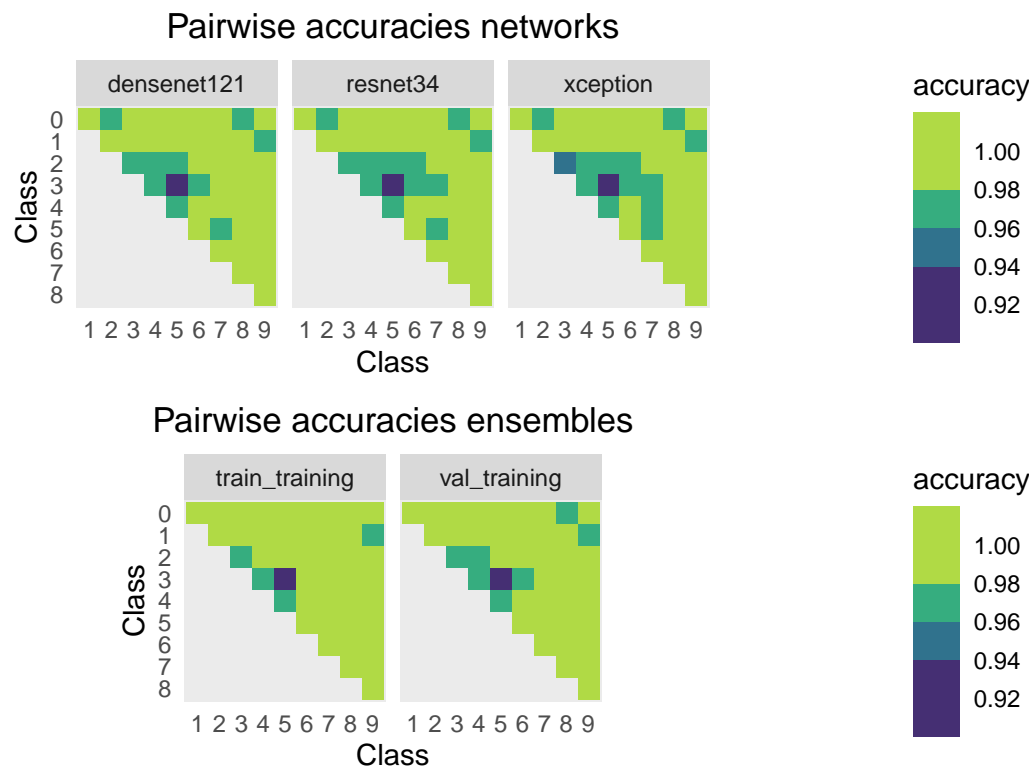
Pairwise accuracies networks



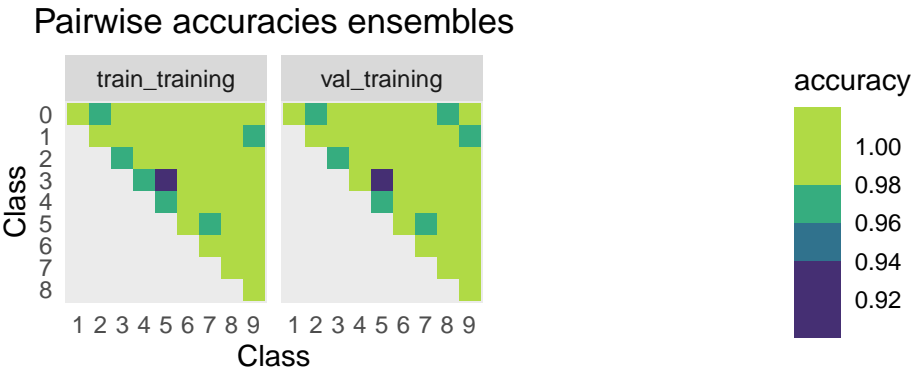
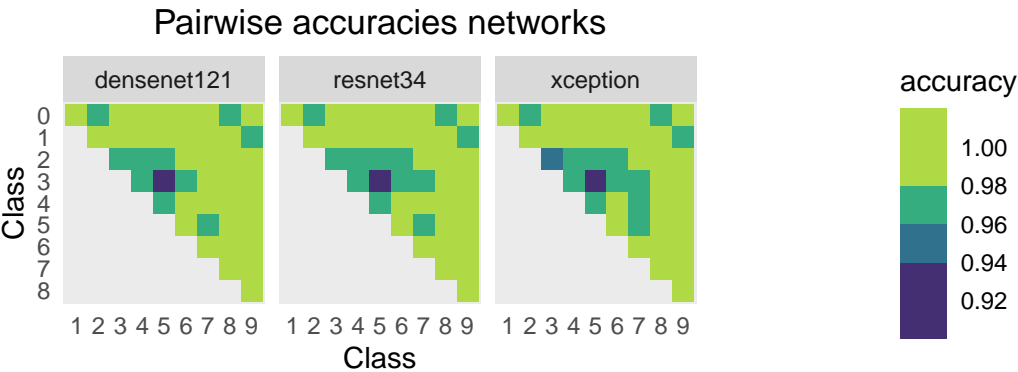
Pairwise accuracies ensembles



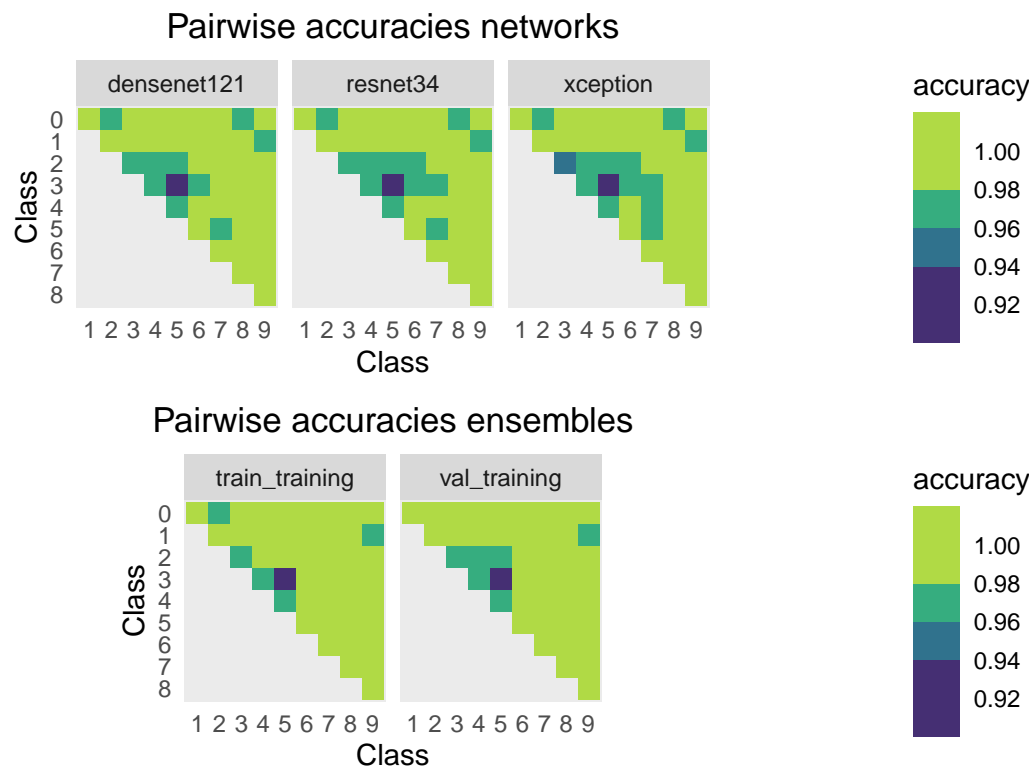
Replication 0 , fold 2



Replication 0 , fold 3

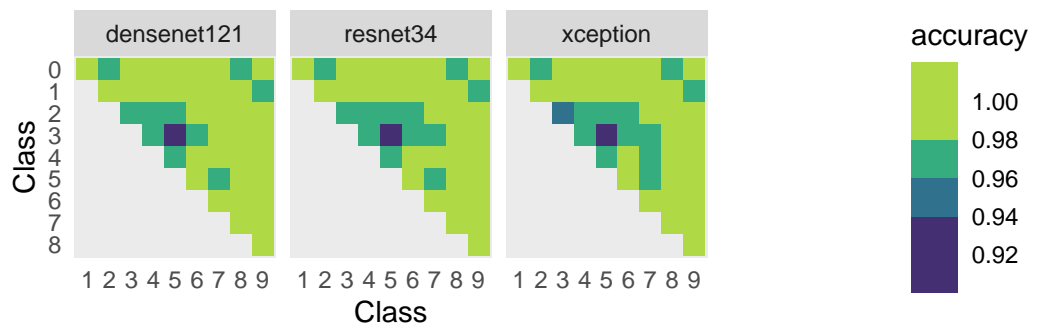


Replication 0 , fold 4

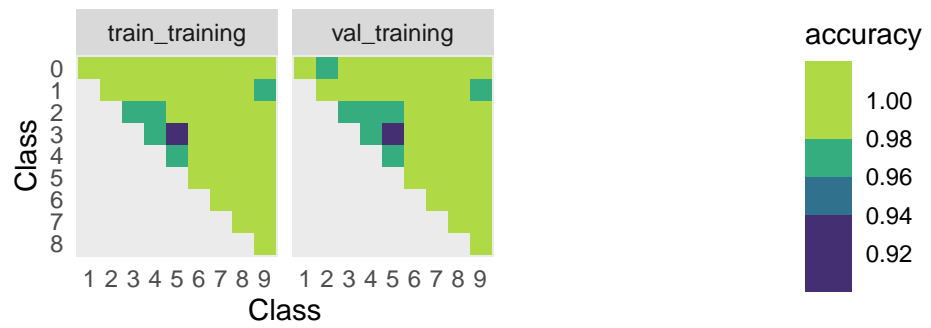


Replication 0 , fold 5

Pairwise accuracies networks

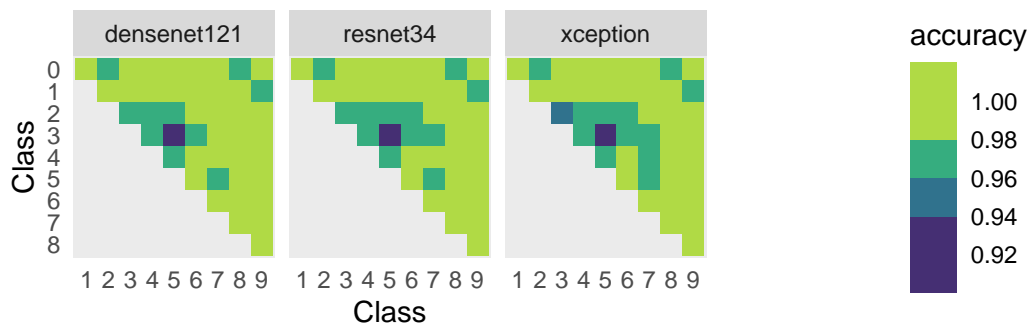


Pairwise accuracies ensembles

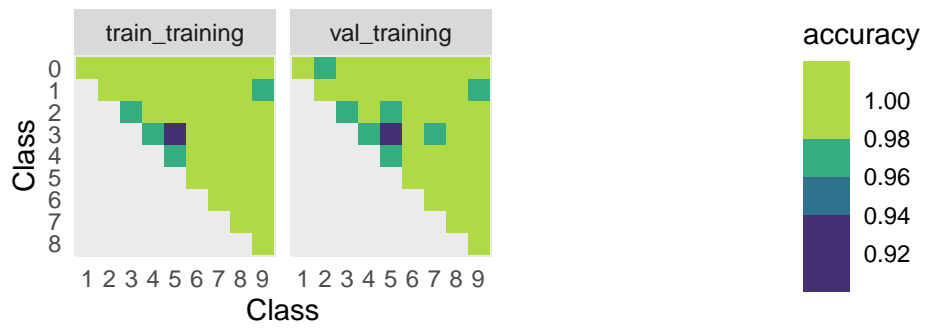


Replication 0 , fold 6

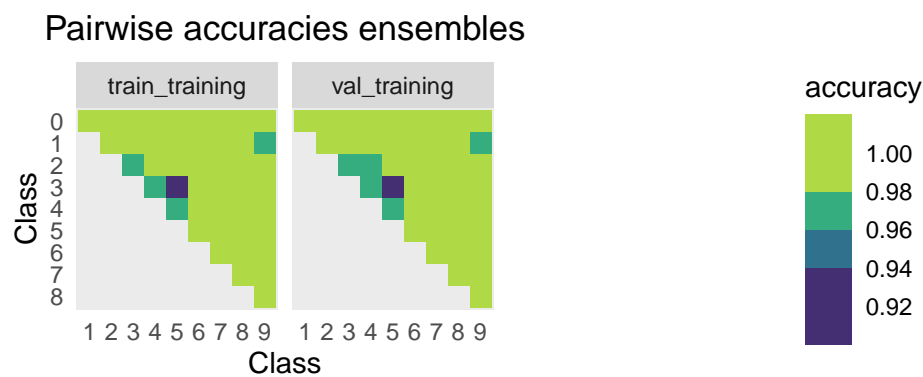
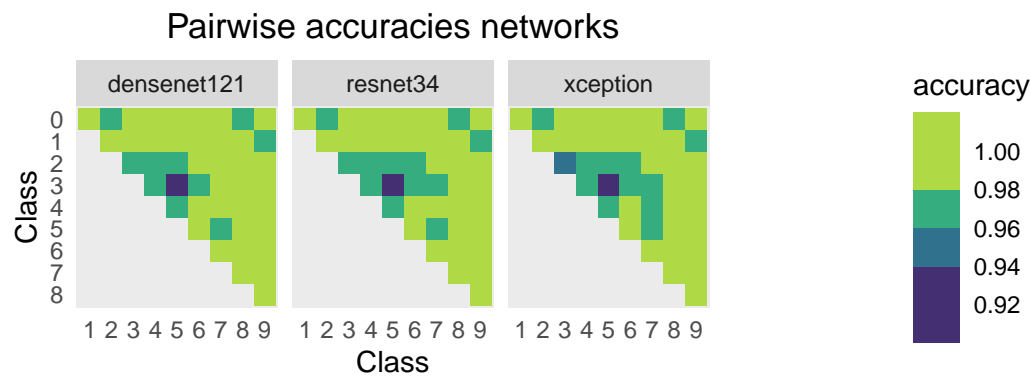
Pairwise accuracies networks



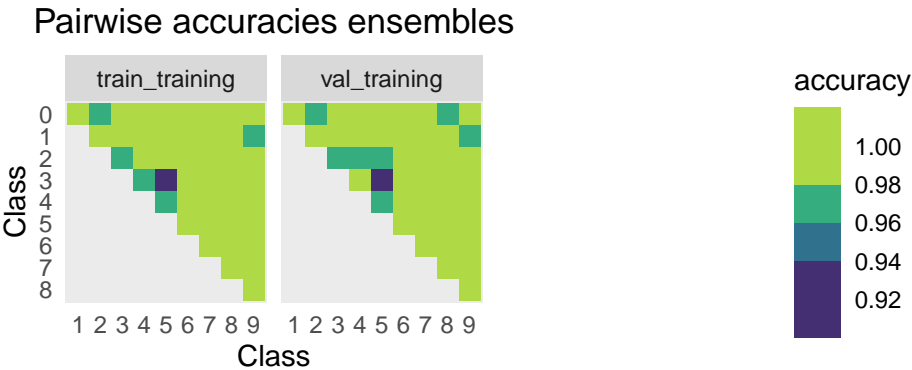
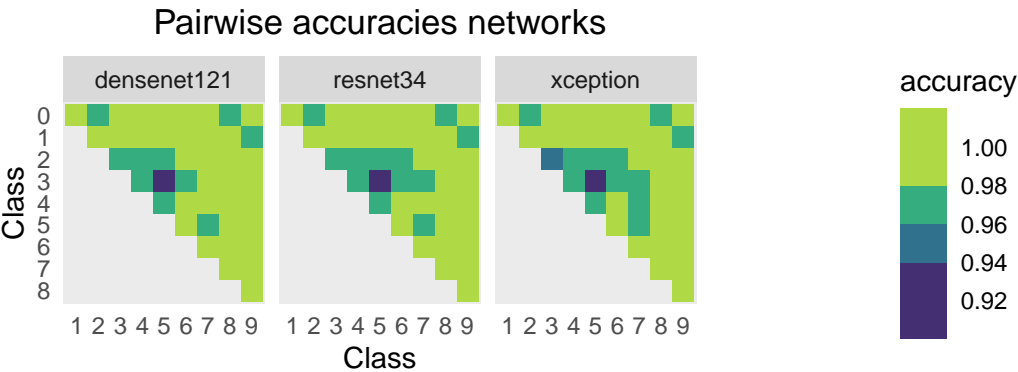
Pairwise accuracies ensembles



Replication 0 , fold 7

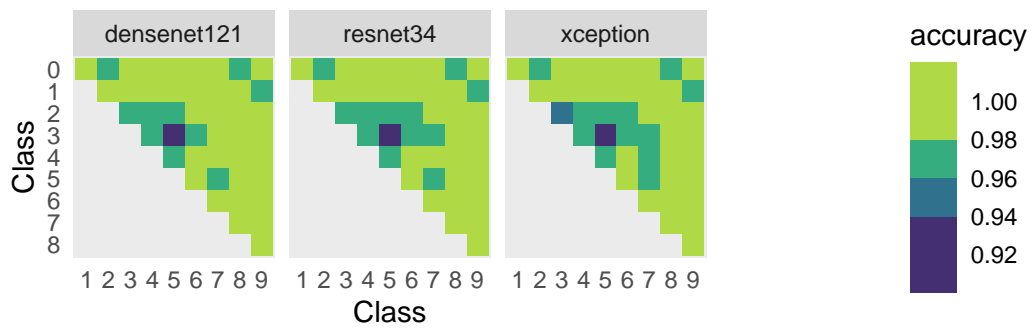


Replication 0 , fold 8

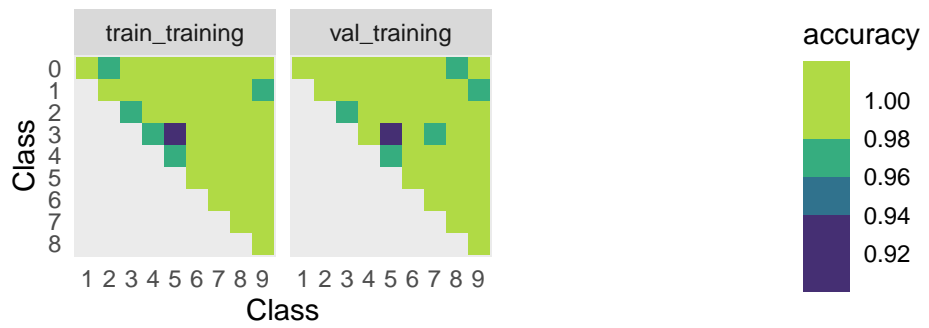


Replication 0 , fold 9

Pairwise accuracies networks

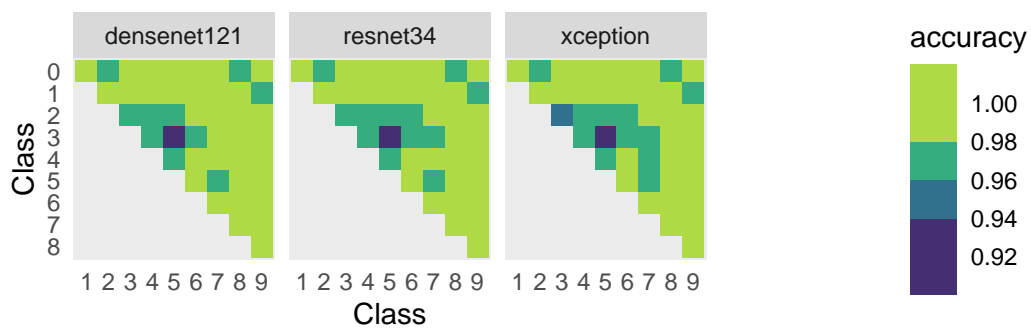


Pairwise accuracies ensembles

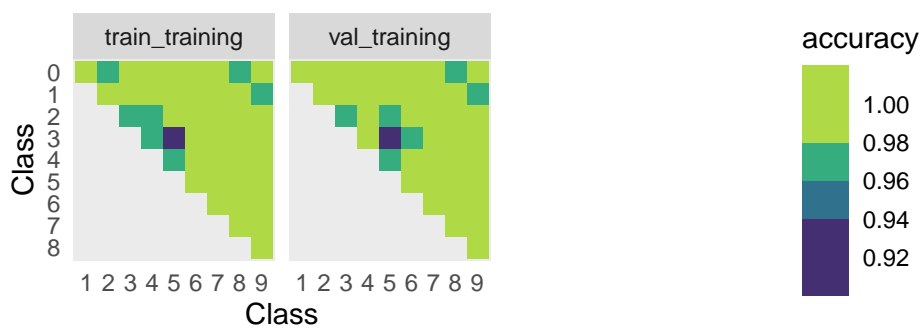


Replication 0 , fold 10

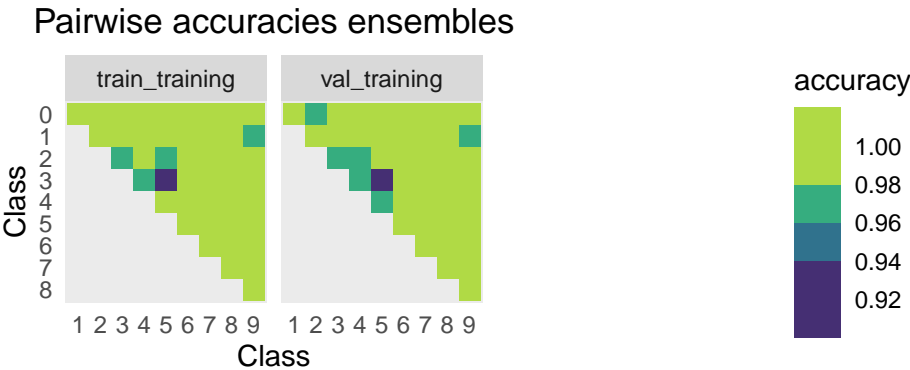
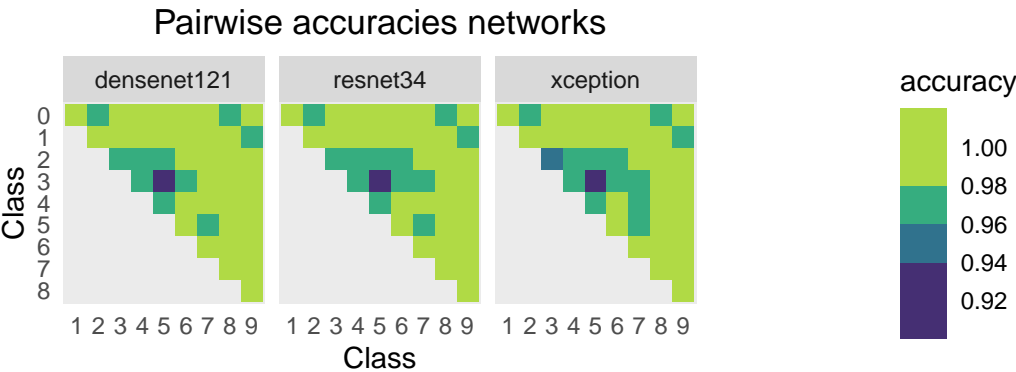
Pairwise accuracies networks



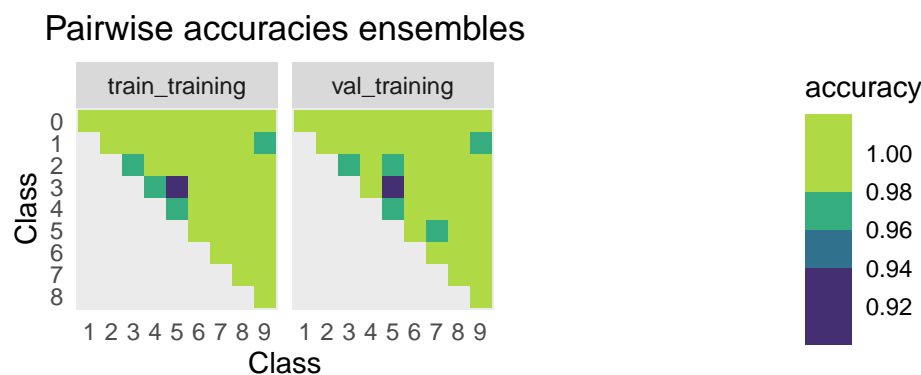
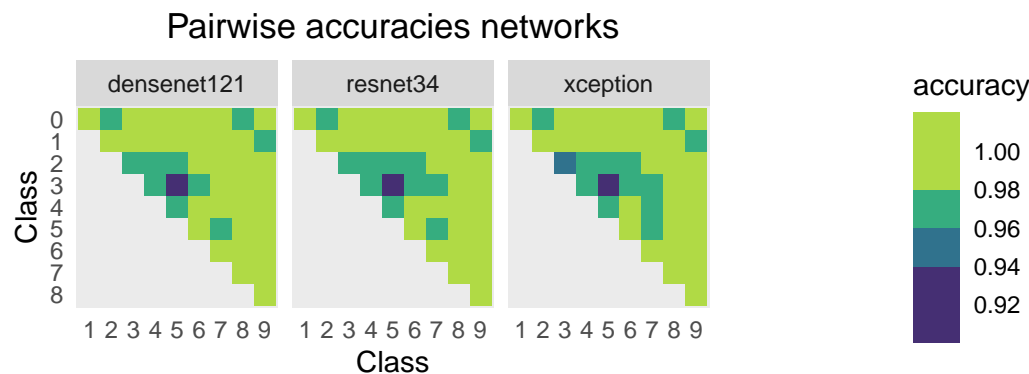
Pairwise accuracies ensembles



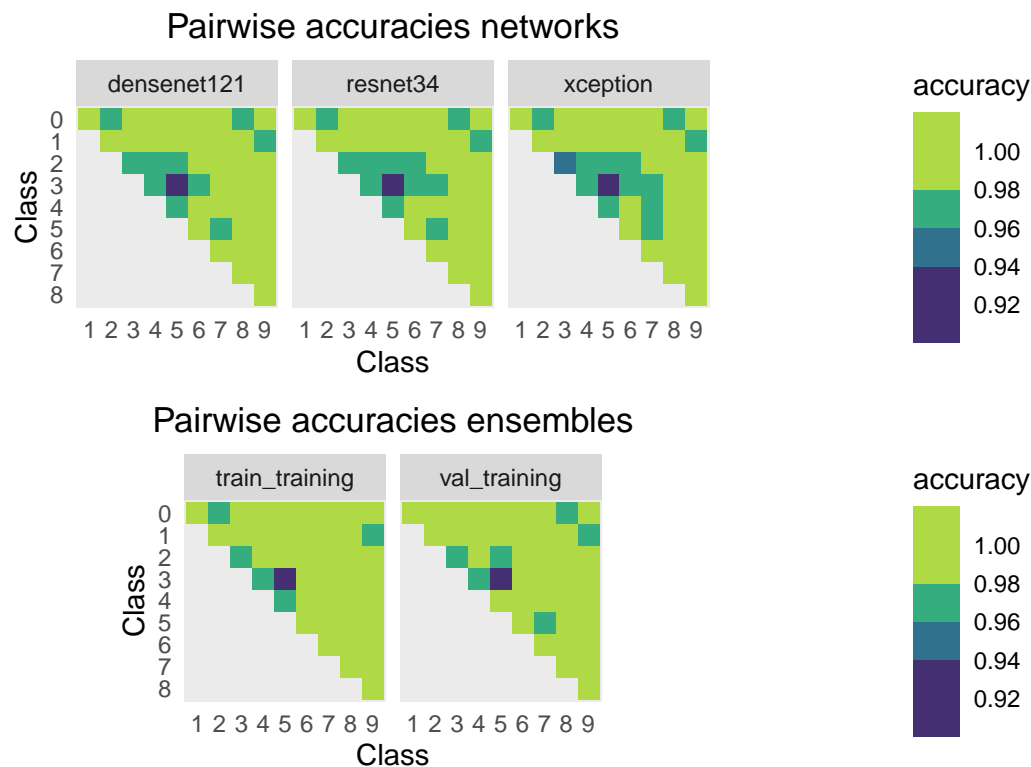
Replication 0 , fold 11



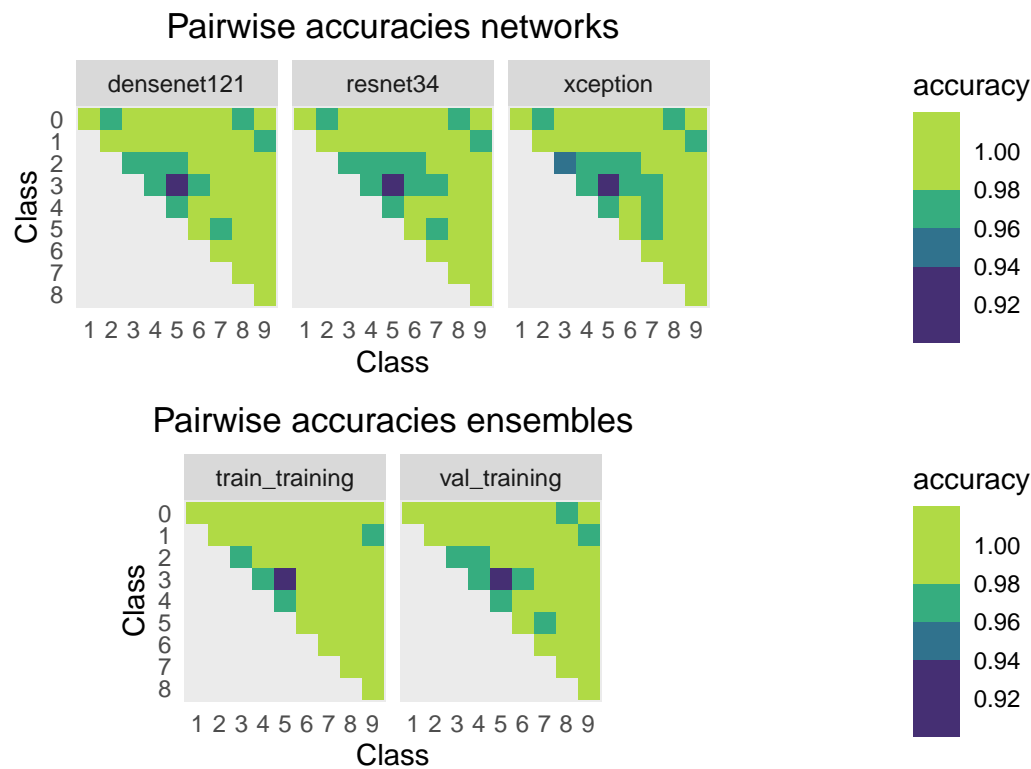
Replication 0 , fold 12



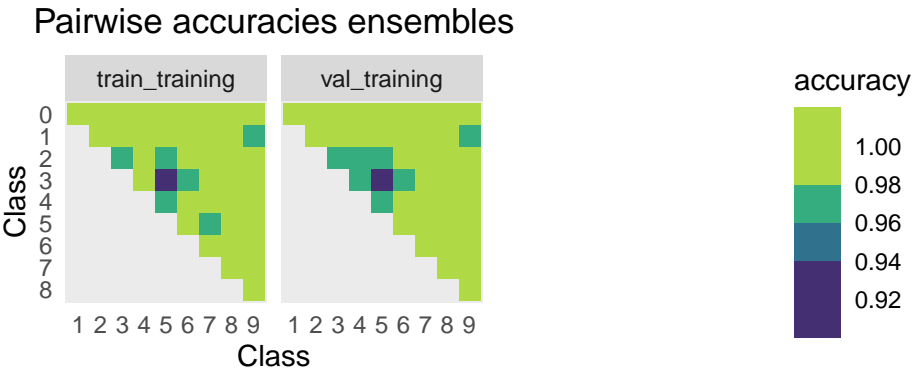
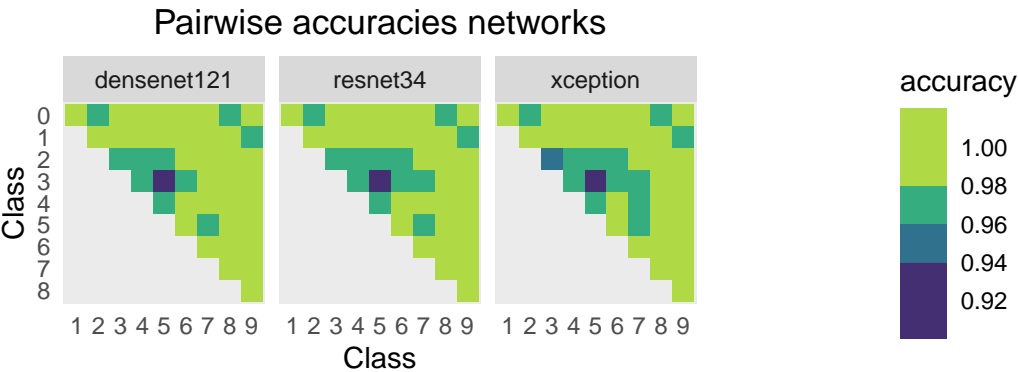
Replication 0 , fold 13



Replication 0 , fold 14

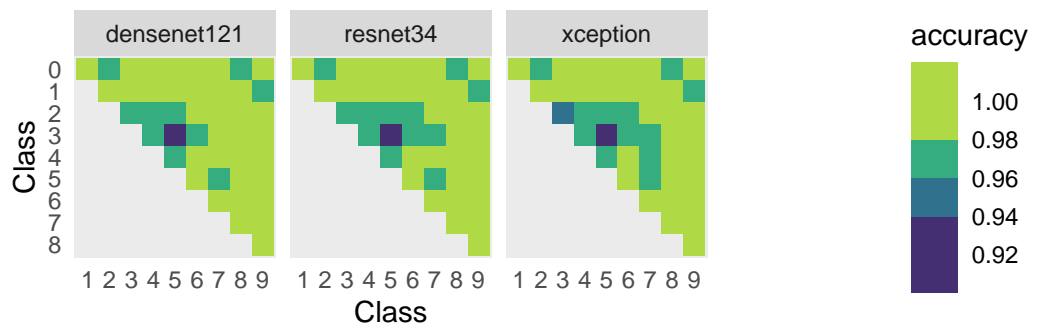


Replication 0 , fold 15

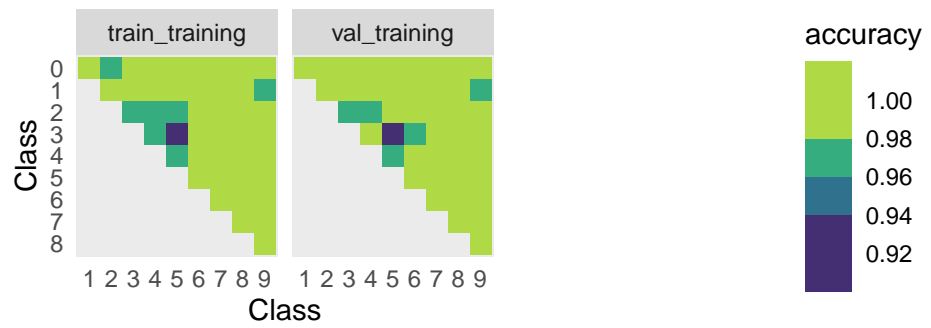


Replication 0 , fold 16

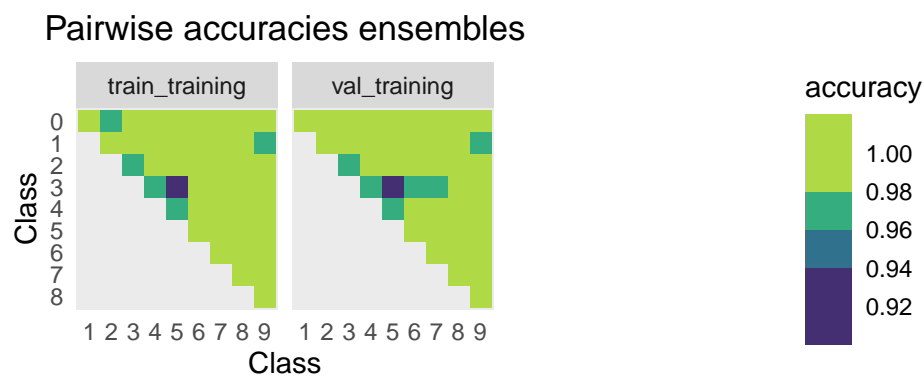
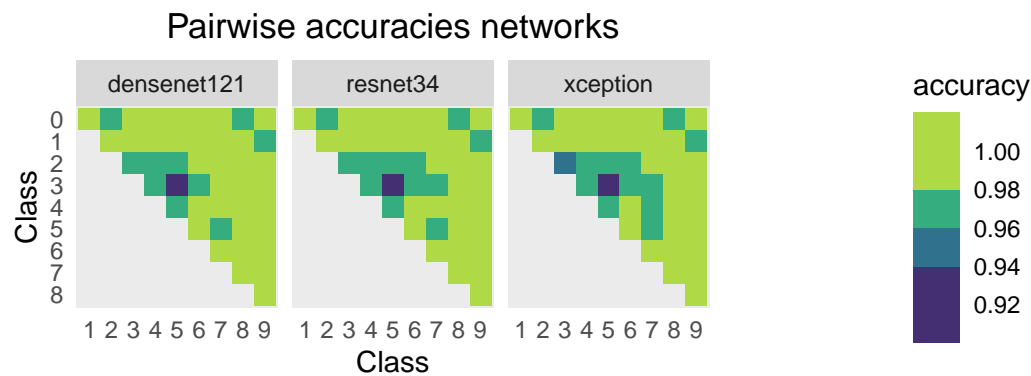
Pairwise accuracies networks



Pairwise accuracies ensembles

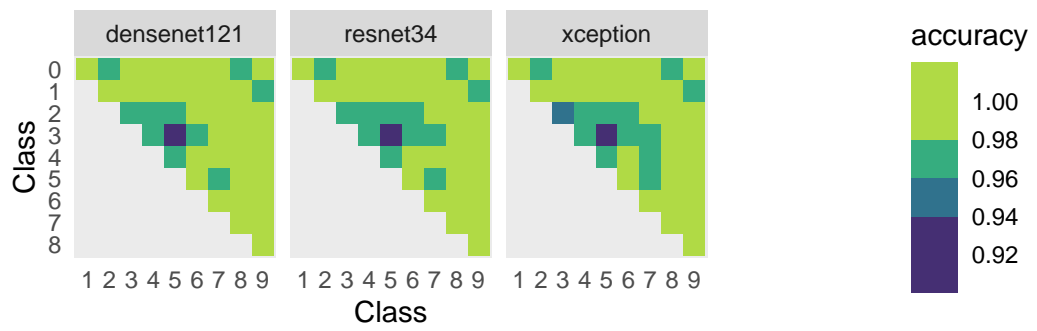


Replication 0 , fold 17

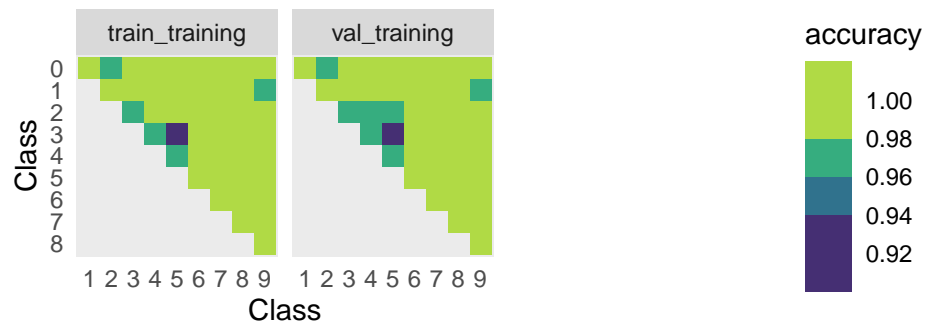


Replication 0 , fold 18

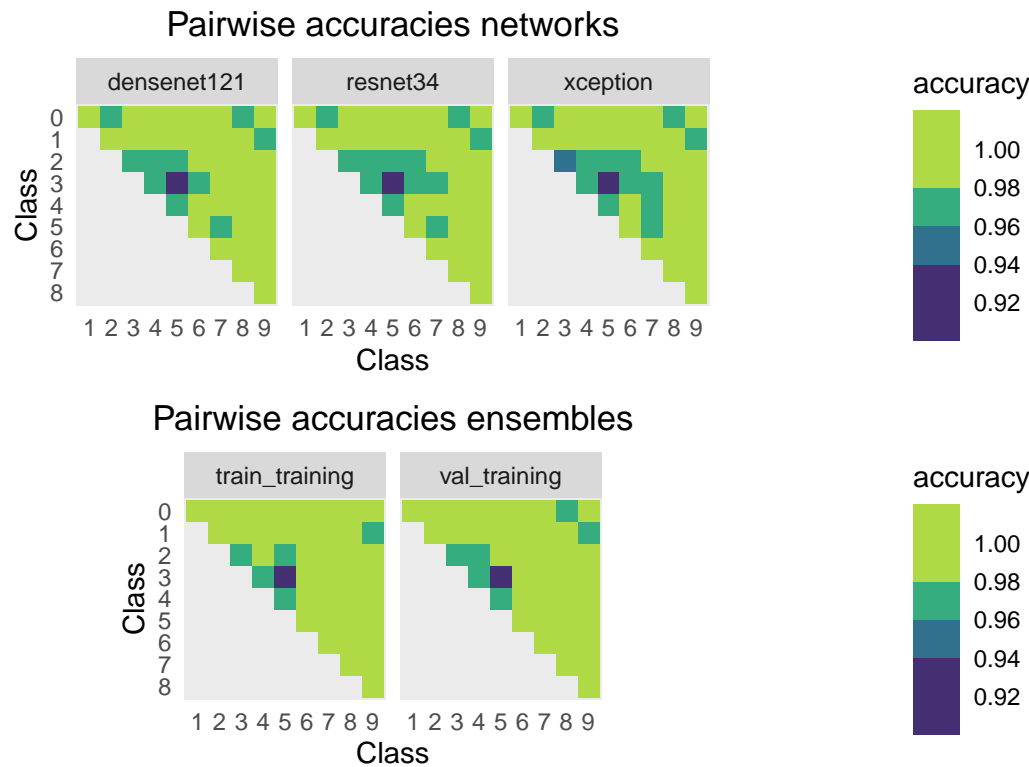
Pairwise accuracies networks



Pairwise accuracies ensembles

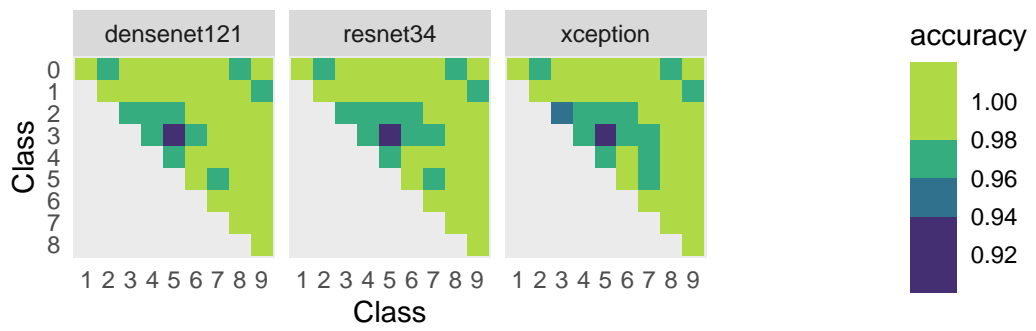


Replication 0 , fold 19

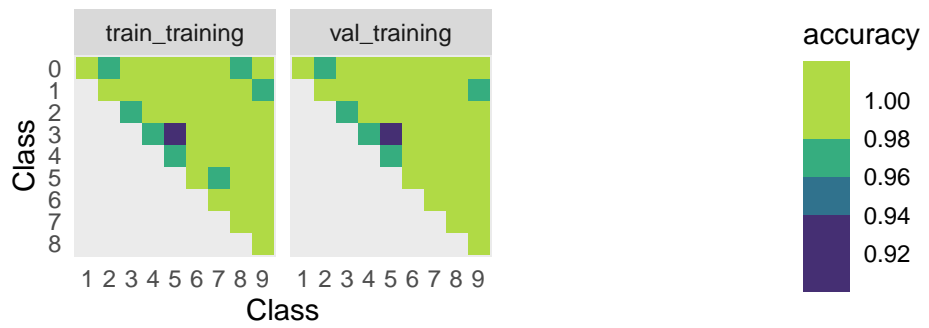


Replication 0 , fold 20

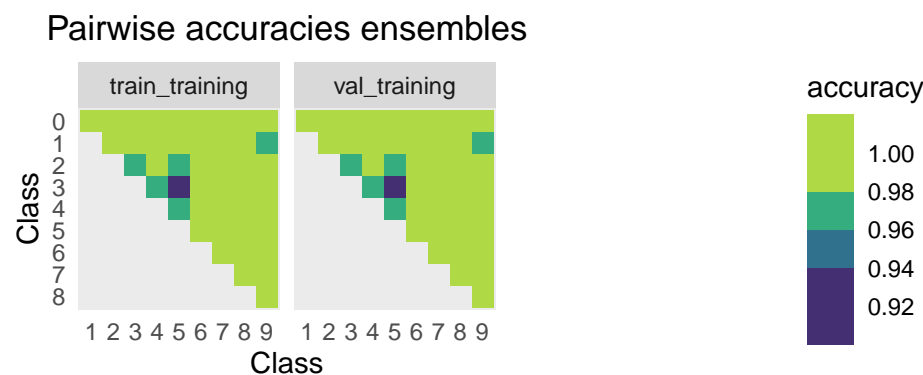
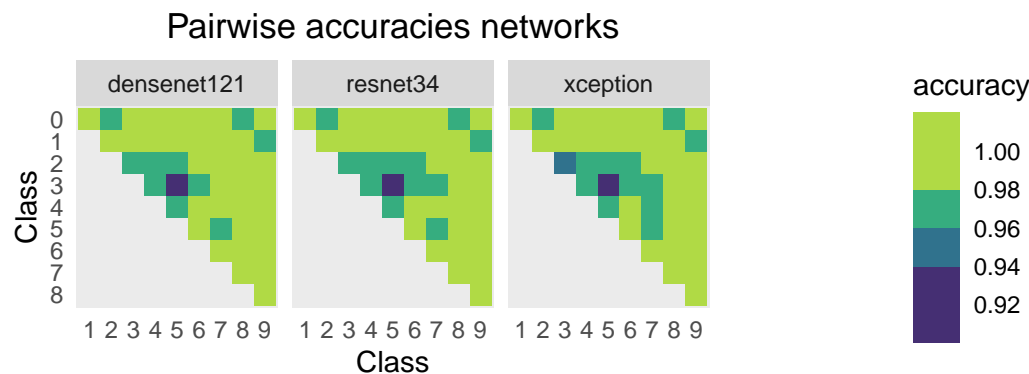
Pairwise accuracies networks



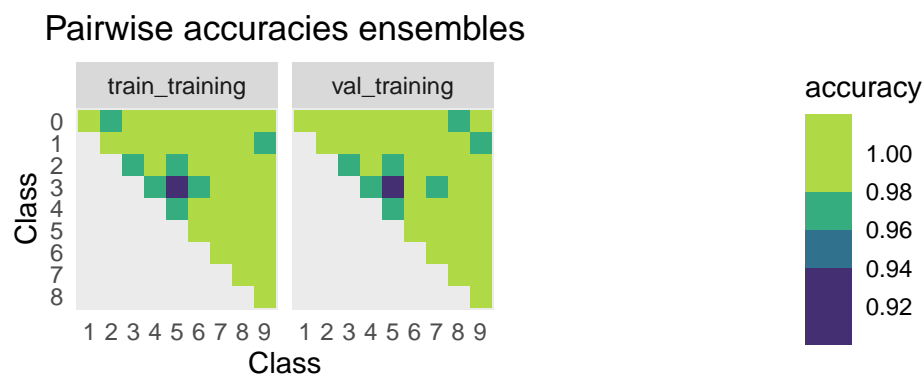
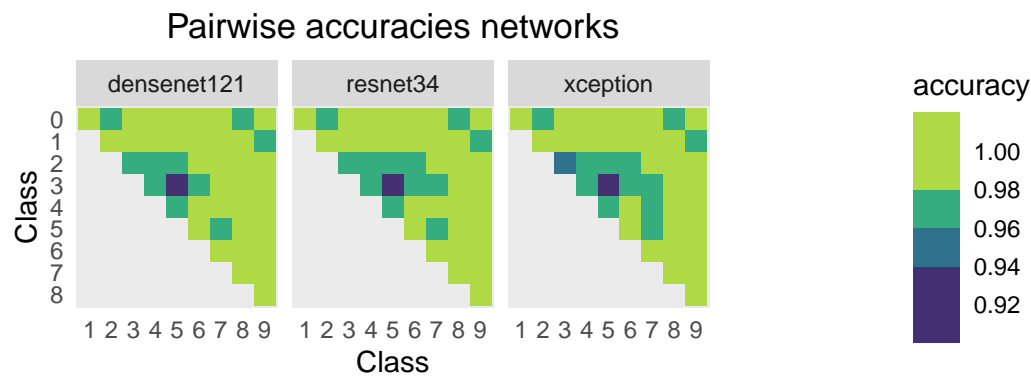
Pairwise accuracies ensembles



Replication 0 , fold 21

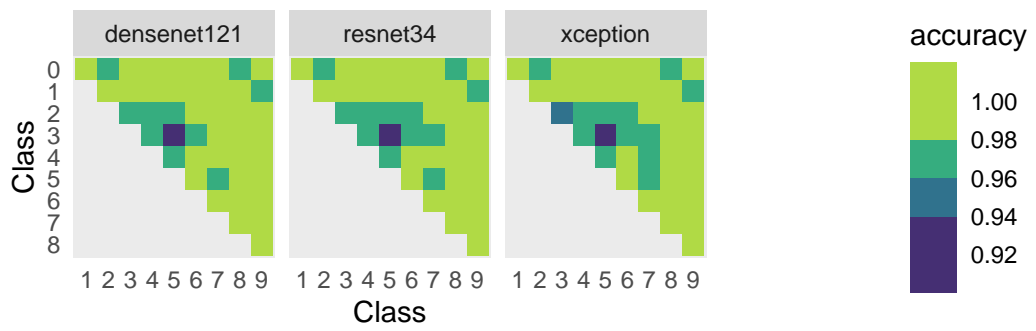


Replication 0 , fold 22



Replication 0 , fold 23

Pairwise accuracies networks

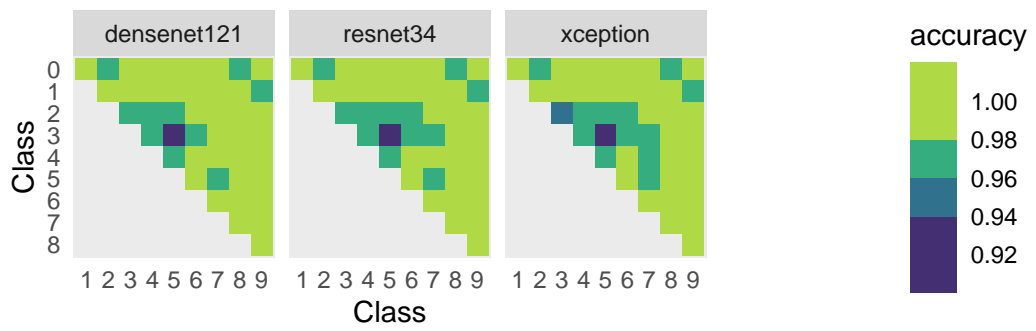


Pairwise accuracies ensembles

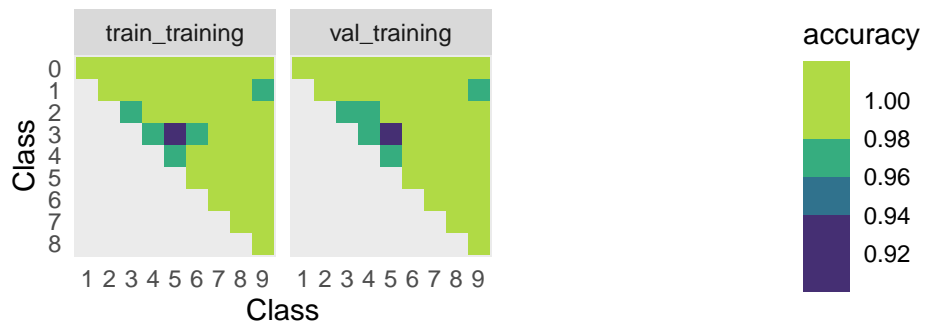


Replication 0 , fold 24

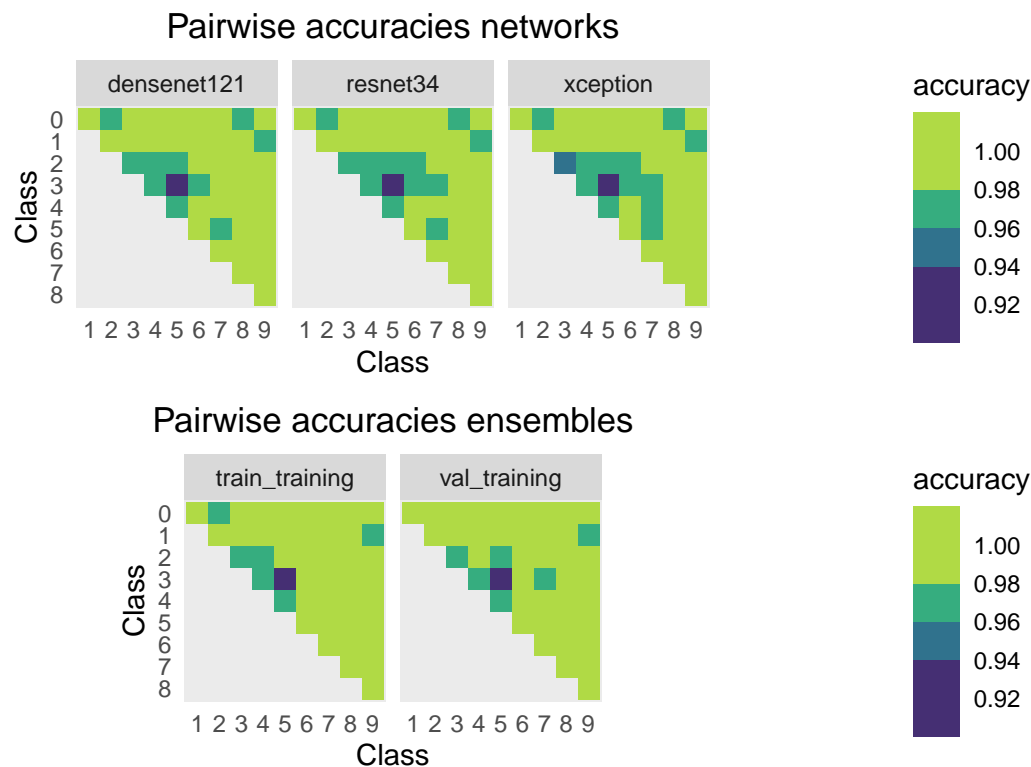
Pairwise accuracies networks



Pairwise accuracies ensembles

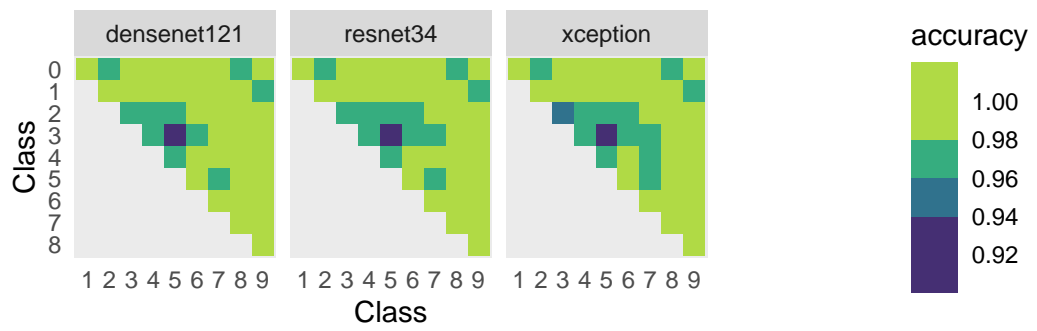


Replication 0 , fold 25

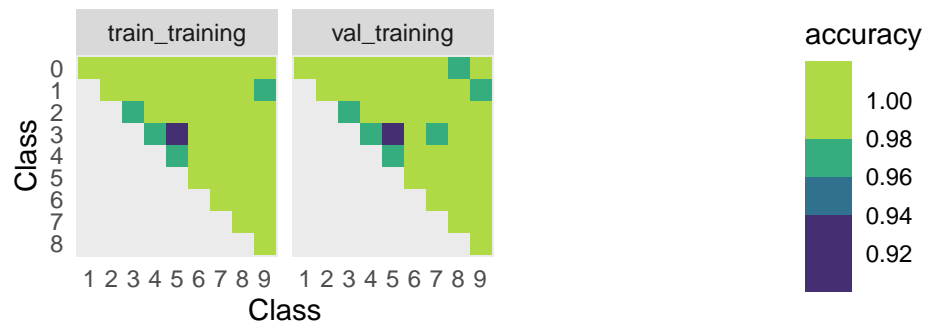


Replication 0 , fold 26

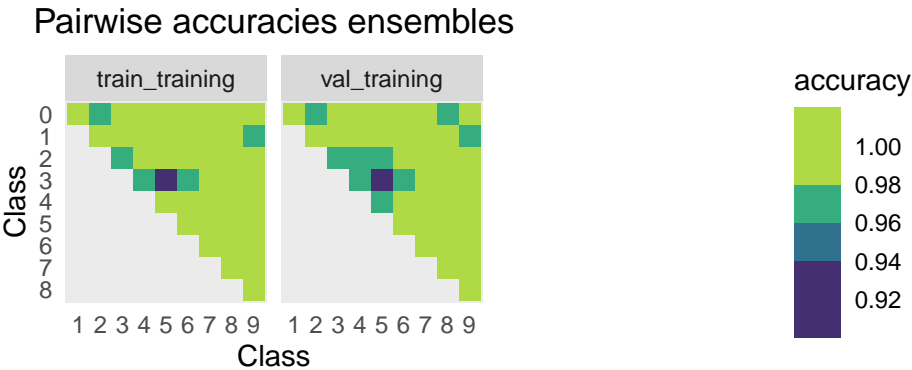
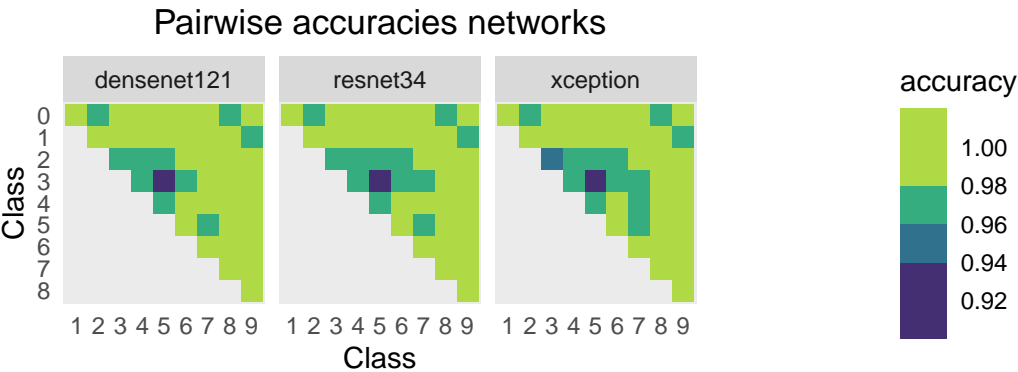
Pairwise accuracies networks



Pairwise accuracies ensembles

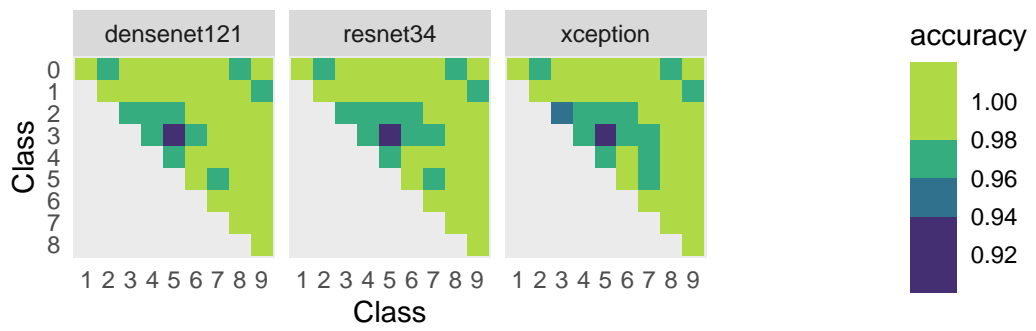


Replication 0 , fold 27

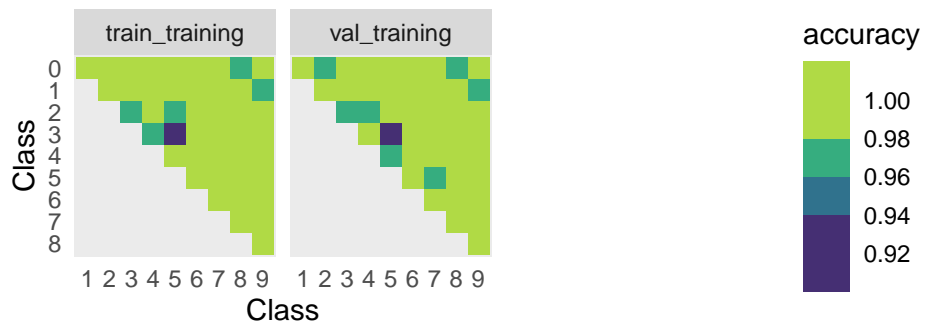


Replication 0 , fold 28

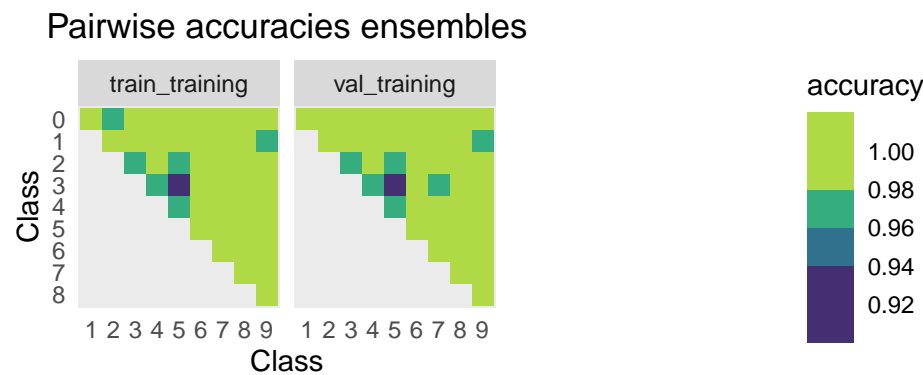
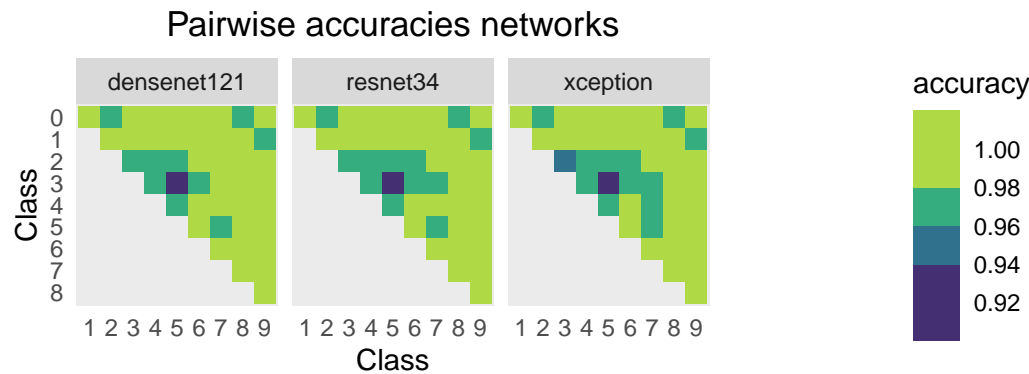
Pairwise accuracies networks



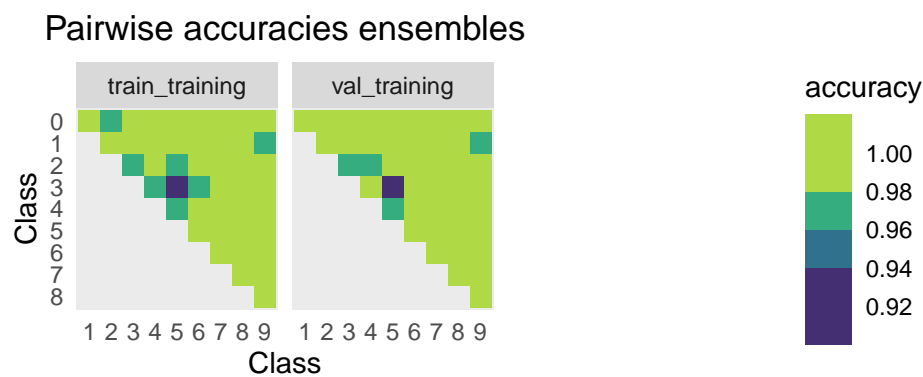
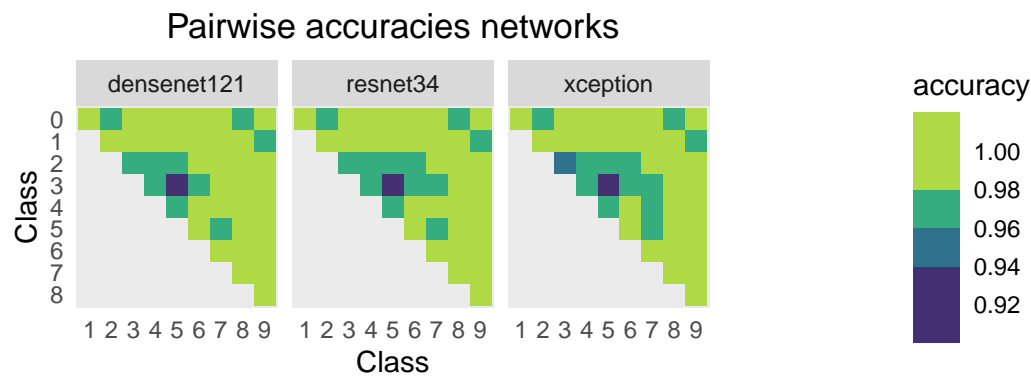
Pairwise accuracies ensembles



Replication 0 , fold 29

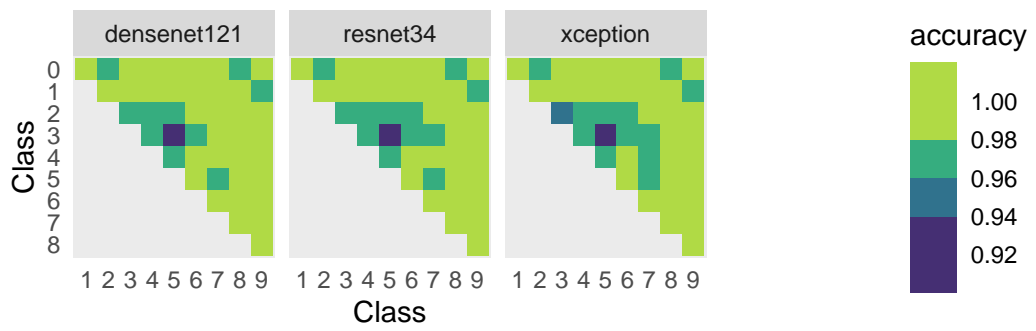


Replication 0 , fold 30

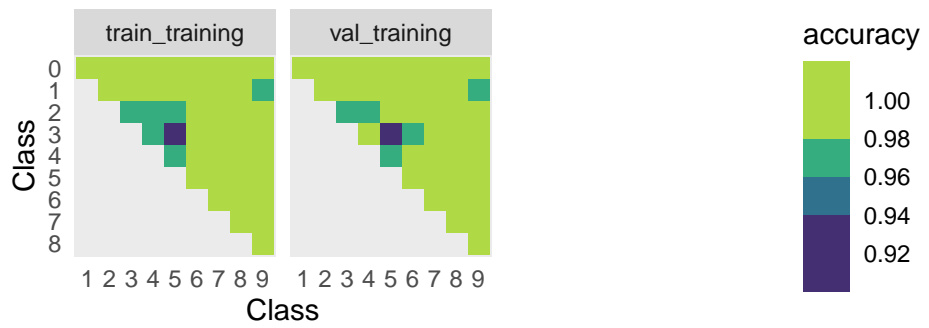


Replication 0 , fold 31

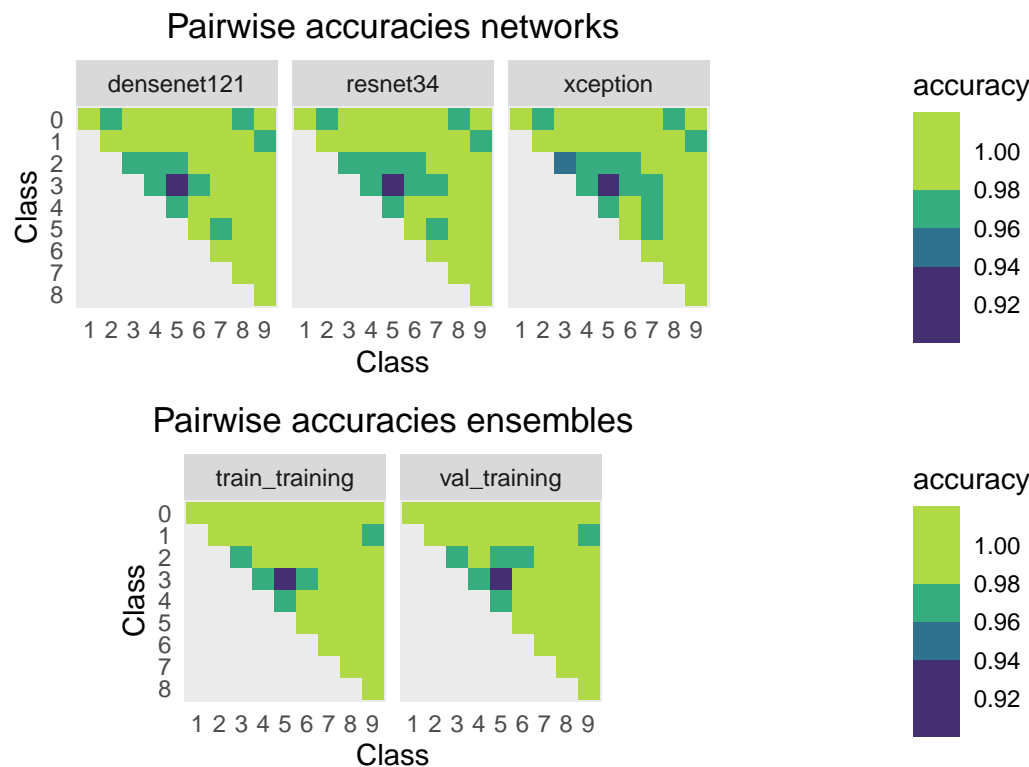
Pairwise accuracies networks



Pairwise accuracies ensembles

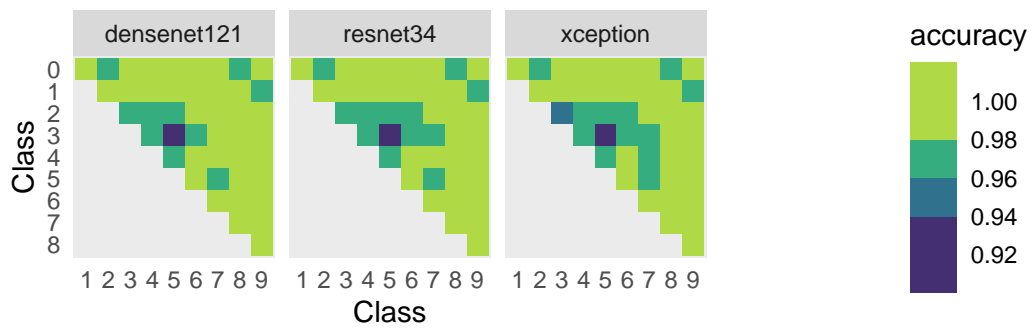


Replication 0 , fold 32

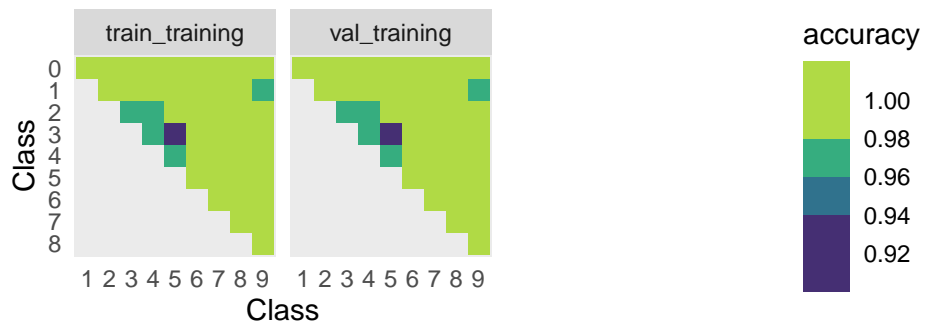


Replication 0 , fold 33

Pairwise accuracies networks

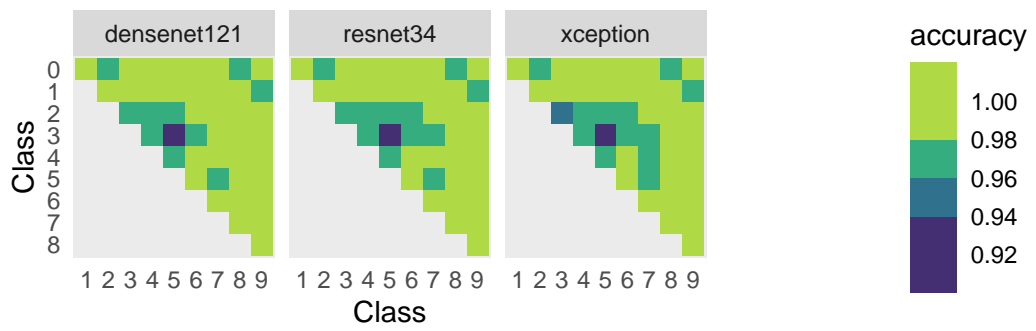


Pairwise accuracies ensembles



Replication 0 , fold 34

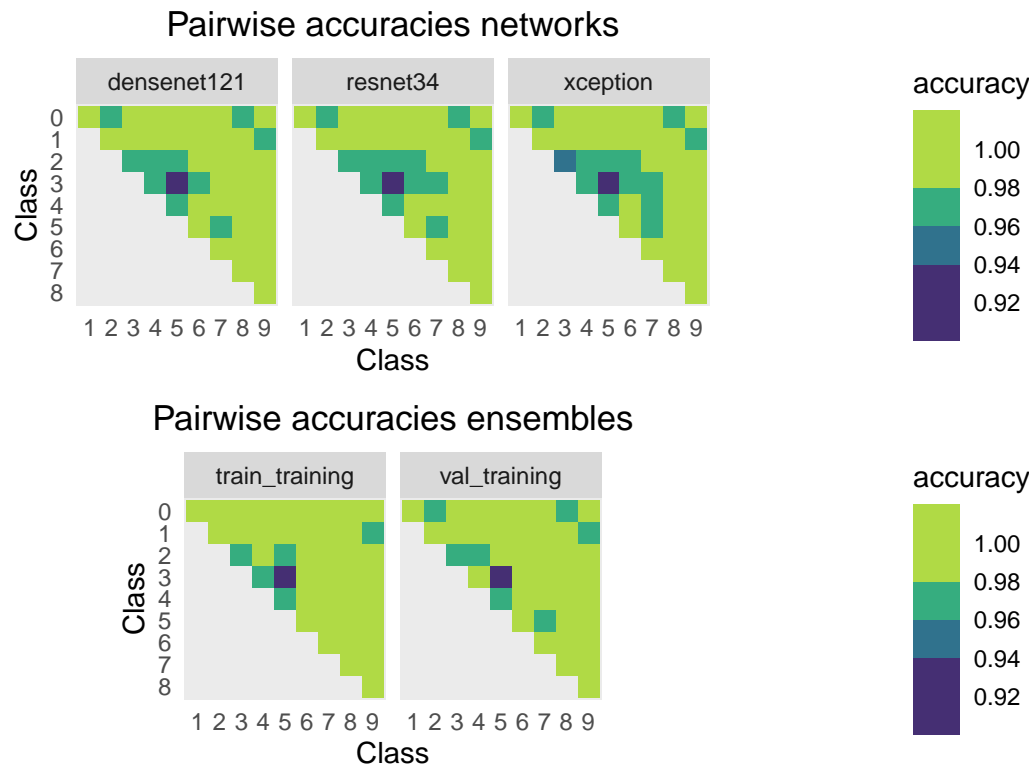
Pairwise accuracies networks



Pairwise accuracies ensembles

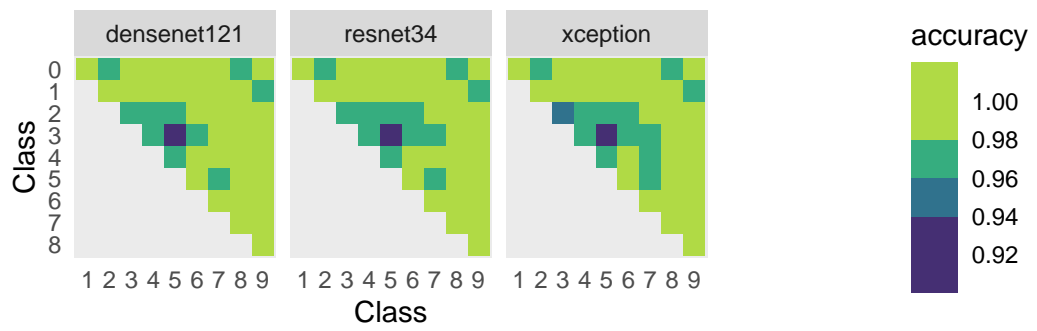


Replication 0 , fold 35

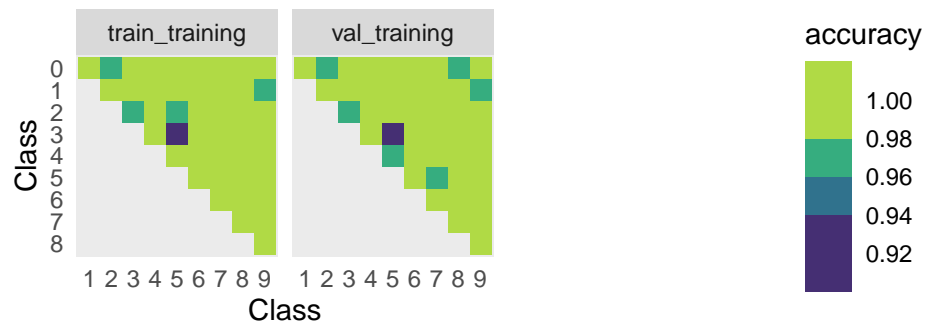


Replication 0 , fold 36

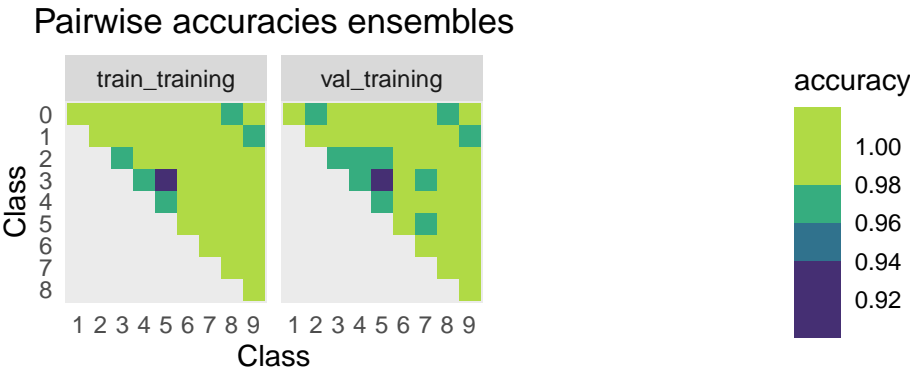
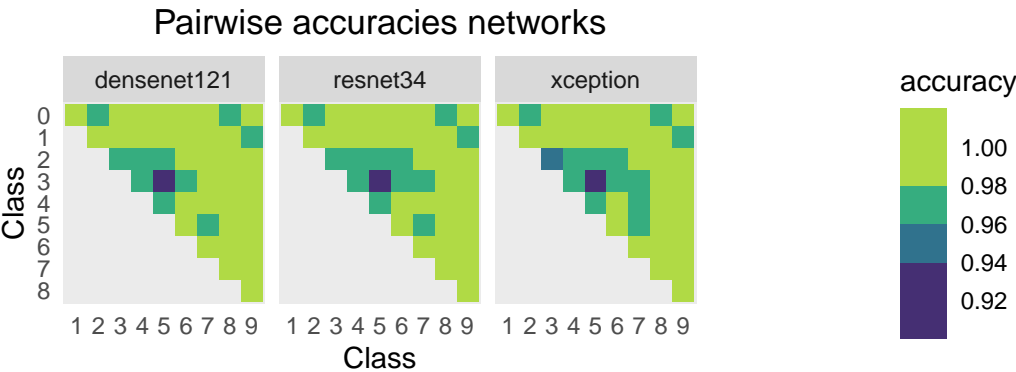
Pairwise accuracies networks



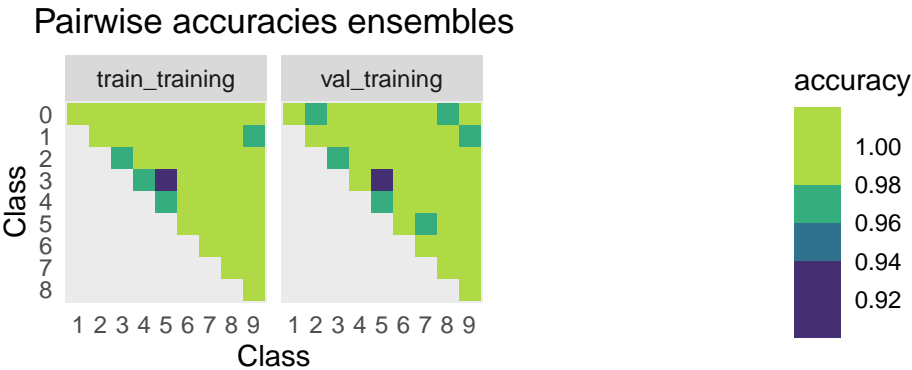
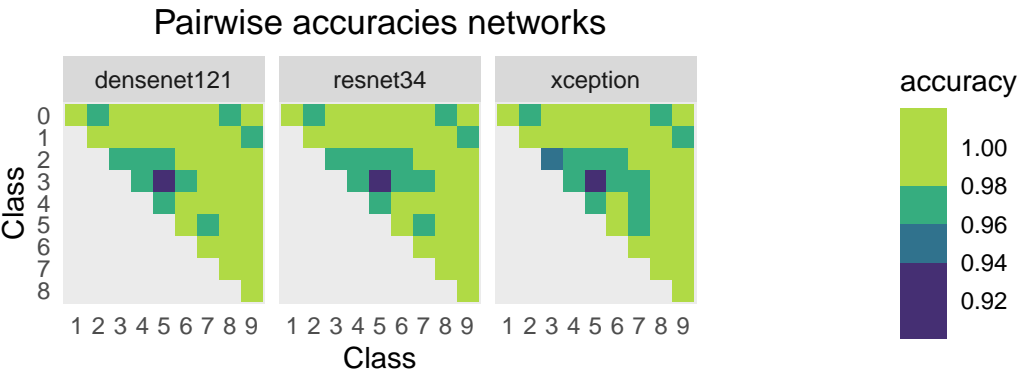
Pairwise accuracies ensembles



Replication 0 , fold 37

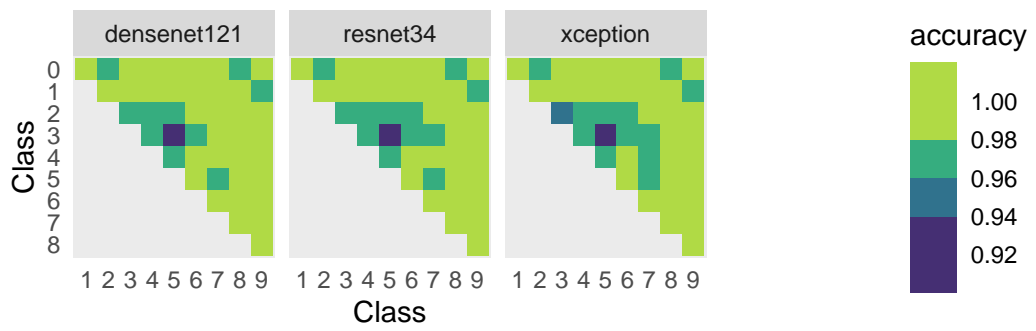


Replication 0 , fold 38

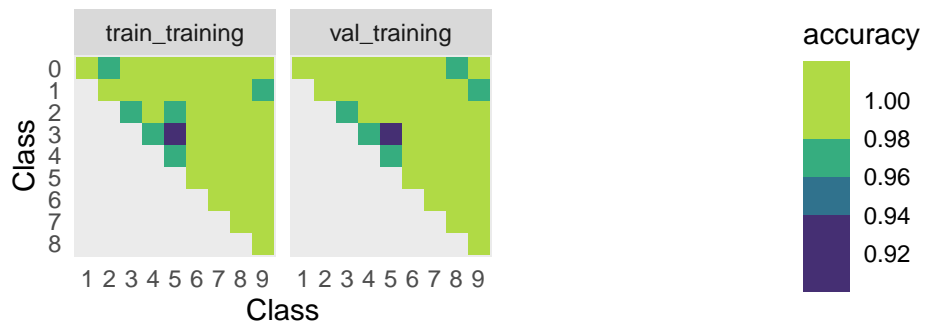


Replication 0 , fold 39

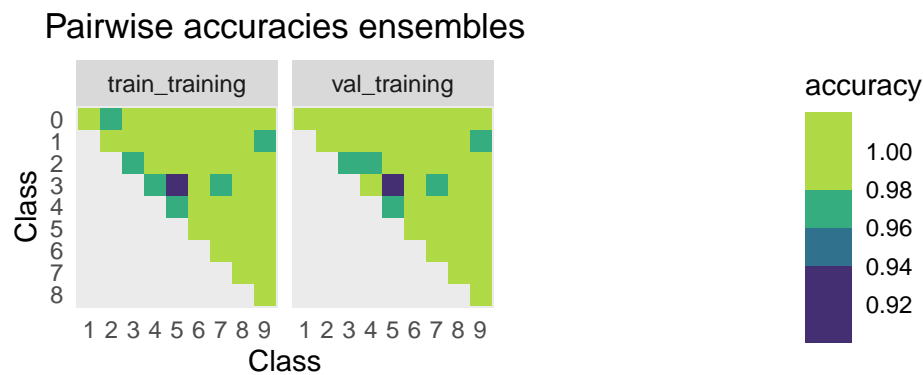
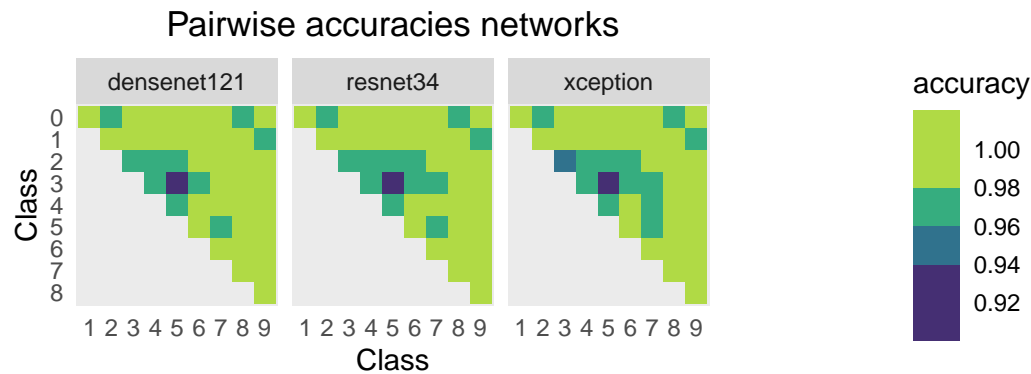
Pairwise accuracies networks



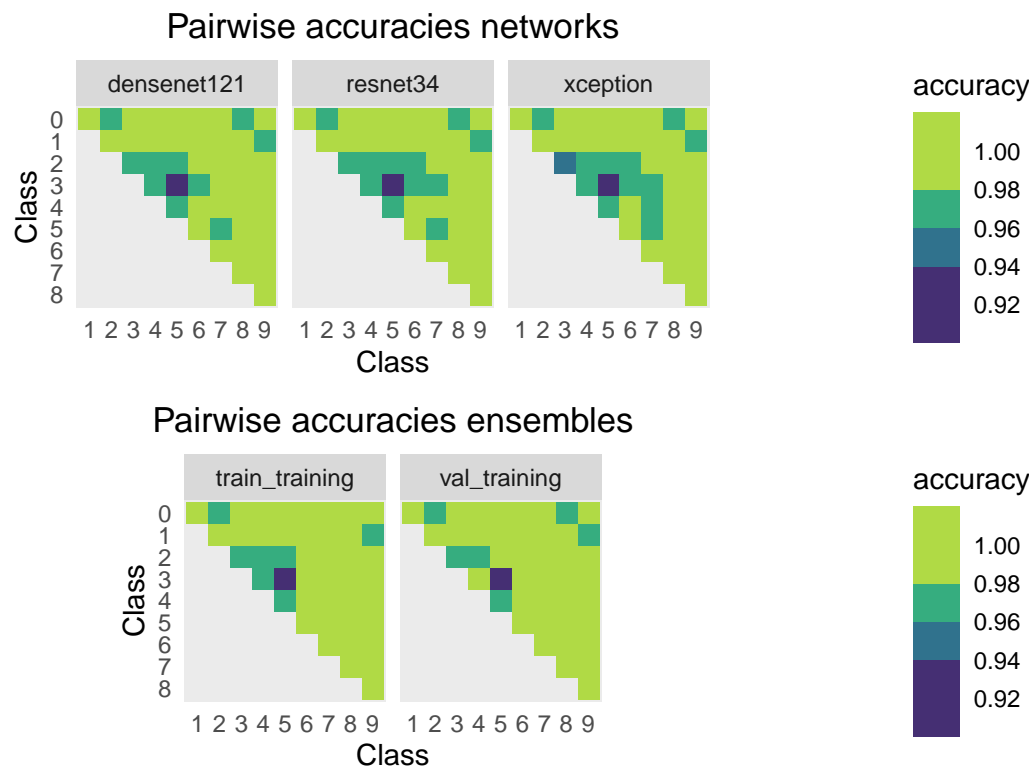
Pairwise accuracies ensembles



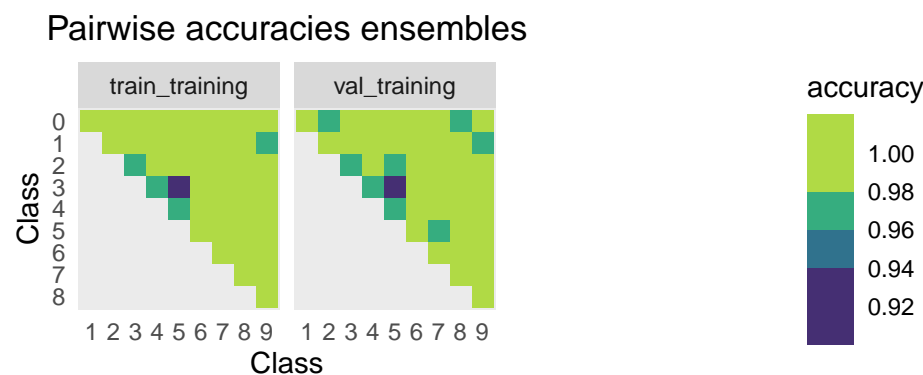
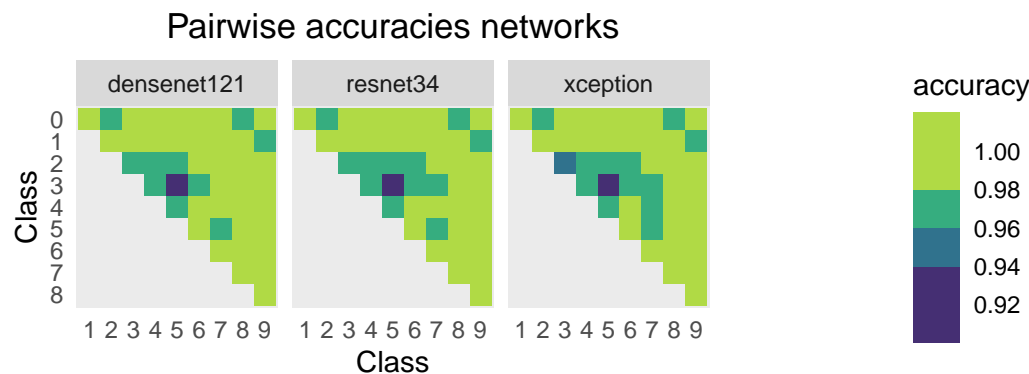
Replication 0 , fold 40



Replication 0 , fold 41

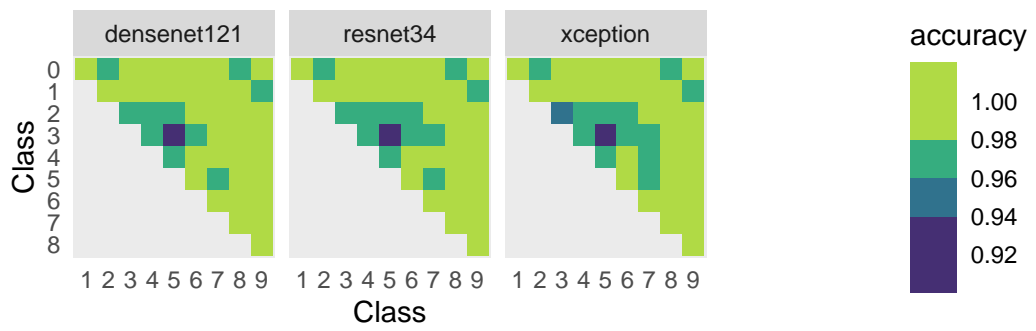


Replication 0 , fold 42

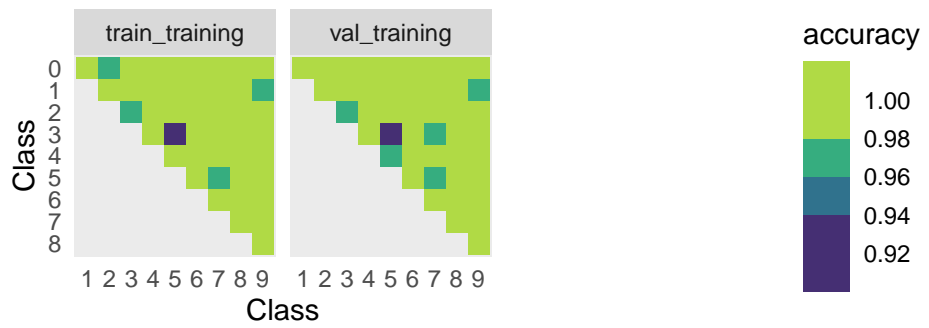


Replication 0 , fold 43

Pairwise accuracies networks

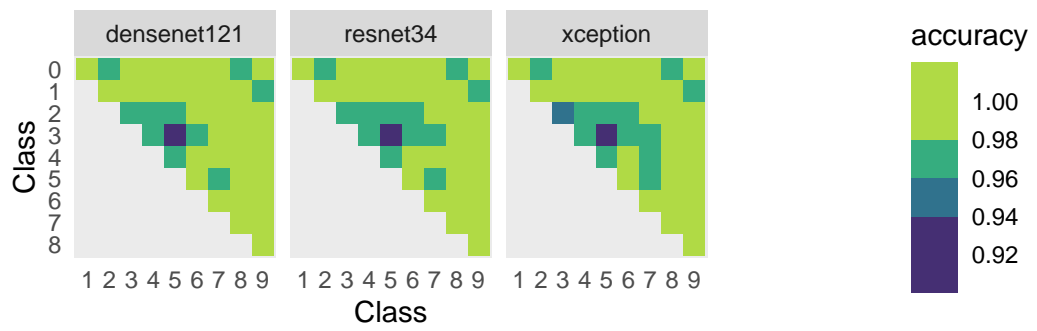


Pairwise accuracies ensembles

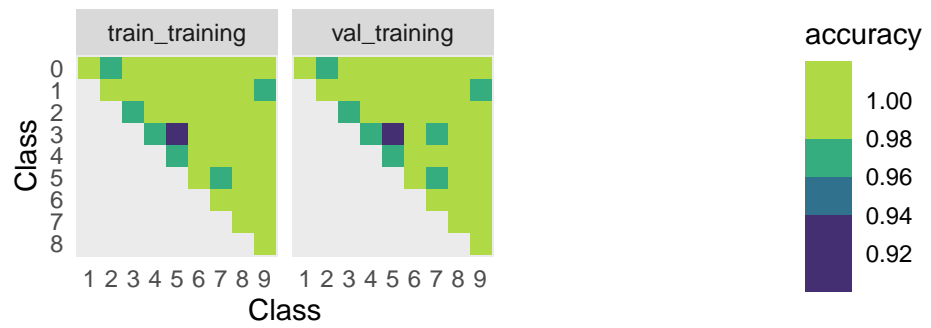


Replication 0 , fold 44

Pairwise accuracies networks

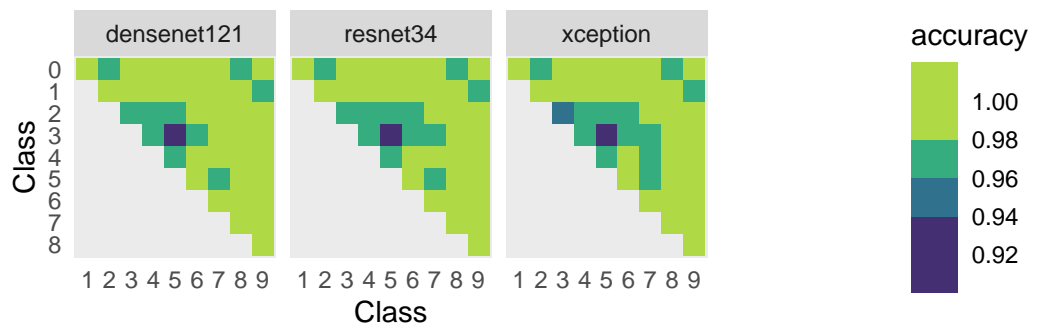


Pairwise accuracies ensembles

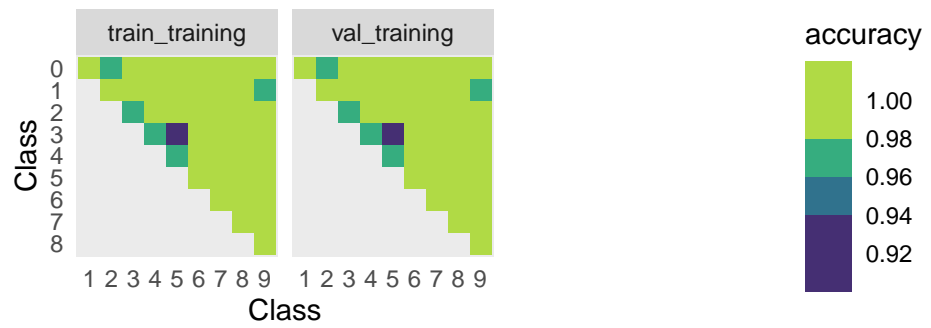


Replication 0 , fold 45

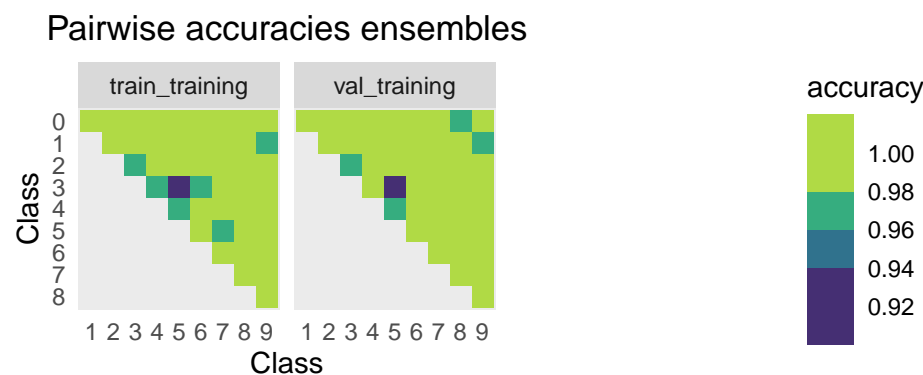
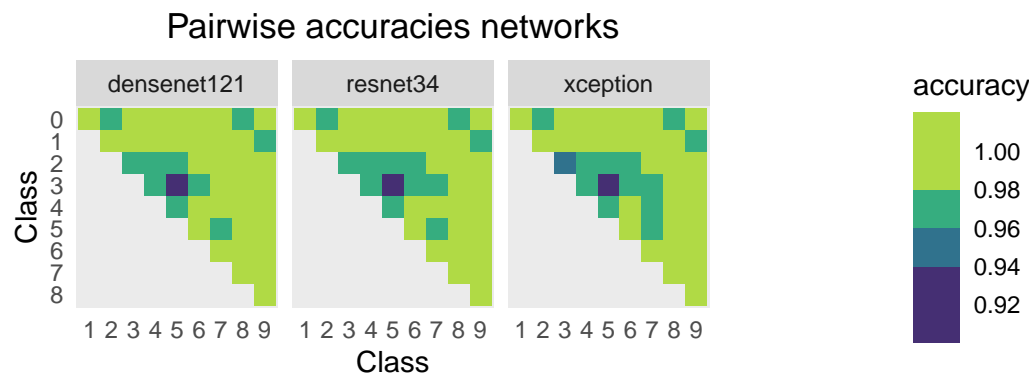
Pairwise accuracies networks



Pairwise accuracies ensembles

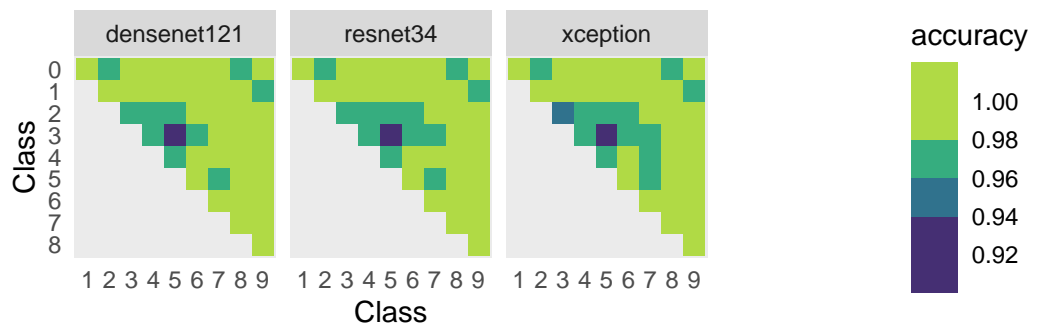


Replication 0 , fold 46

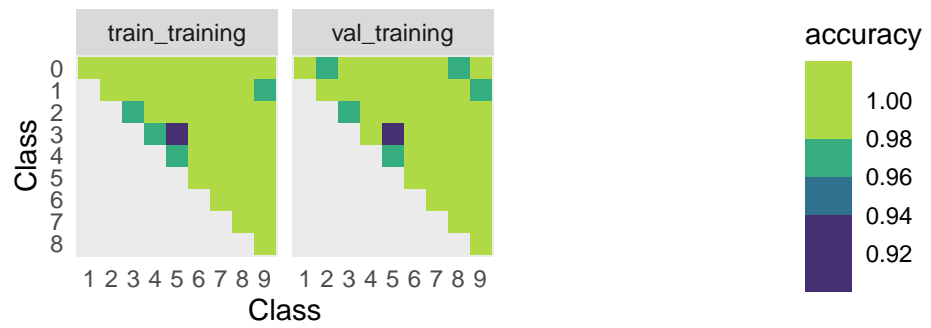


Replication 0 , fold 47

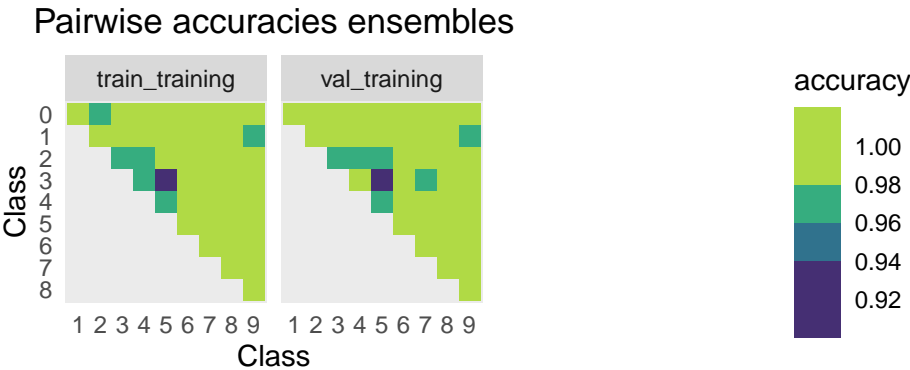
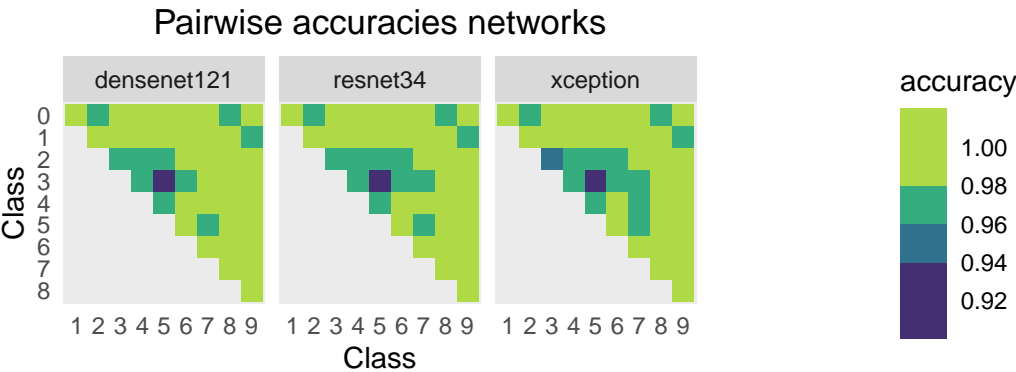
Pairwise accuracies networks



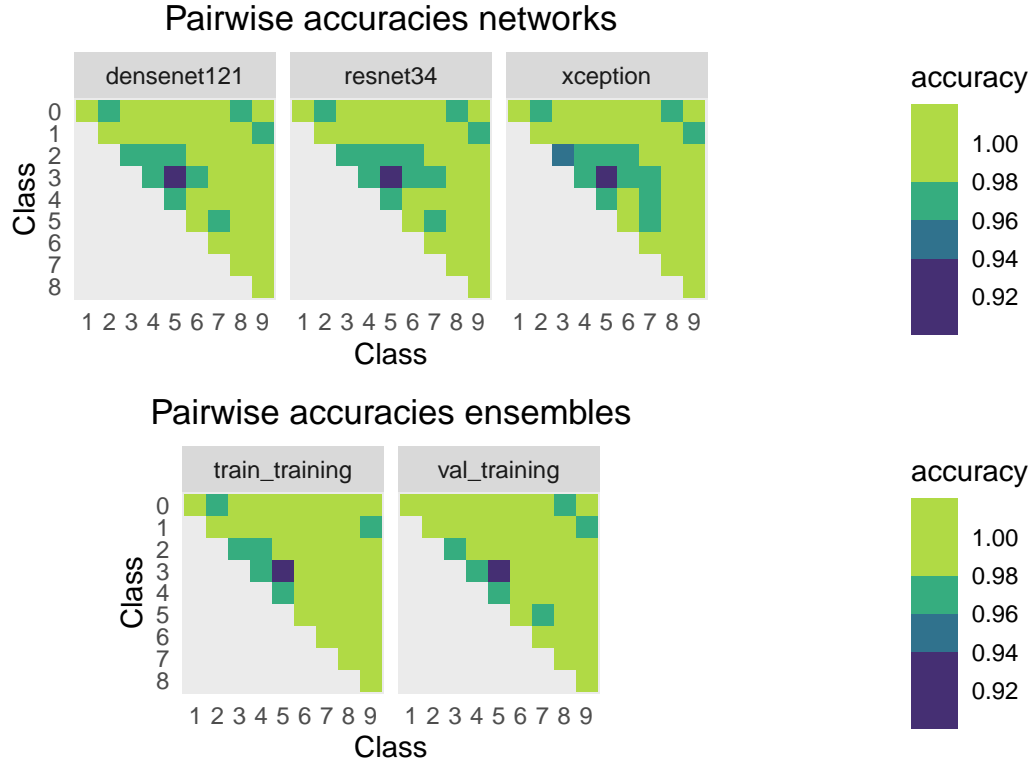
Pairwise accuracies ensembles



Replication 0 , fold 48



Replication 0 , fold 49



Networks are same across all the folds. vt and tt for a given fold have no special relationship, they are displayed together just for convenience. tt again seems to be more successfull at improving the pairwise probabilities.

CIFAR 10 - validation set of size 25000

```
base_dir <- "../data/data_train_val_half_c100"
repls <- 0:9
folds <- 0:4
classes <- 100

net_pw_results <- read.csv(file.path(base_dir, "net_pw_accuracies.csv"))
ens_pw_results <- read.csv(file.path(base_dir, "ensemble_pw_accuracies.csv"))
net_pw_results[, c("class1", "class2")] <- lapply(net_pw_results[, c("class1", "class2")], as.factor)
ens_pw_results[, c("class1", "class2")] <- lapply(ens_pw_results[, c("class1", "class2")], as.factor)

for (ri in repls)
{
  net_plot <- net_pw_results %>% filter(repli == ri) %>%
    ggplot(mapping=aes(x=class2, y=class1, fill=accuracy)) + geom_raster() + facet_wrap(~network) +
    xlab("Class") +
    ylab("Class") +
    scale_y_discrete(limits=rev, breaks=seq(0, classes, 20)) +
    scale_x_discrete(breaks=seq(0, classes, 20)) +
```

```

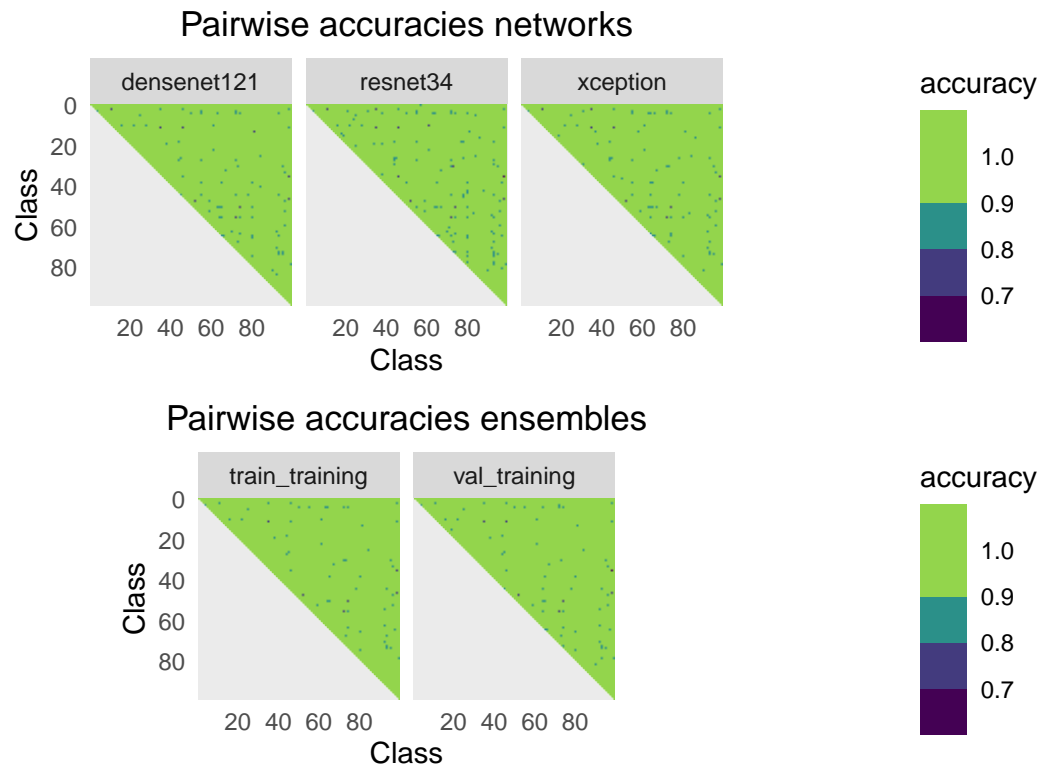
scale_fill_binned(type="viridis", name="accuracy", limits=c(0.7, 1)) +
coord_fixed() +
ggtitle("Pairwise accuracies networks") +
theme(plot.title = element_text(hjust = 0.5),
      axis.ticks = element_blank(),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank())

for (fi in folds)
{
  ens_plot <- ens_pw_results %>% filter(repli == ri & fold == fi) %>%
    ggplot(mapping=aes(x=class2, y=class1, fill=accuracy)) + geom_raster() + facet_wrap(~train_set) +
    xlab("Class") +
    ylab("Class") +
    scale_y_discrete(limits=rev, breaks=seq(0, classes, 20)) +
    scale_x_discrete(breaks=seq(0, classes, 20)) +
    coord_fixed() +
    ggtitle("Pairwise accuracies ensembles") +
    scale_fill_binned(type="viridis", name="accuracy", limits=c(0.7, 1)) +
    theme(plot.title = element_text(hjust = 0.5),
          axis.ticks = element_blank(),
          panel.grid.major = element_blank(),
          panel.grid.minor = element_blank())

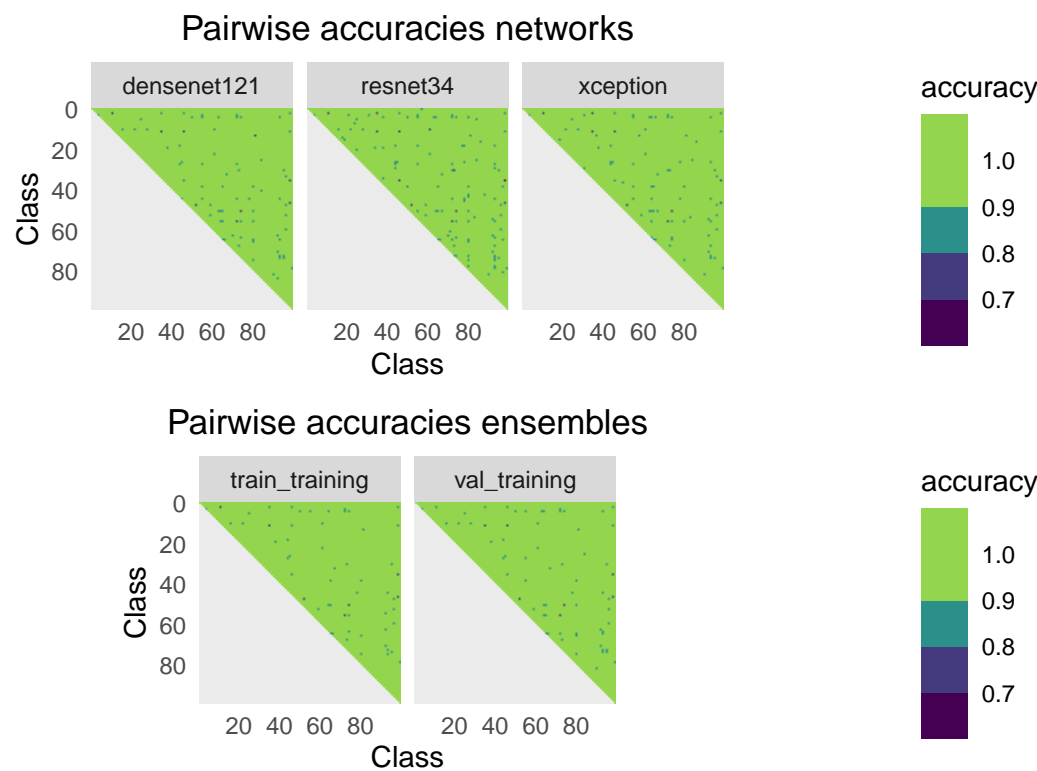
  print((net_plot/ens_plot) + plot_annotation(title=paste("Replication ", ri, ", fold ", fi)))
}
}

```

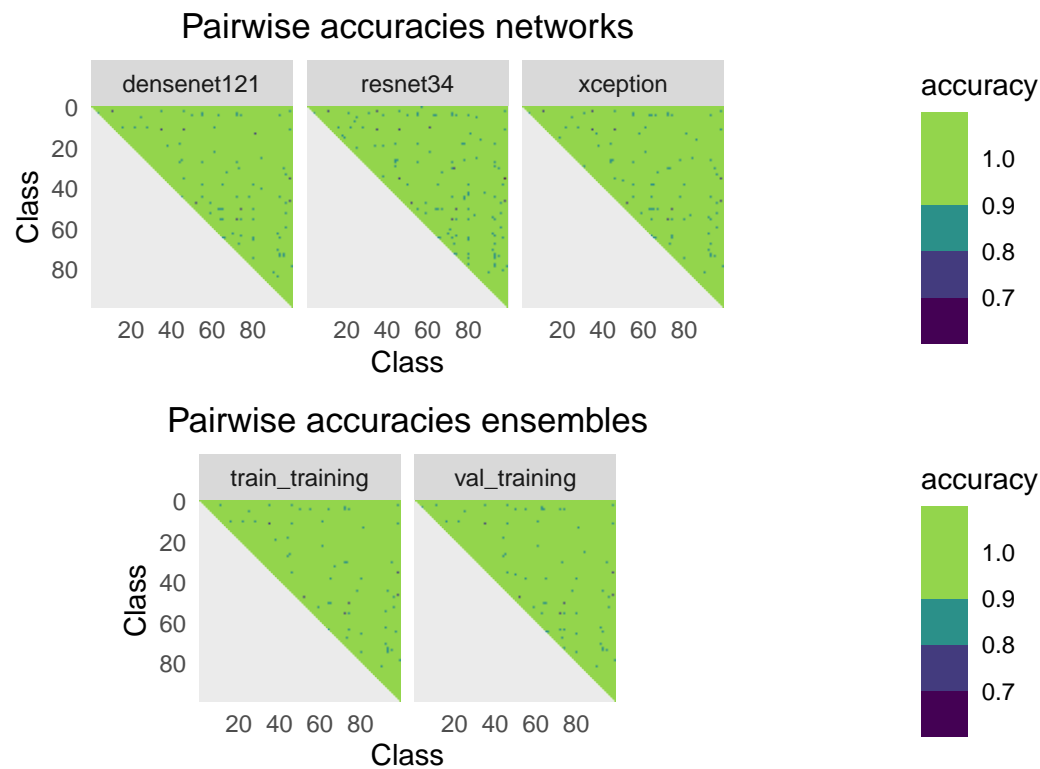
Replication 0 , fold 0



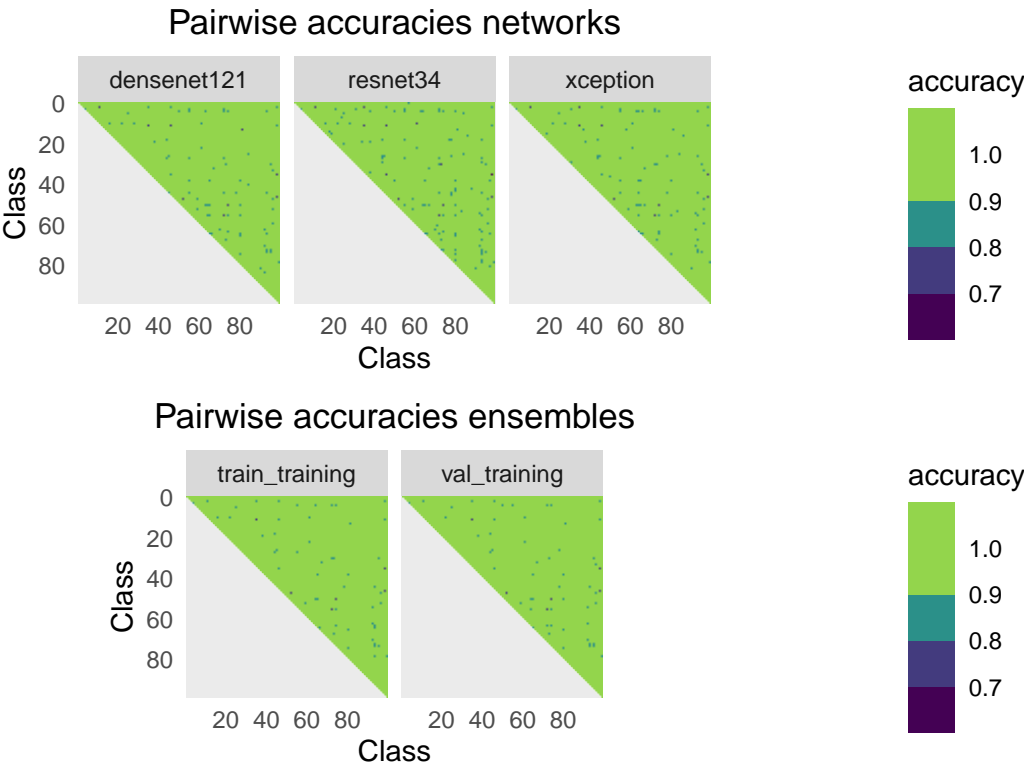
Replication 0 , fold 1



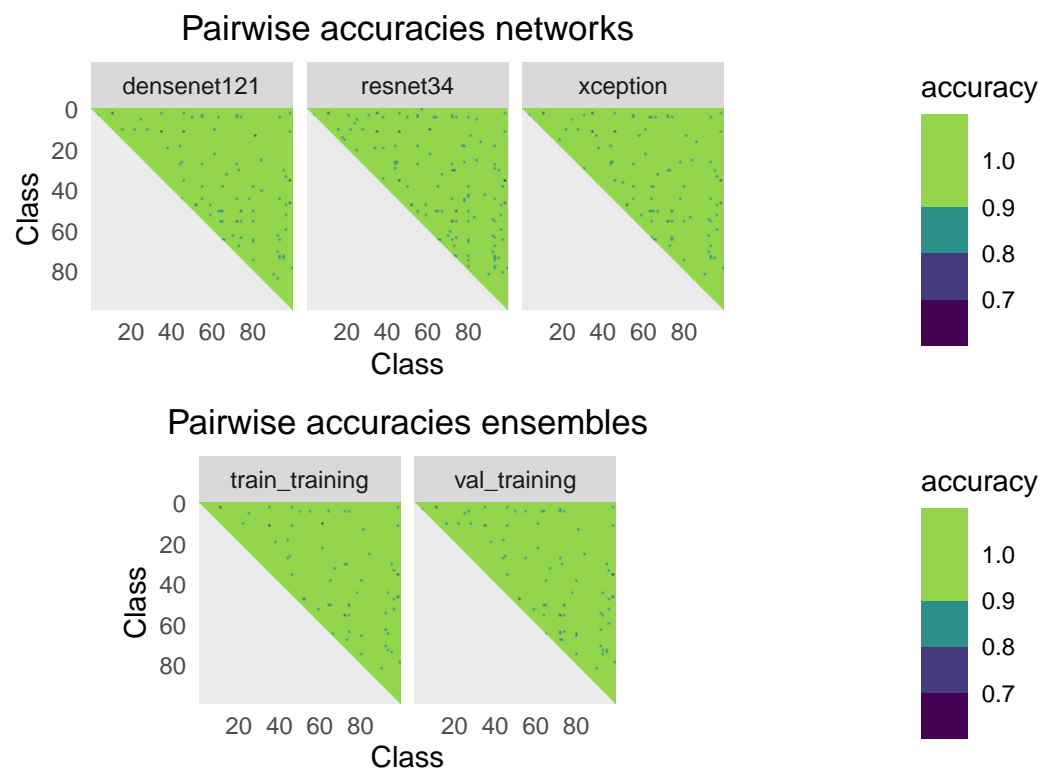
Replication 0 , fold 2



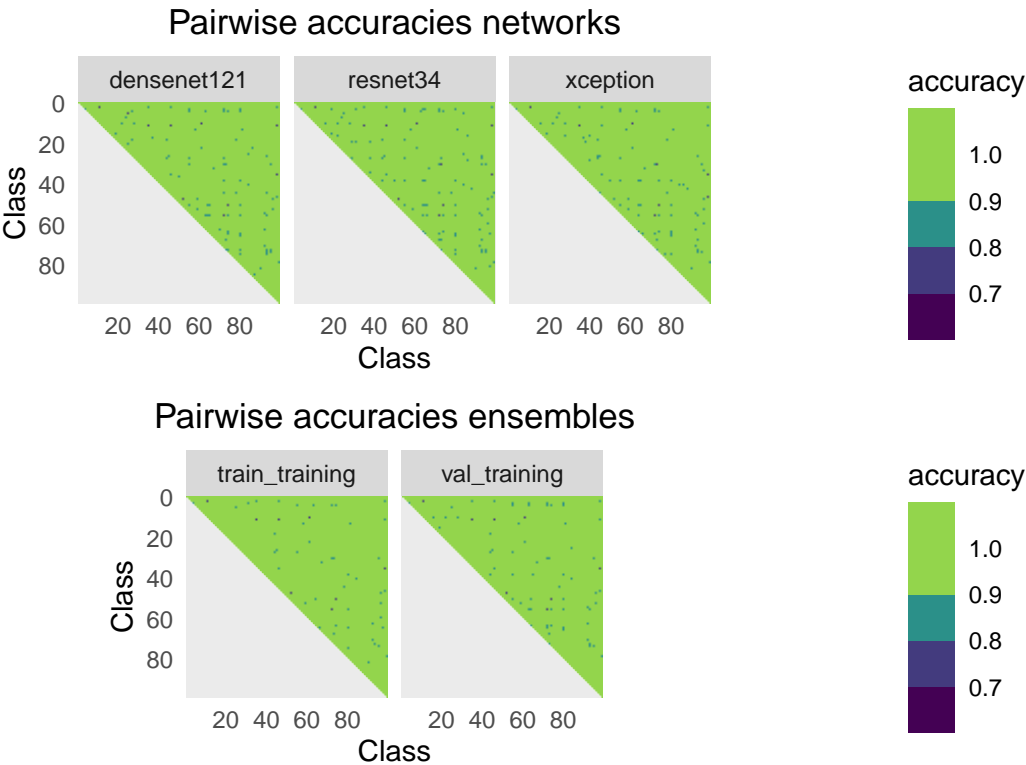
Replication 0 , fold 3



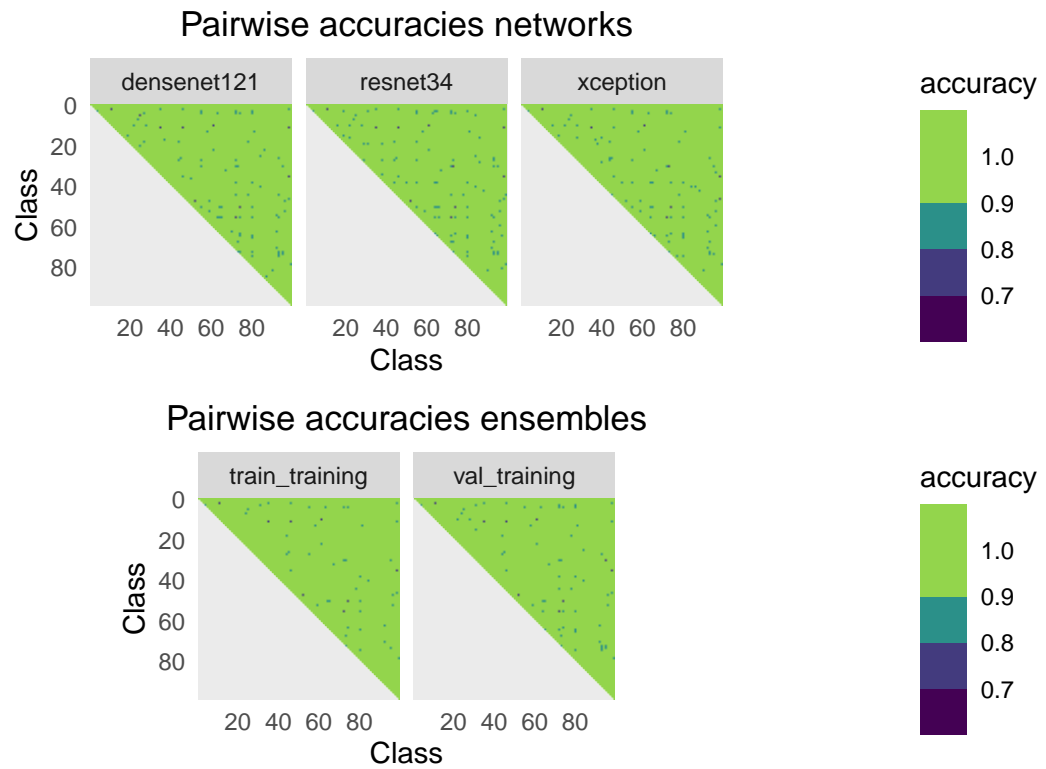
Replication 0 , fold 4



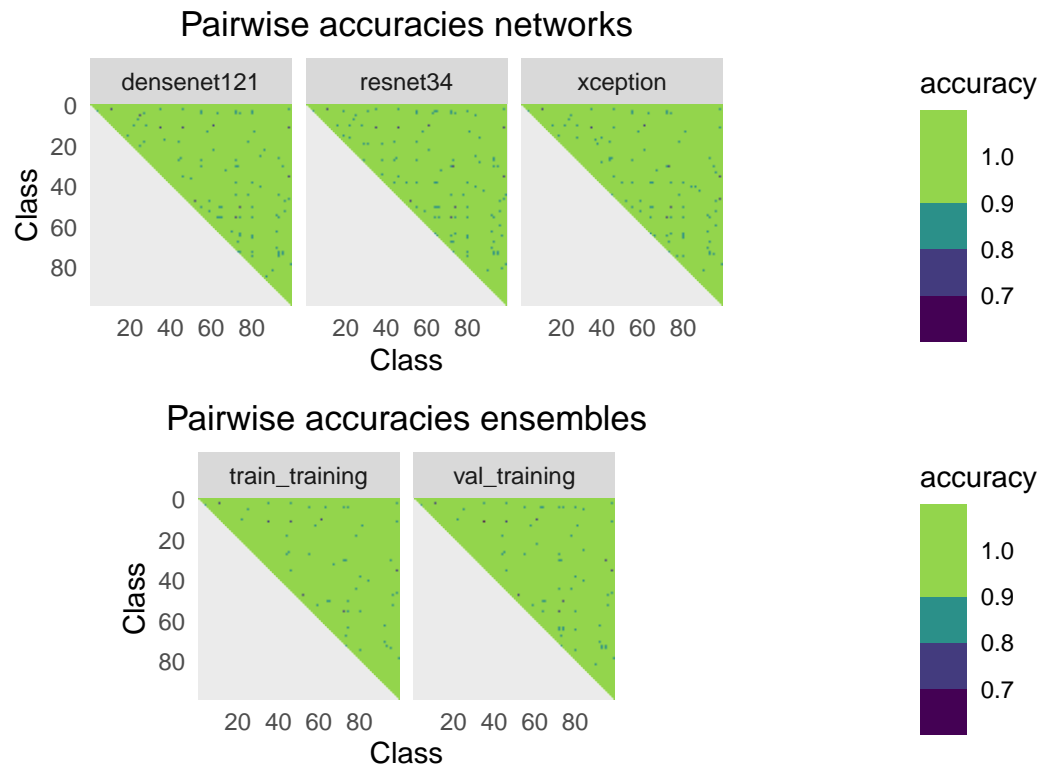
Replication 1 , fold 0



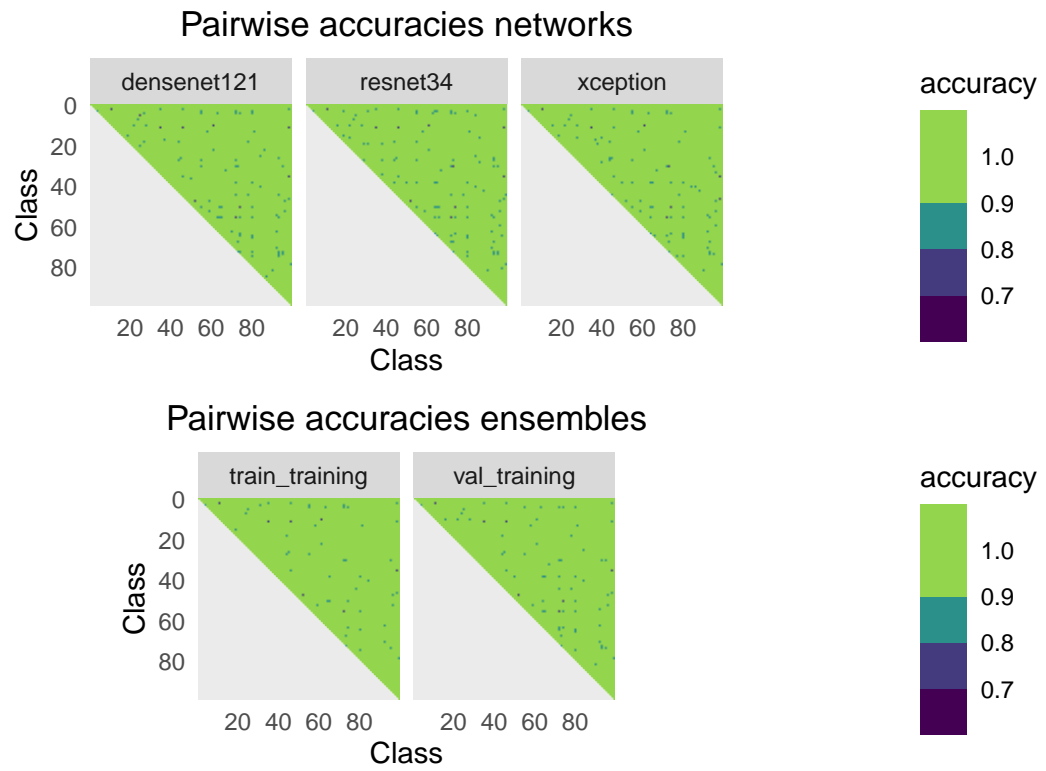
Replication 1 , fold 1



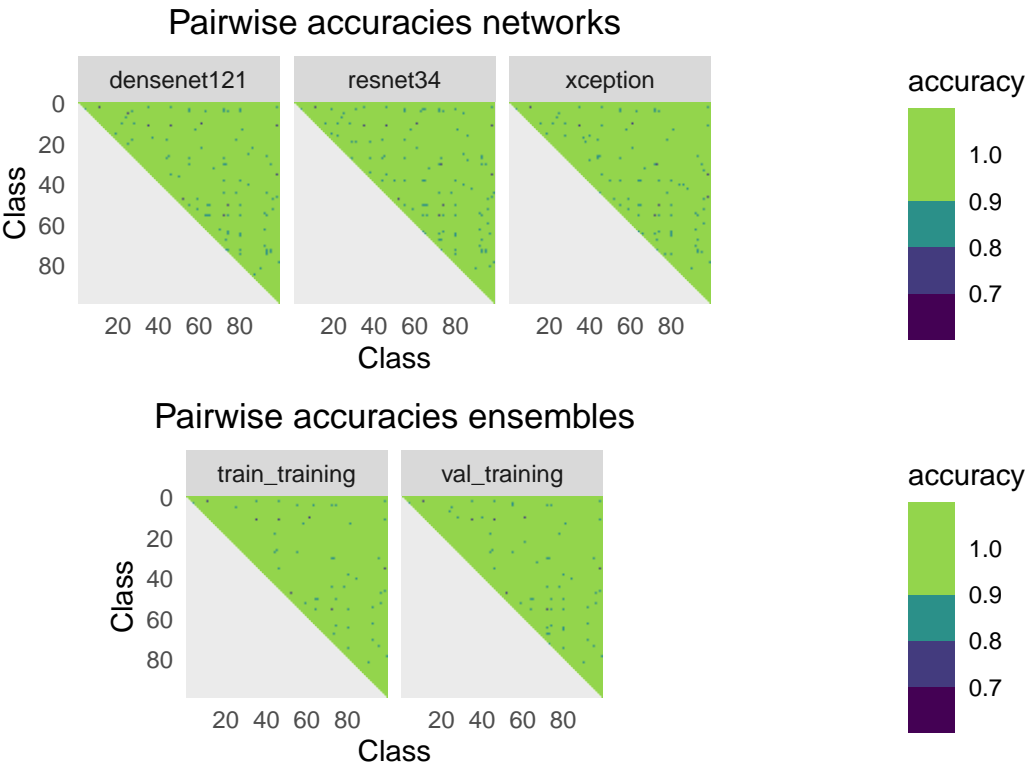
Replication 1 , fold 2



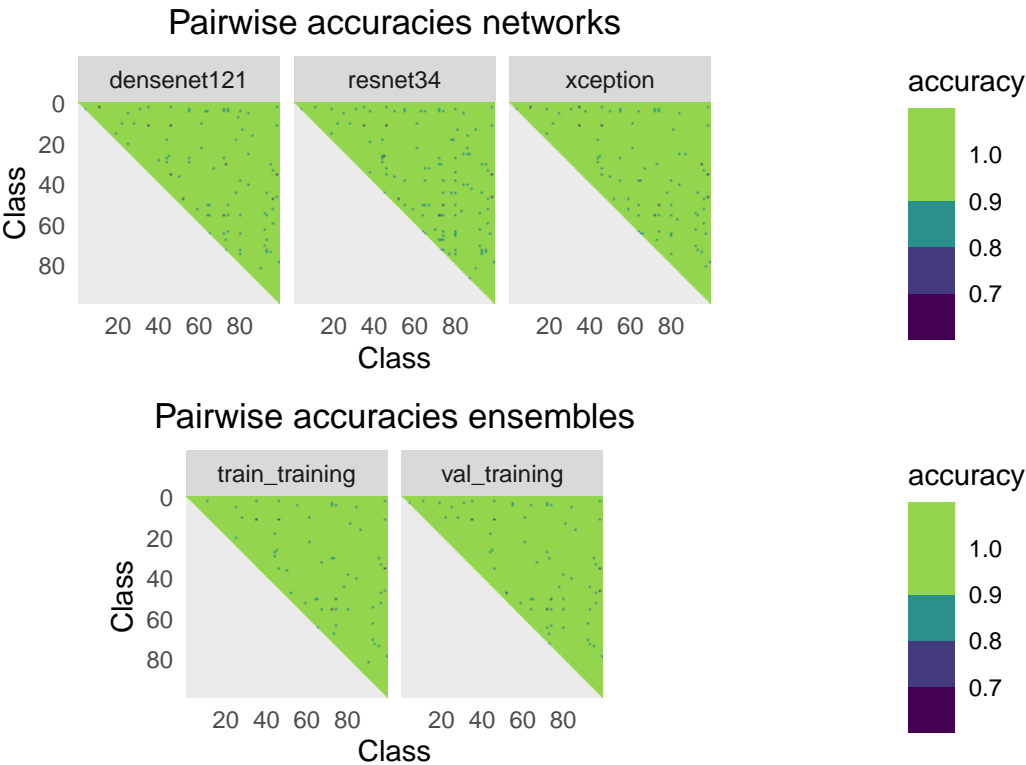
Replication 1 , fold 3



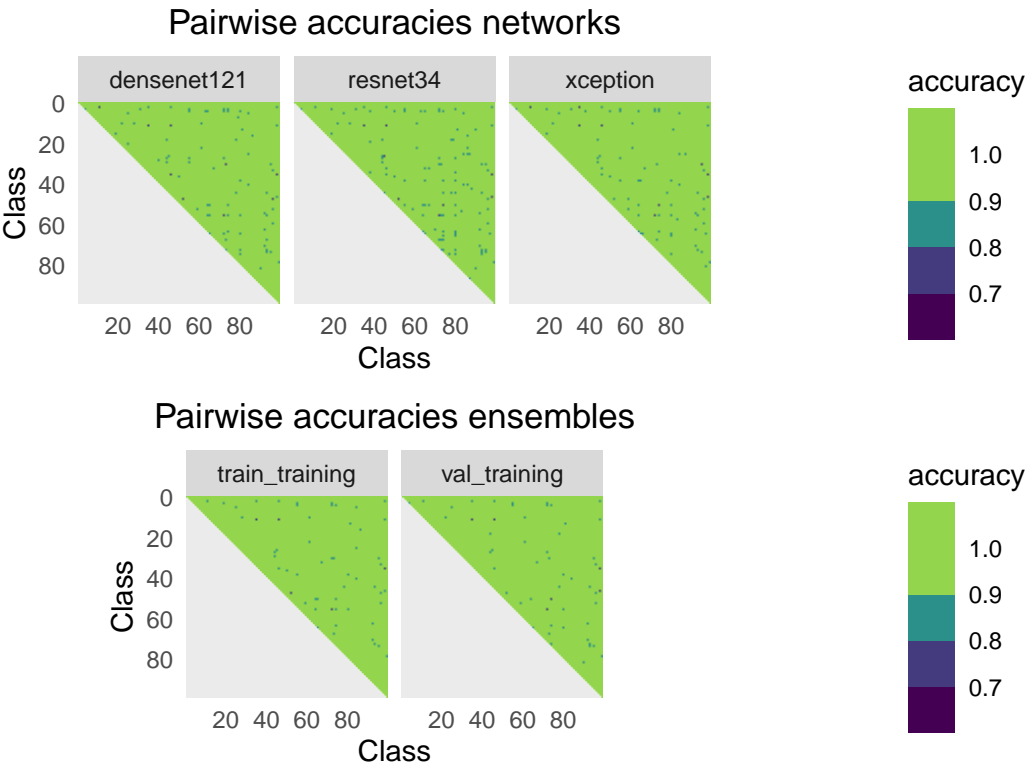
Replication 1 , fold 4



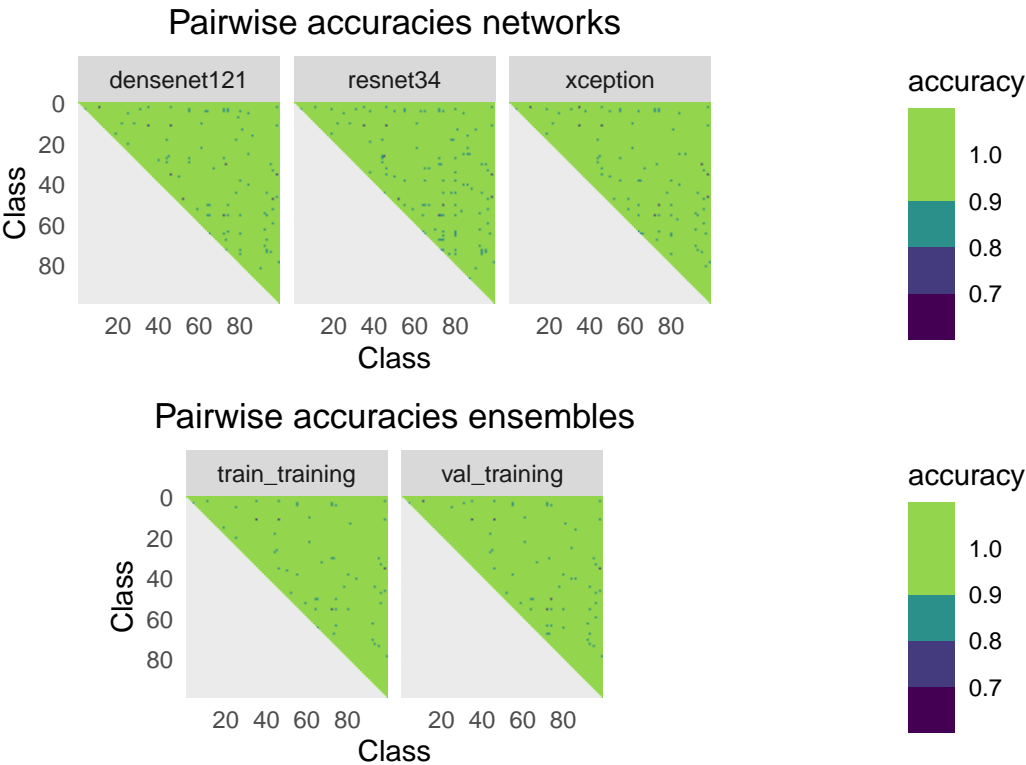
Replication 2 , fold 0



Replication 2 , fold 1

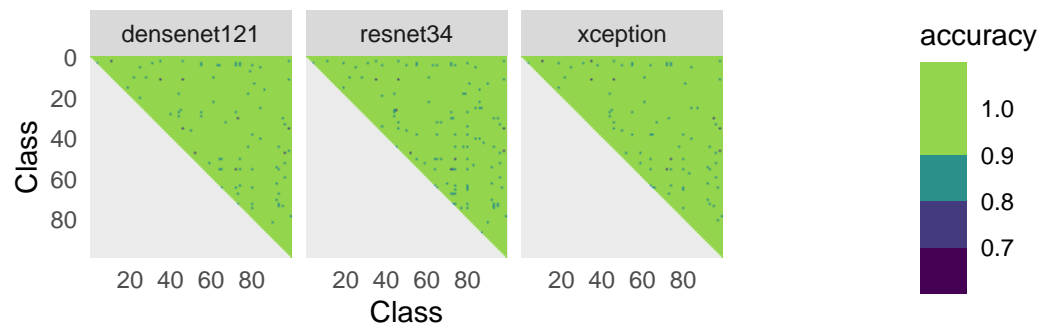


Replication 2 , fold 2

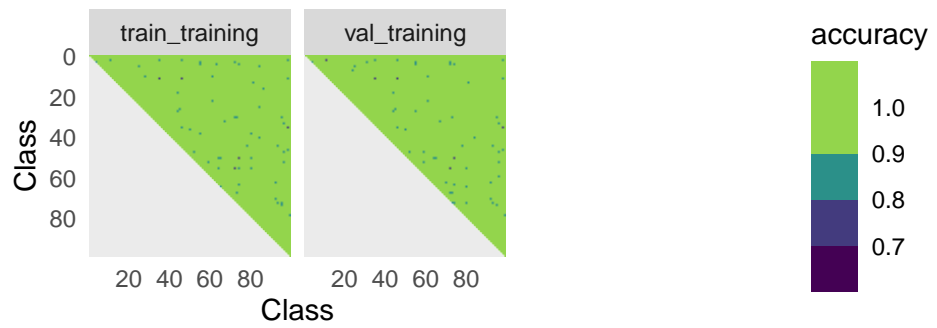


Replication 2 , fold 3

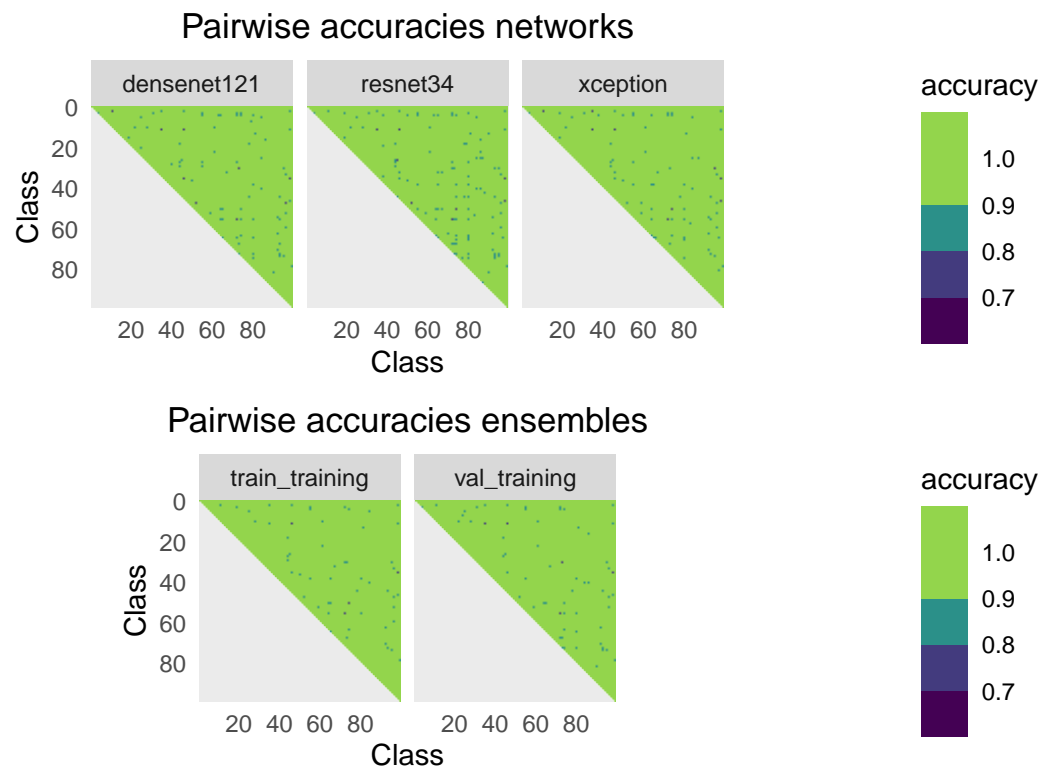
Pairwise accuracies networks



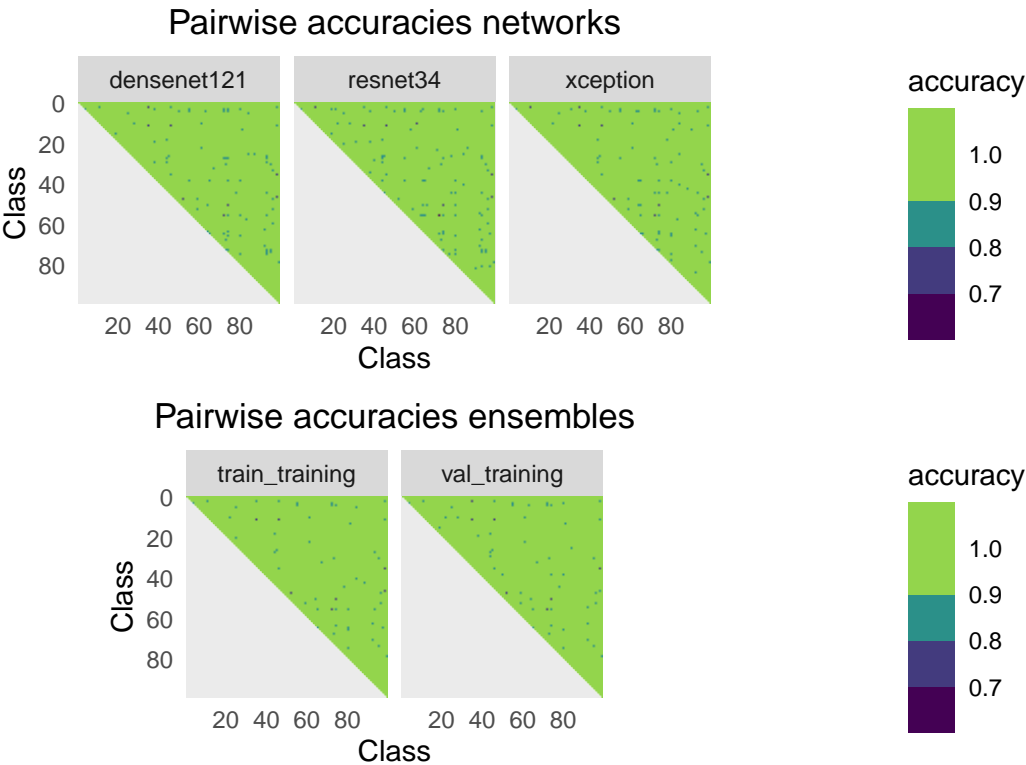
Pairwise accuracies ensembles



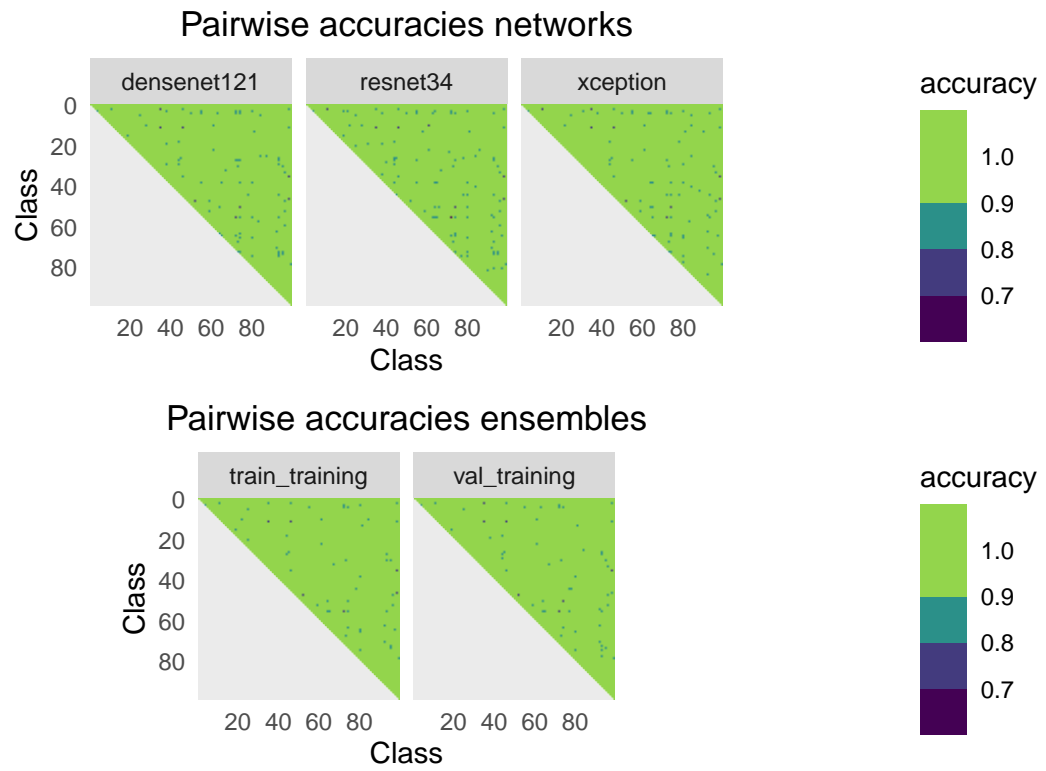
Replication 2 , fold 4



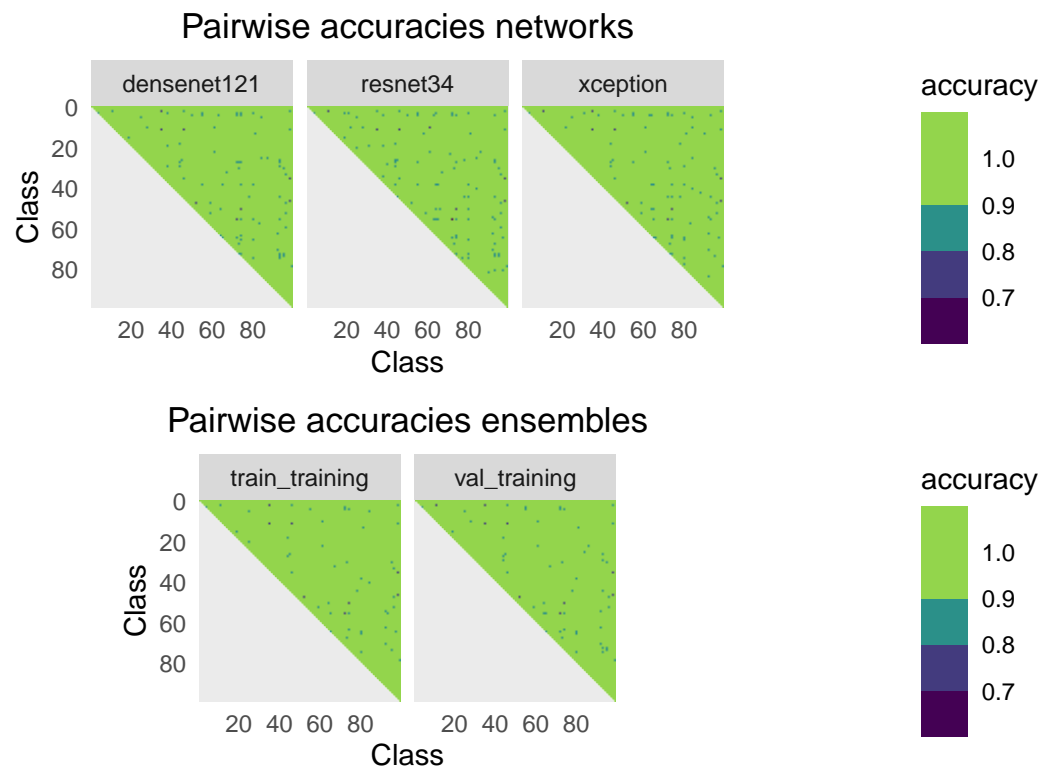
Replication 3 , fold 0



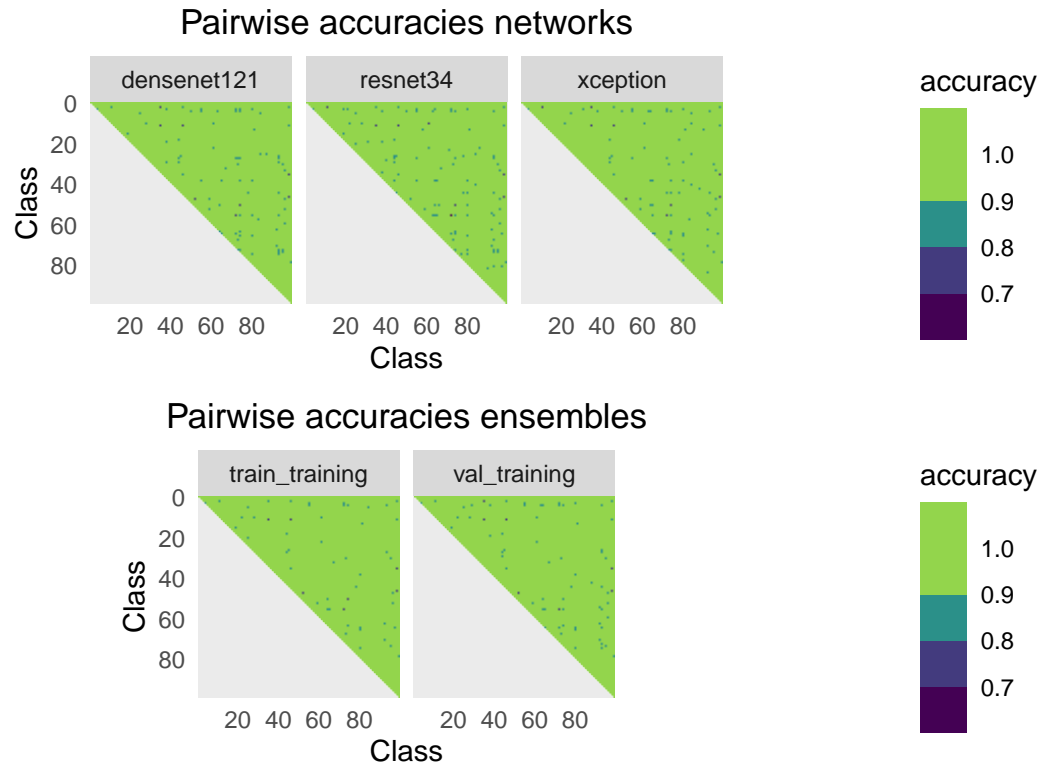
Replication 3 , fold 1



Replication 3 , fold 2

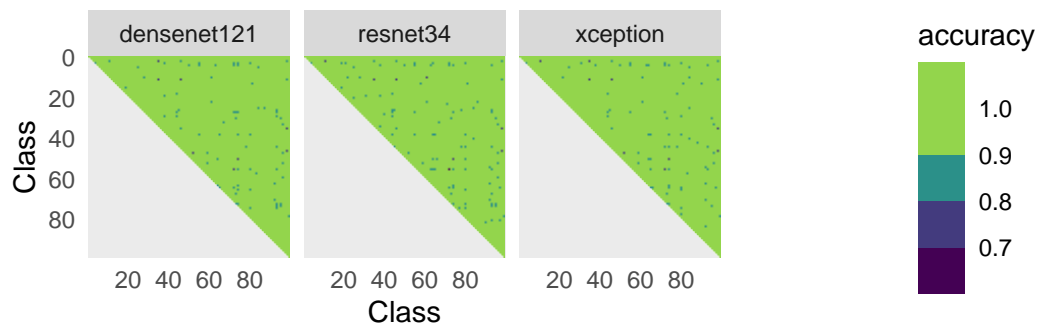


Replication 3 , fold 3

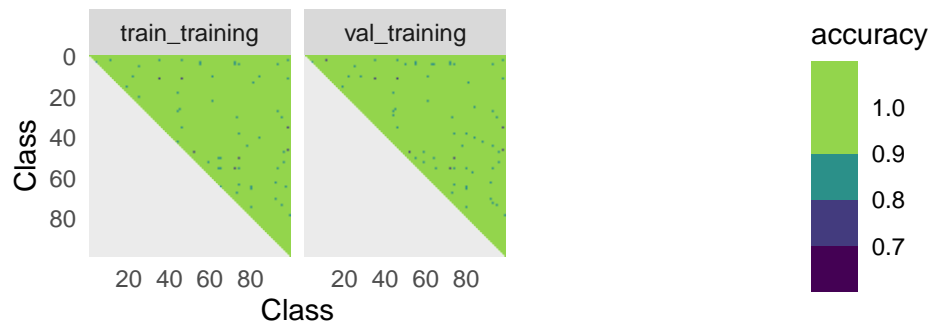


Replication 3 , fold 4

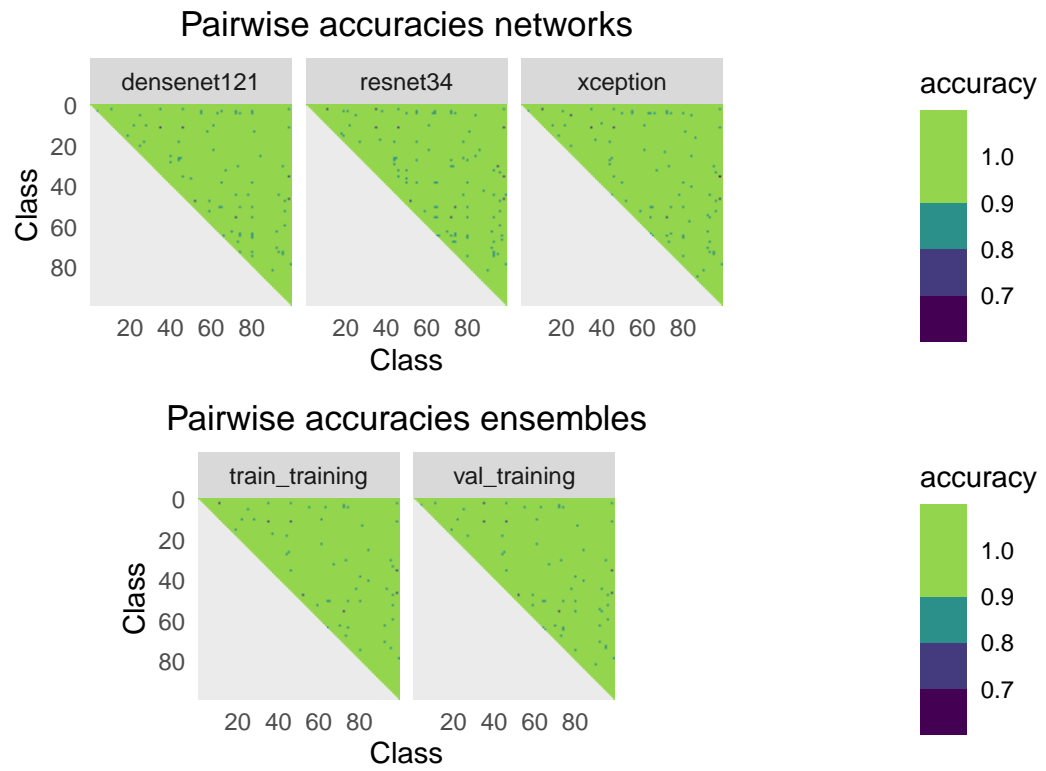
Pairwise accuracies networks



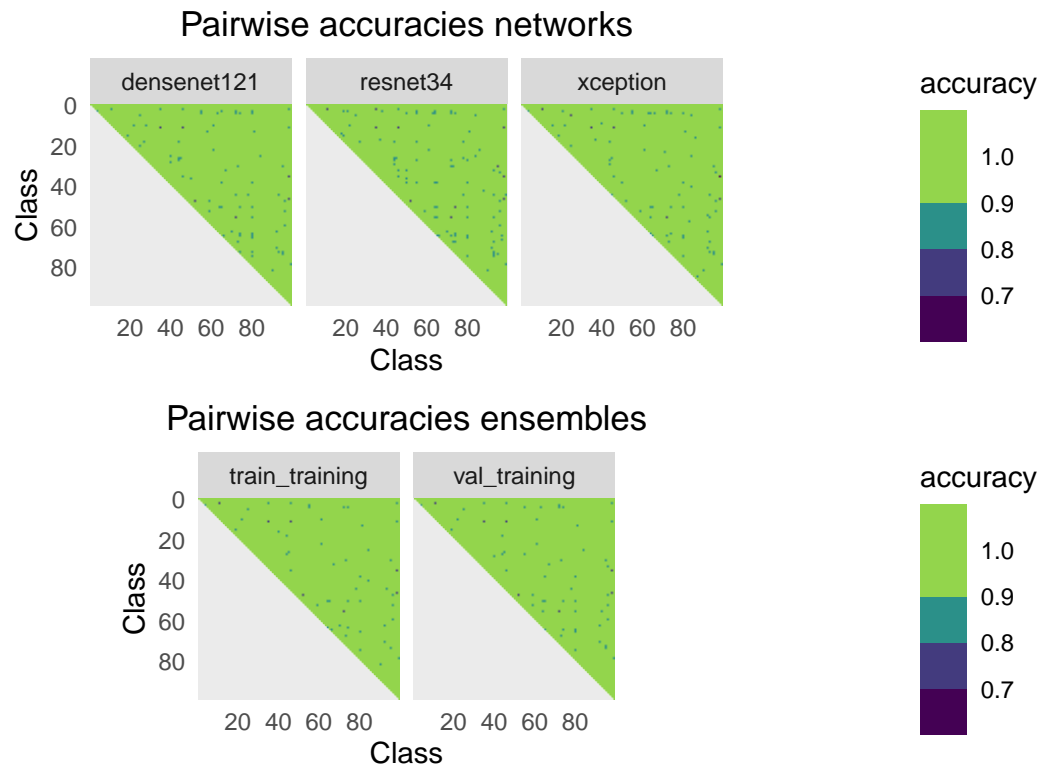
Pairwise accuracies ensembles



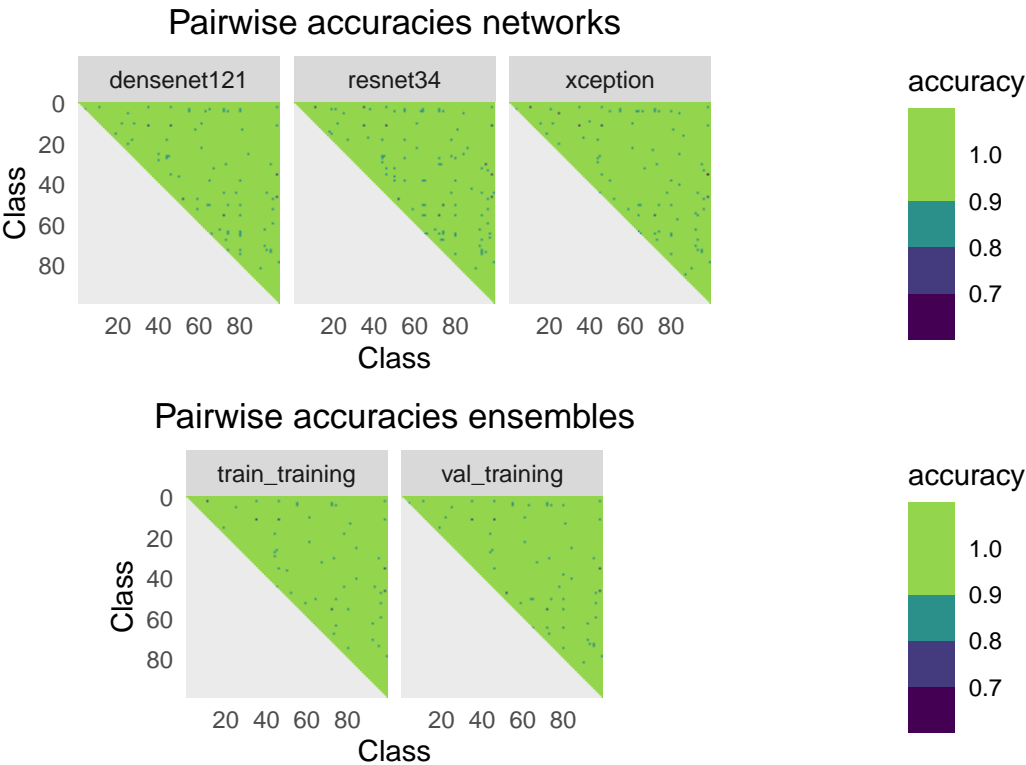
Replication 4 , fold 0



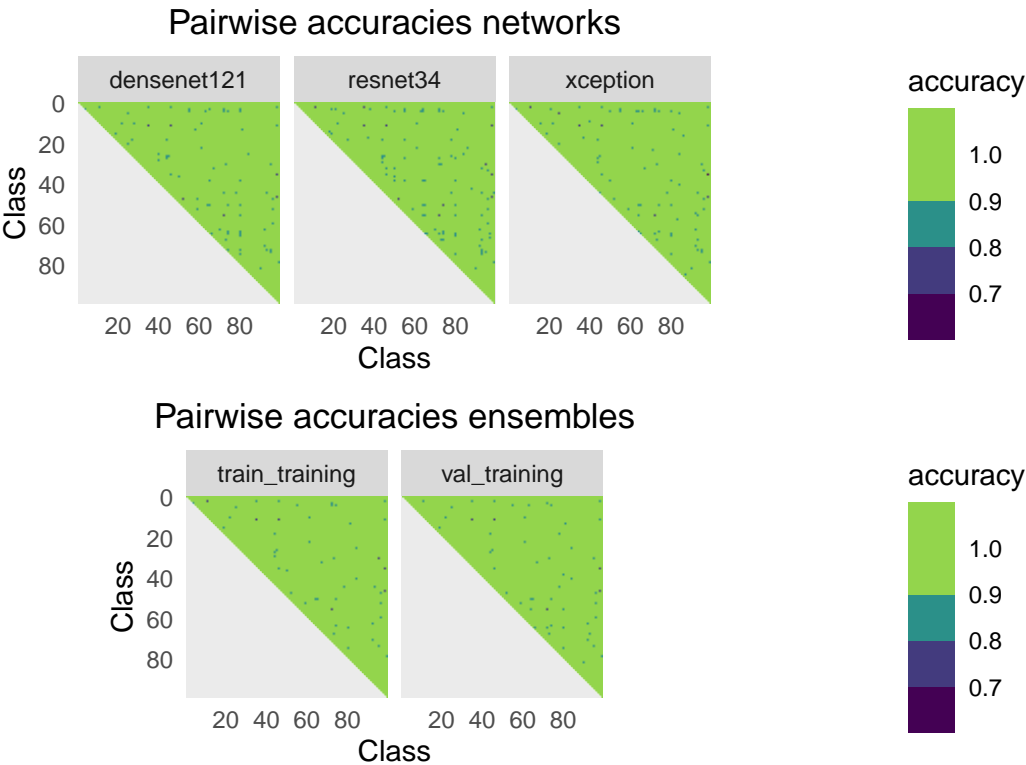
Replication 4 , fold 1



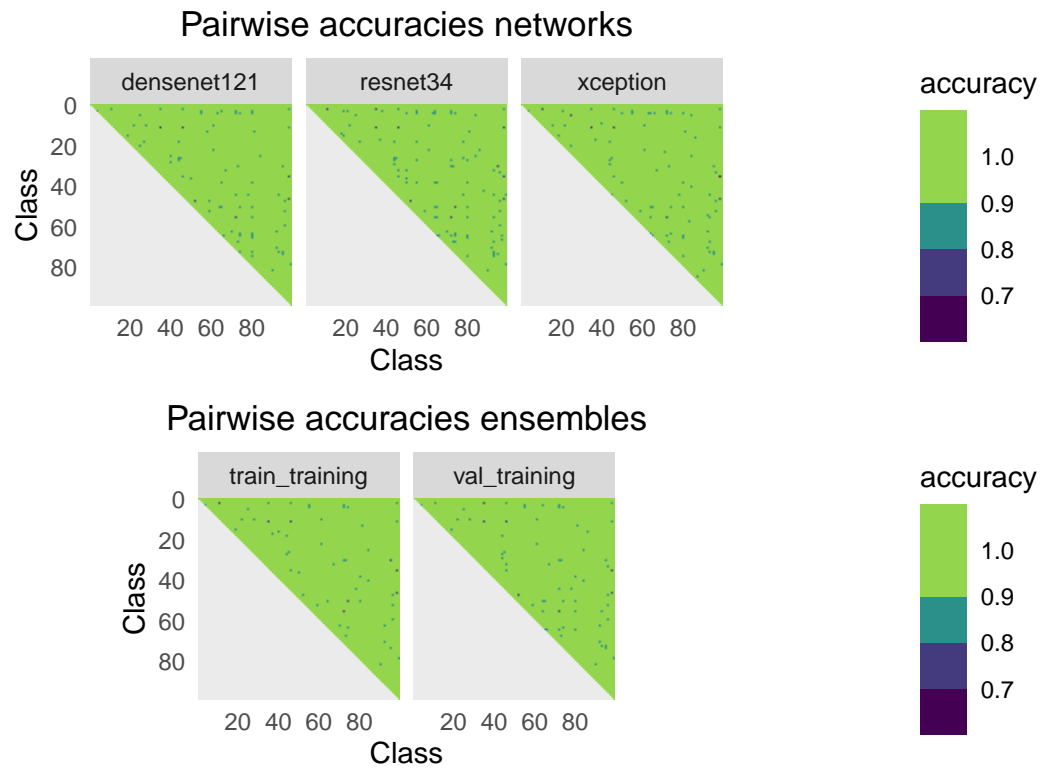
Replication 4 , fold 2



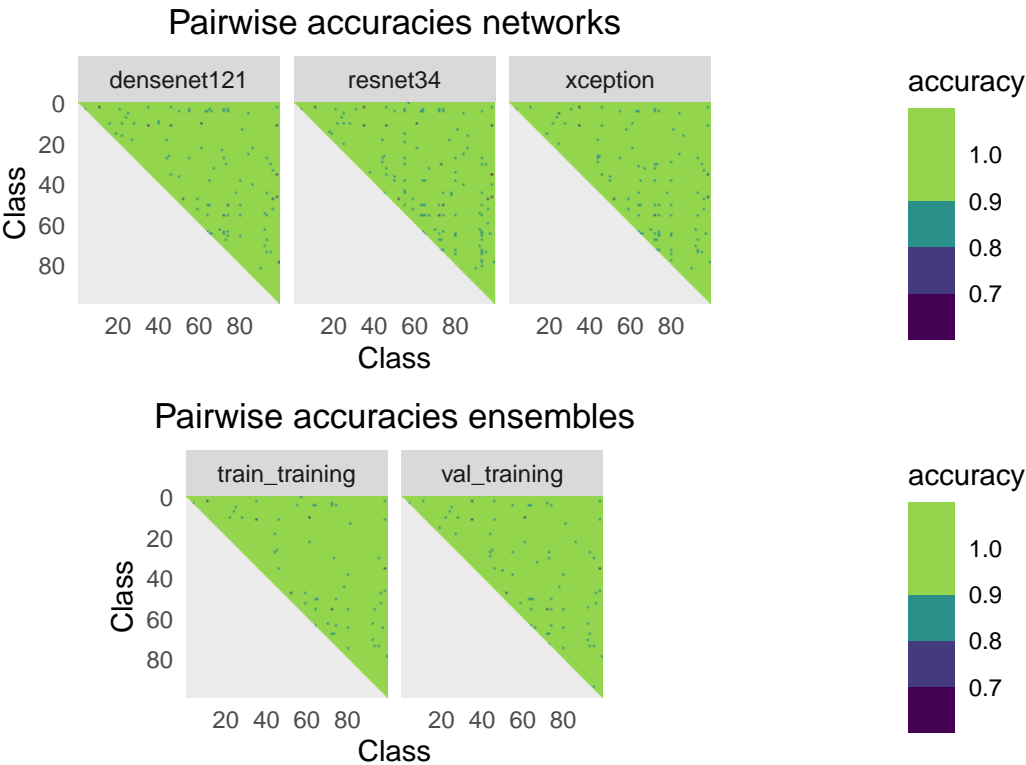
Replication 4 , fold 3



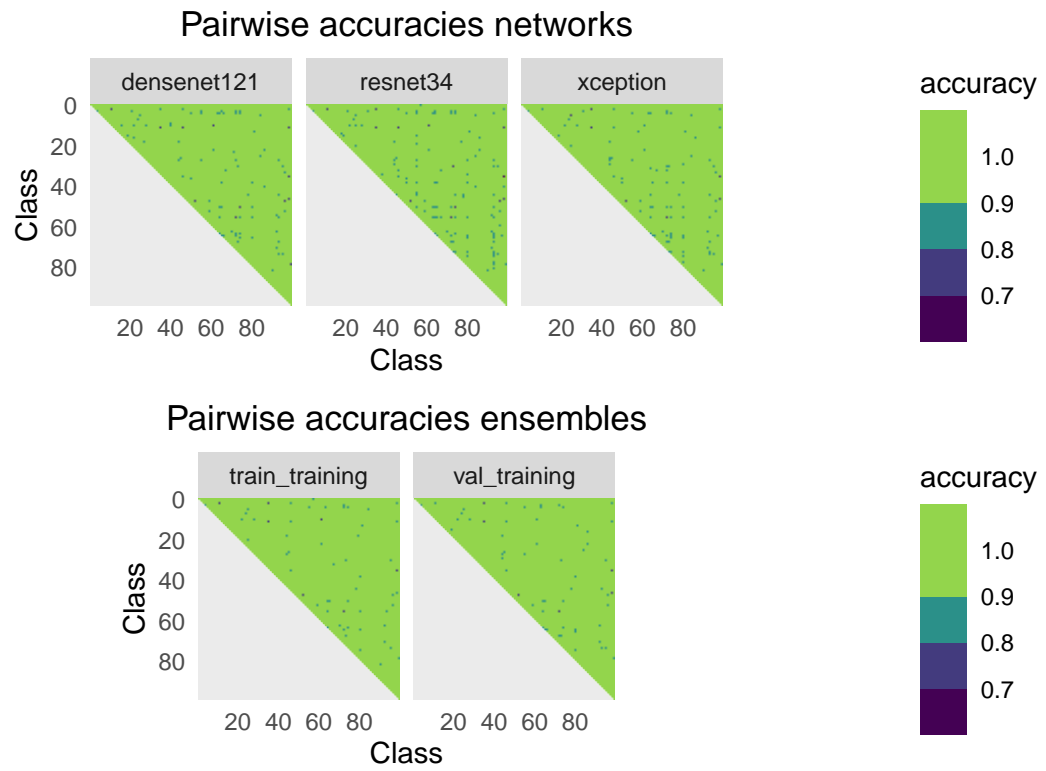
Replication 4 , fold 4



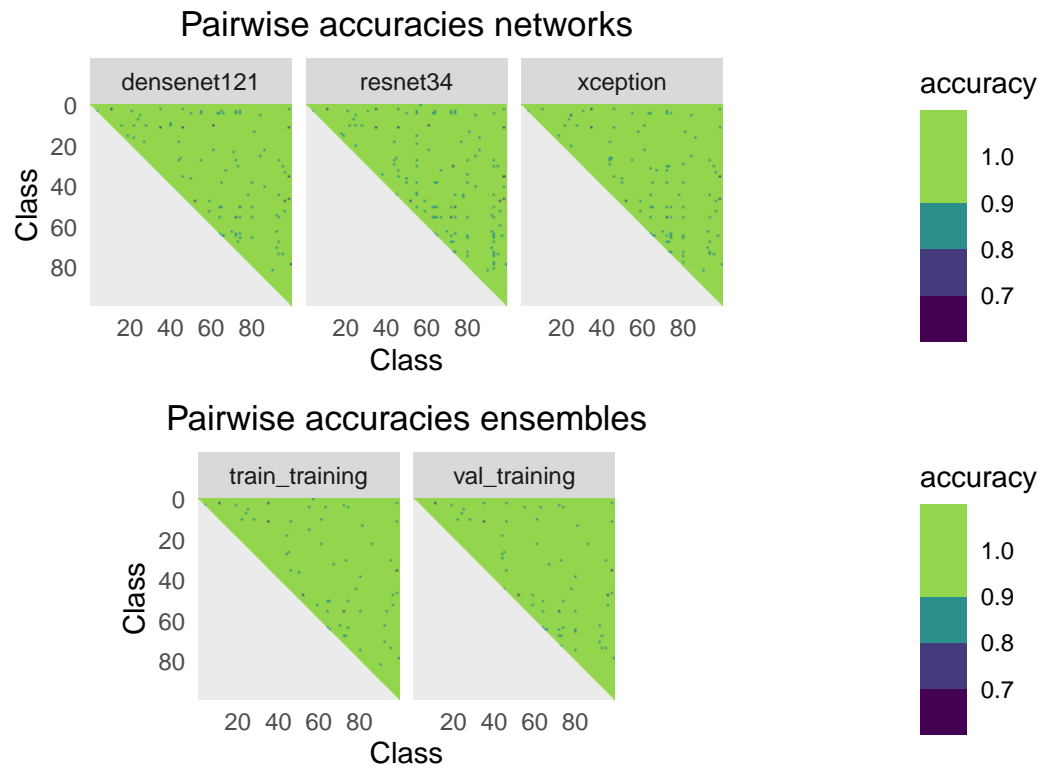
Replication 5 , fold 0



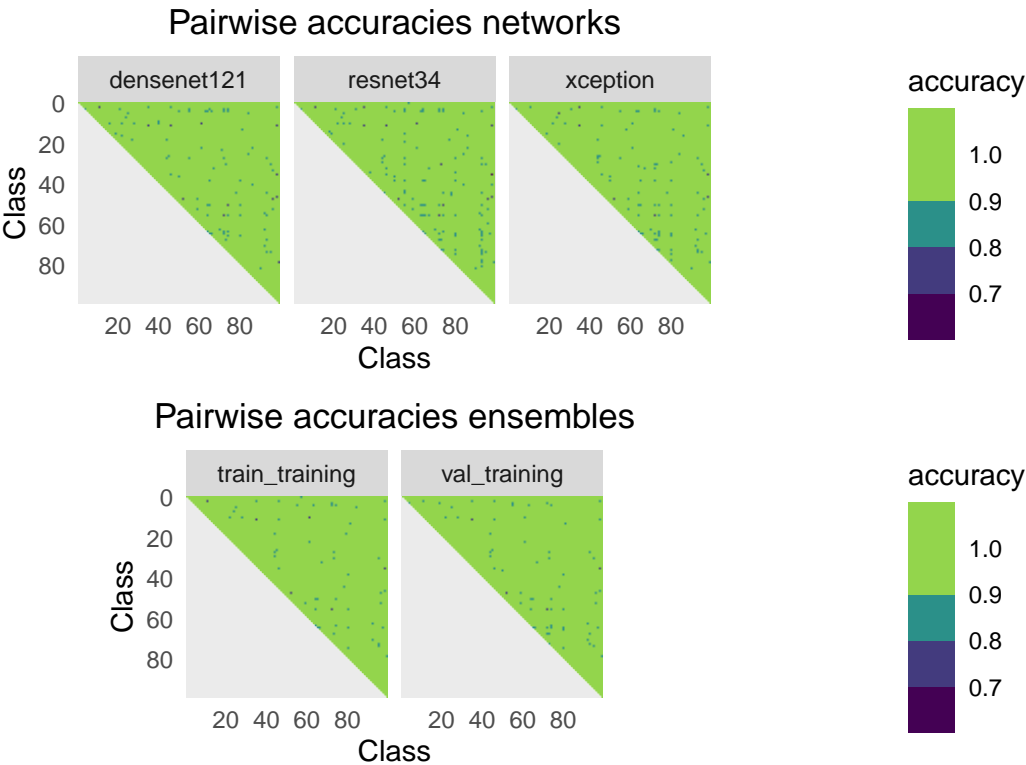
Replication 5 , fold 1



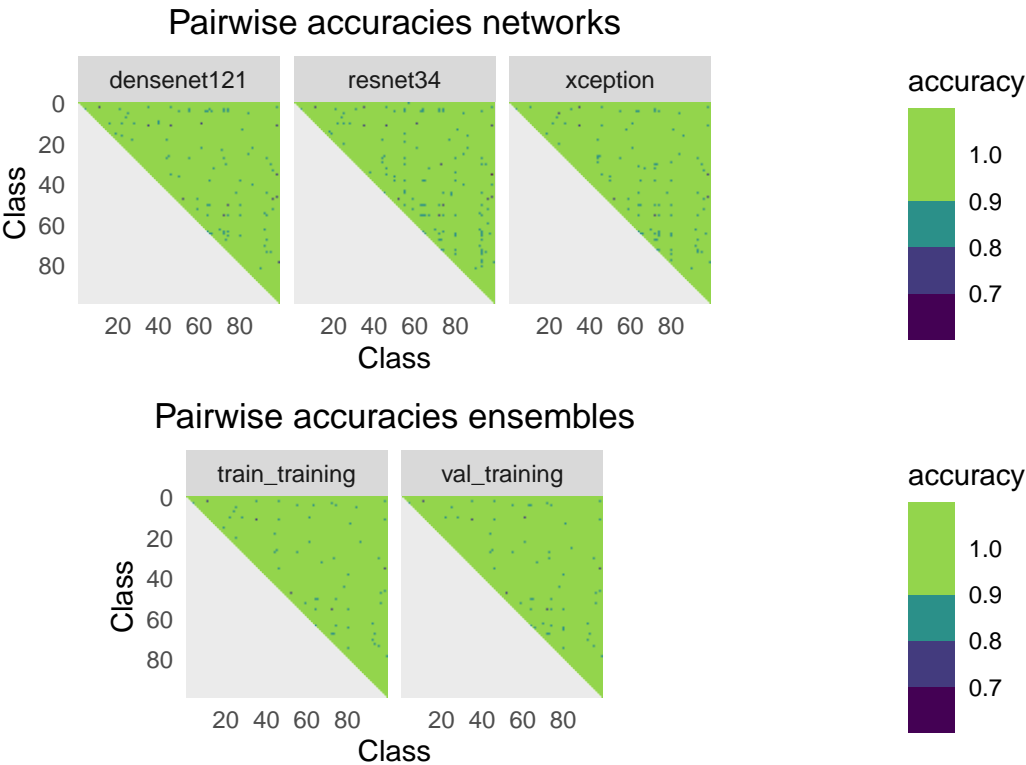
Replication 5 , fold 2



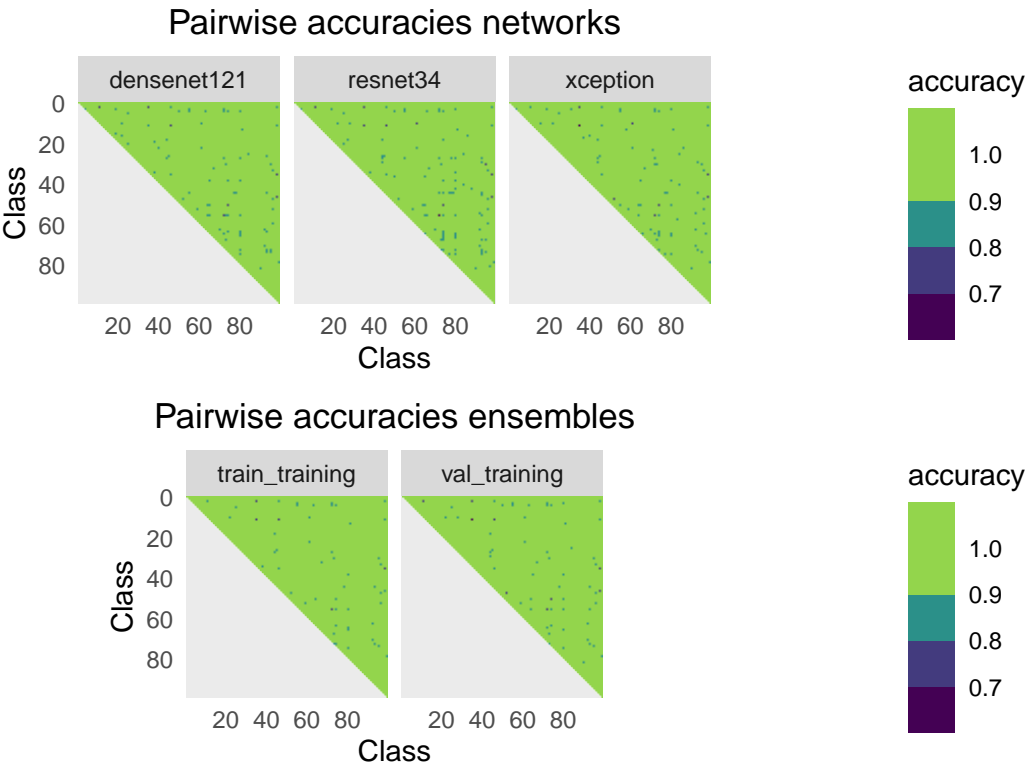
Replication 5 , fold 3



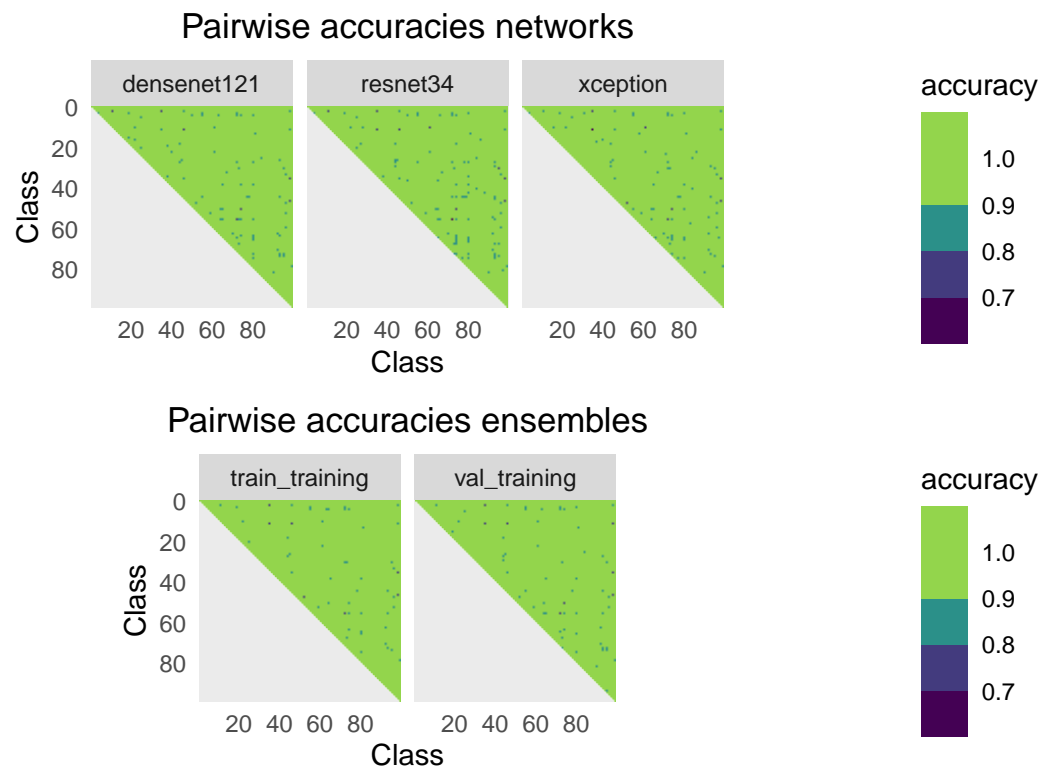
Replication 5 , fold 4



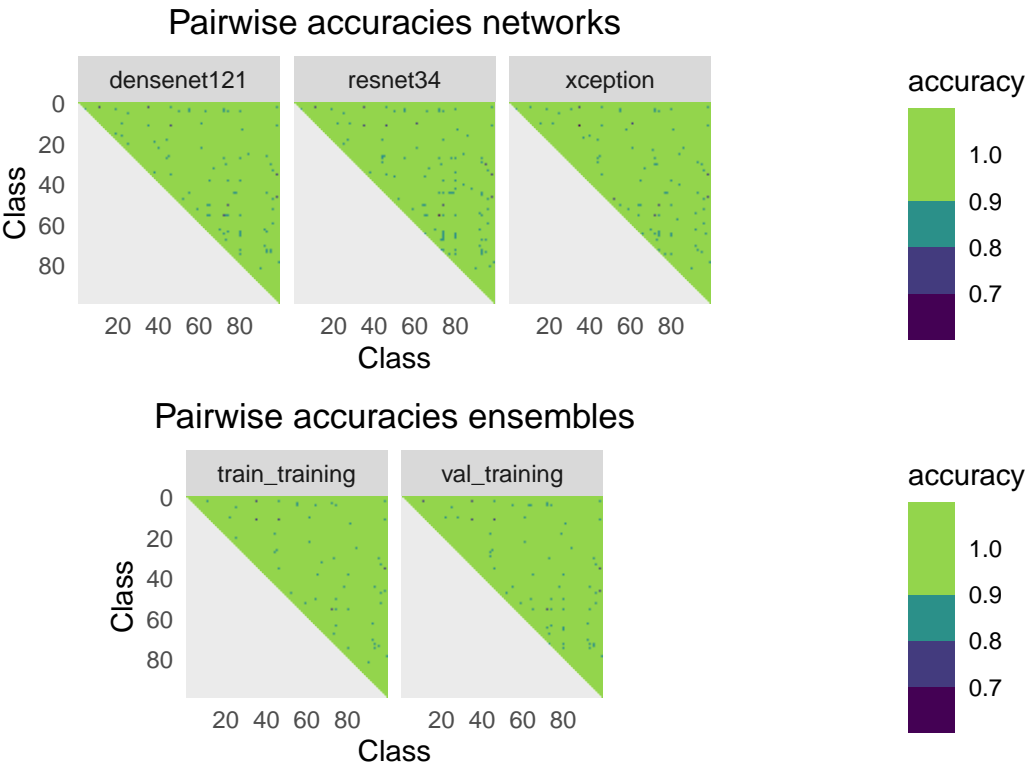
Replication 6 , fold 0



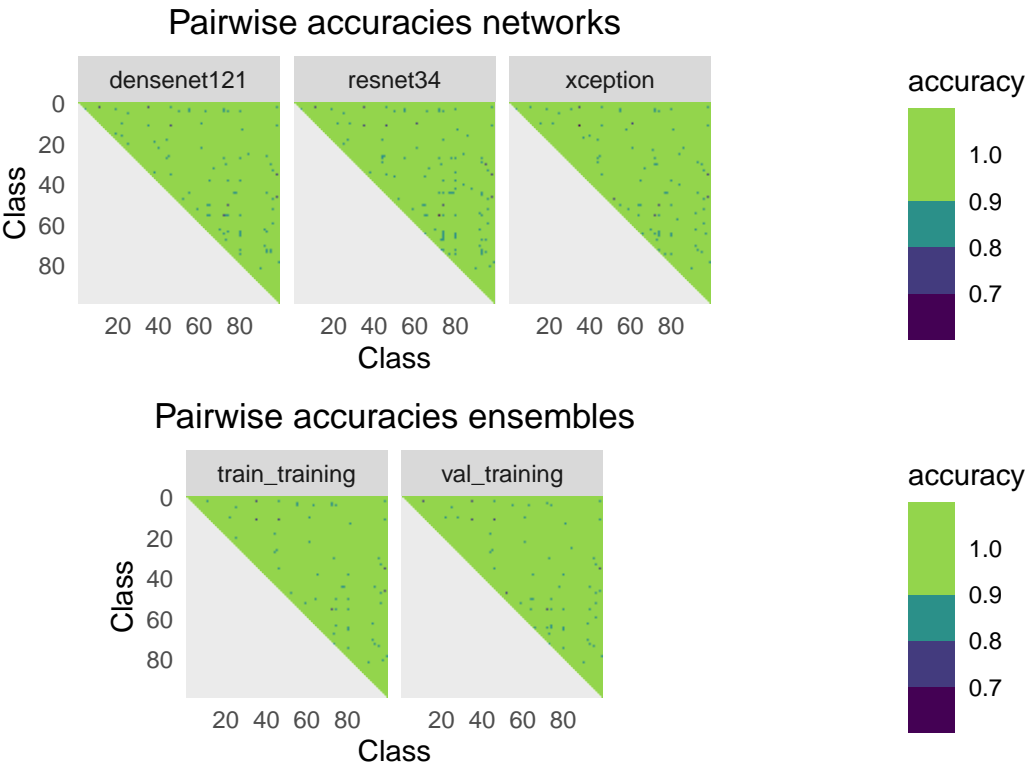
Replication 6 , fold 1



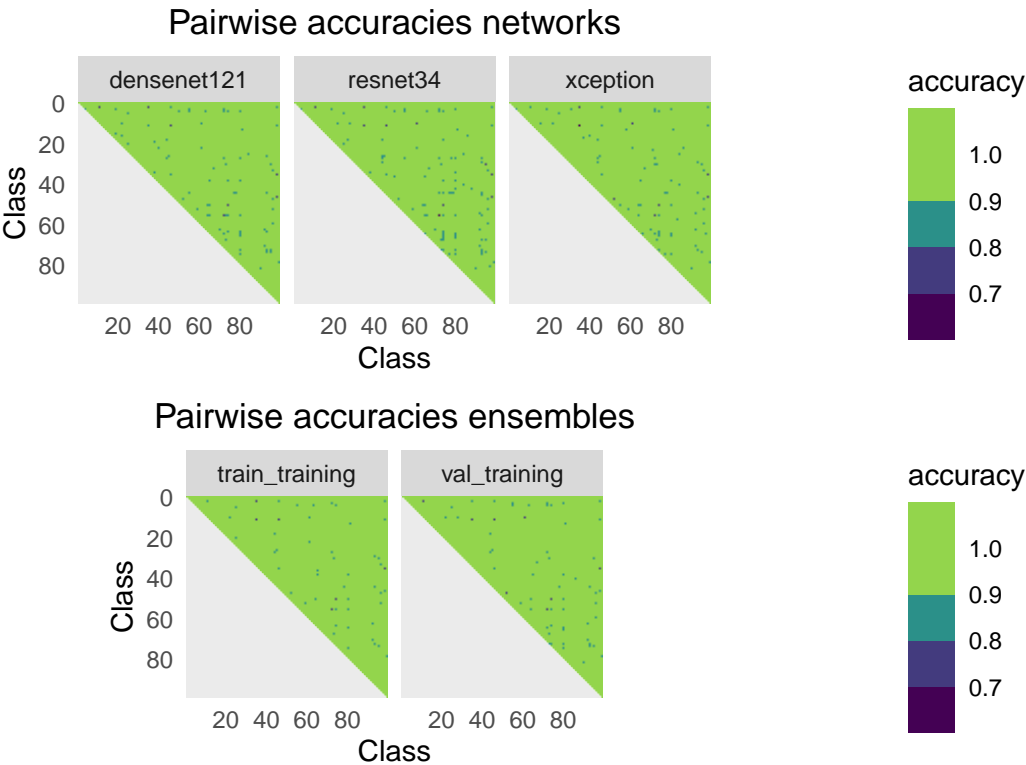
Replication 6 , fold 2



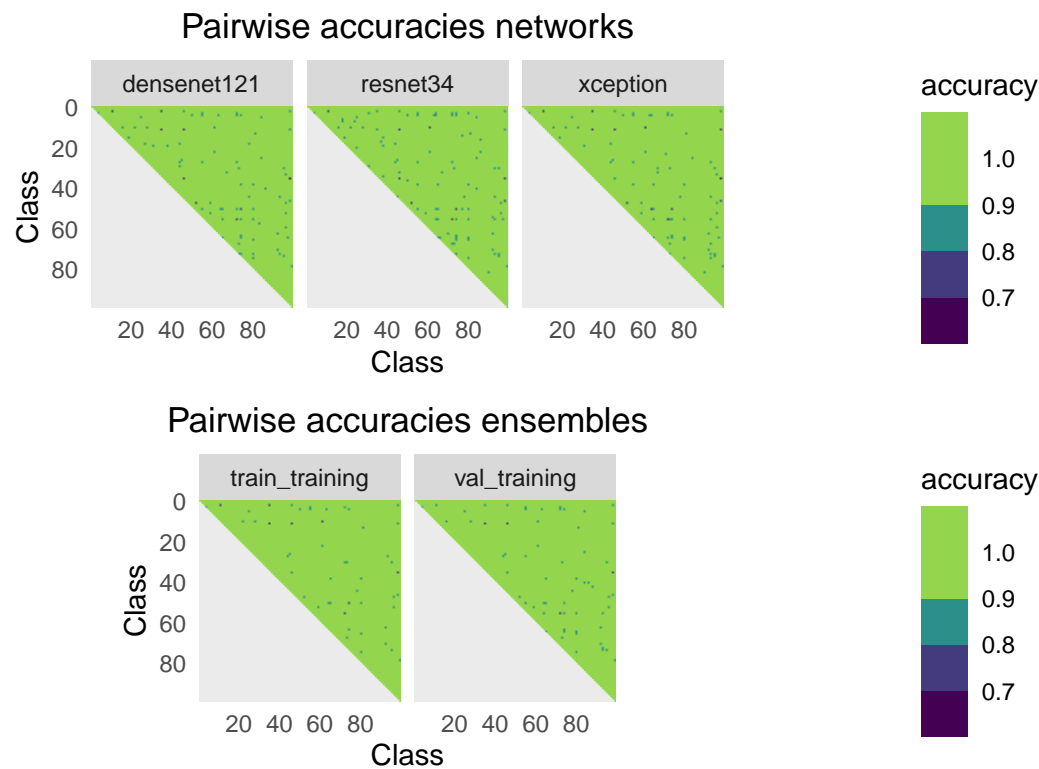
Replication 6 , fold 3



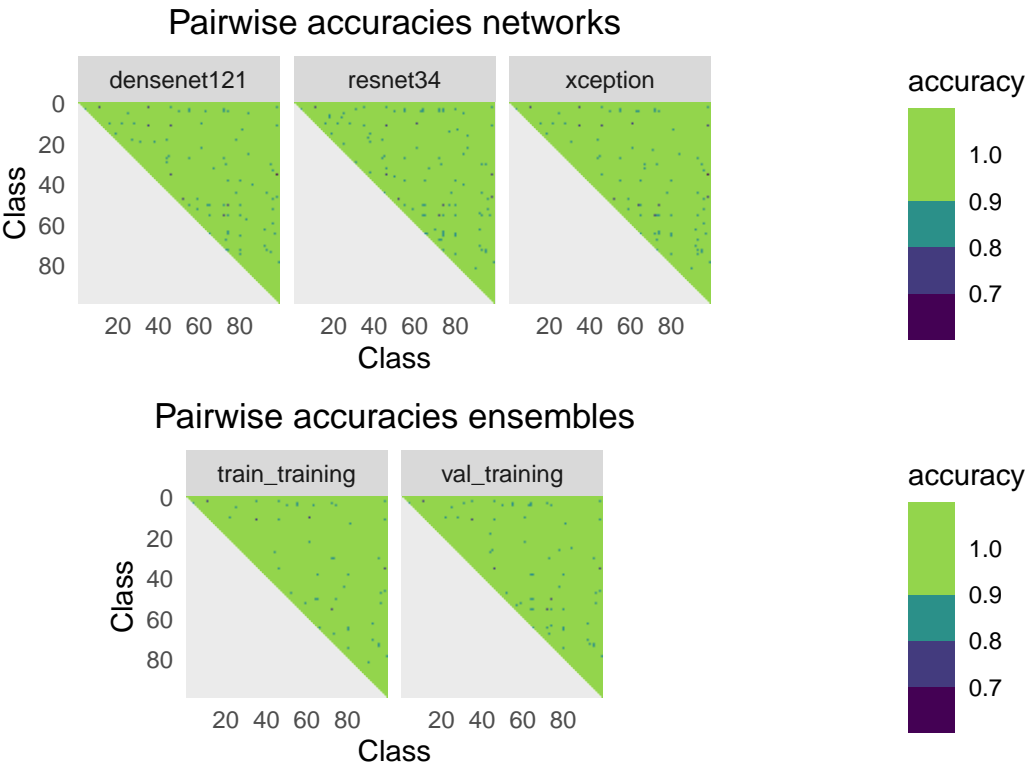
Replication 6 , fold 4



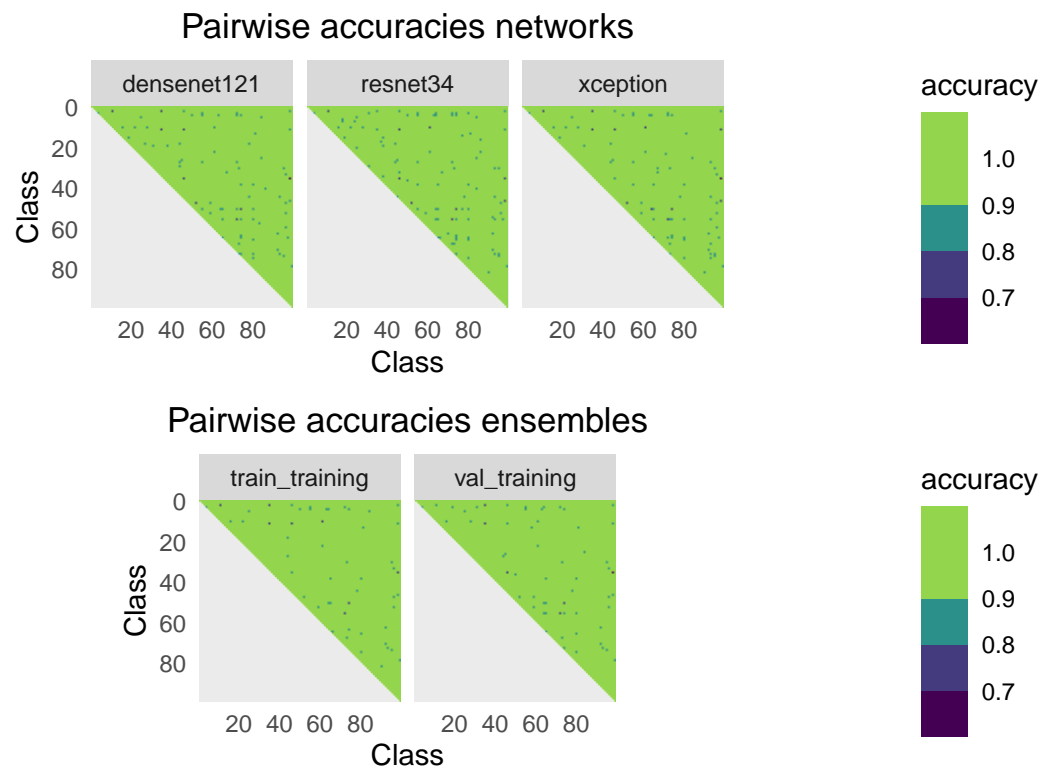
Replication 7 , fold 0



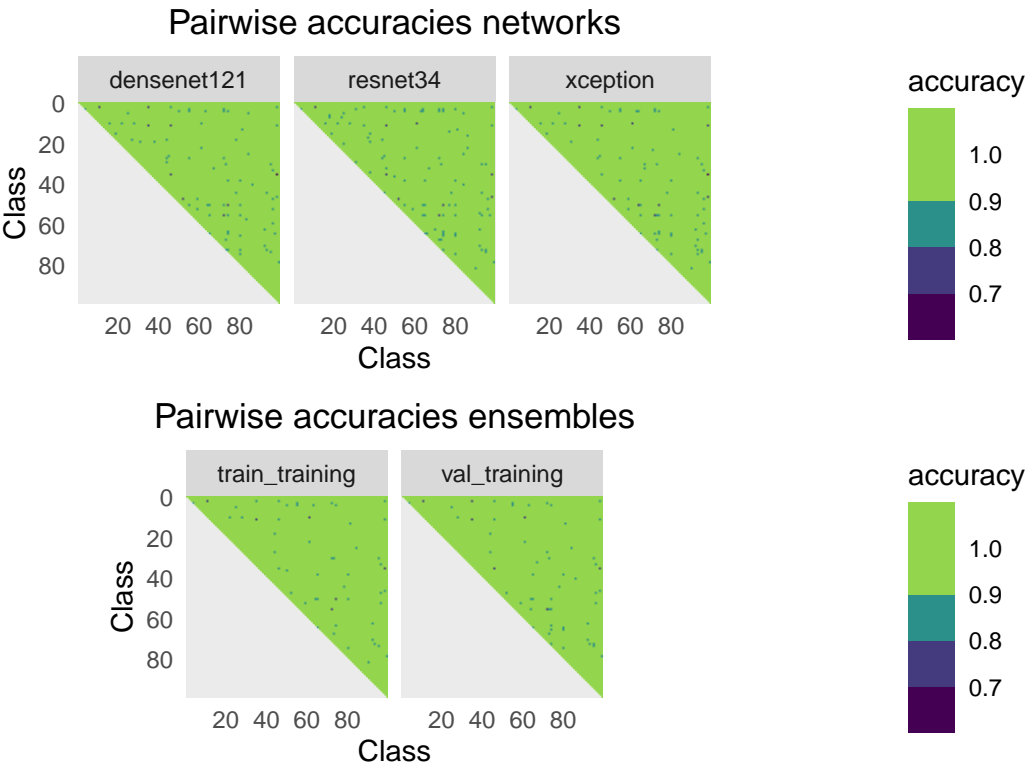
Replication 7 , fold 1



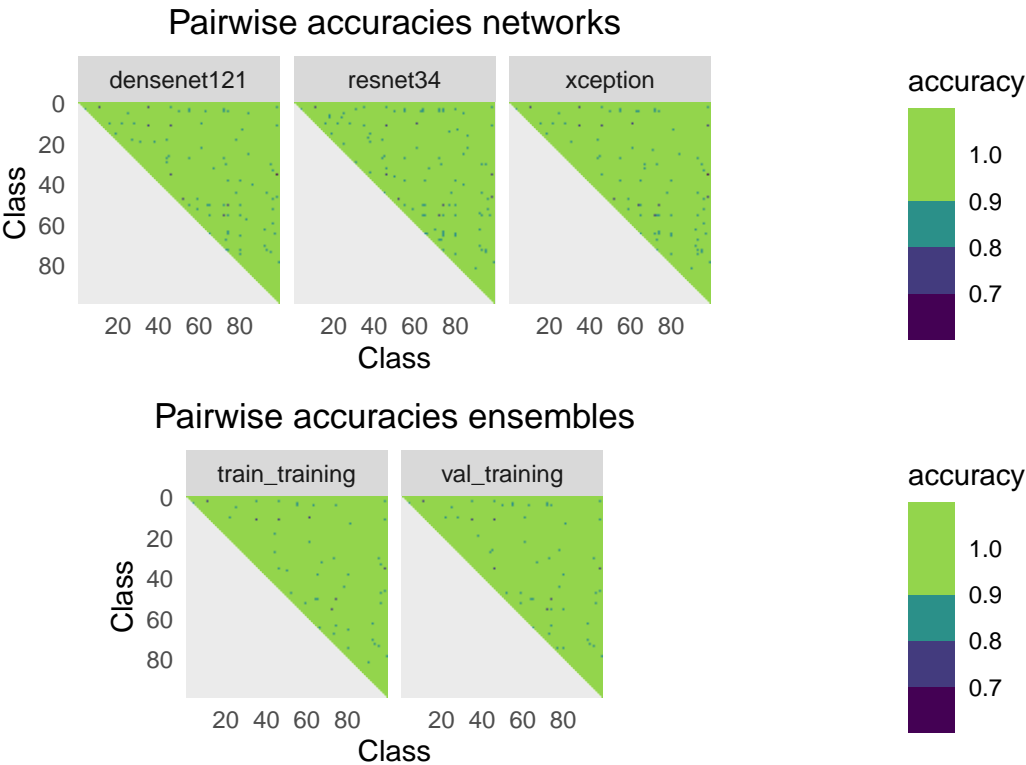
Replication 7 , fold 2



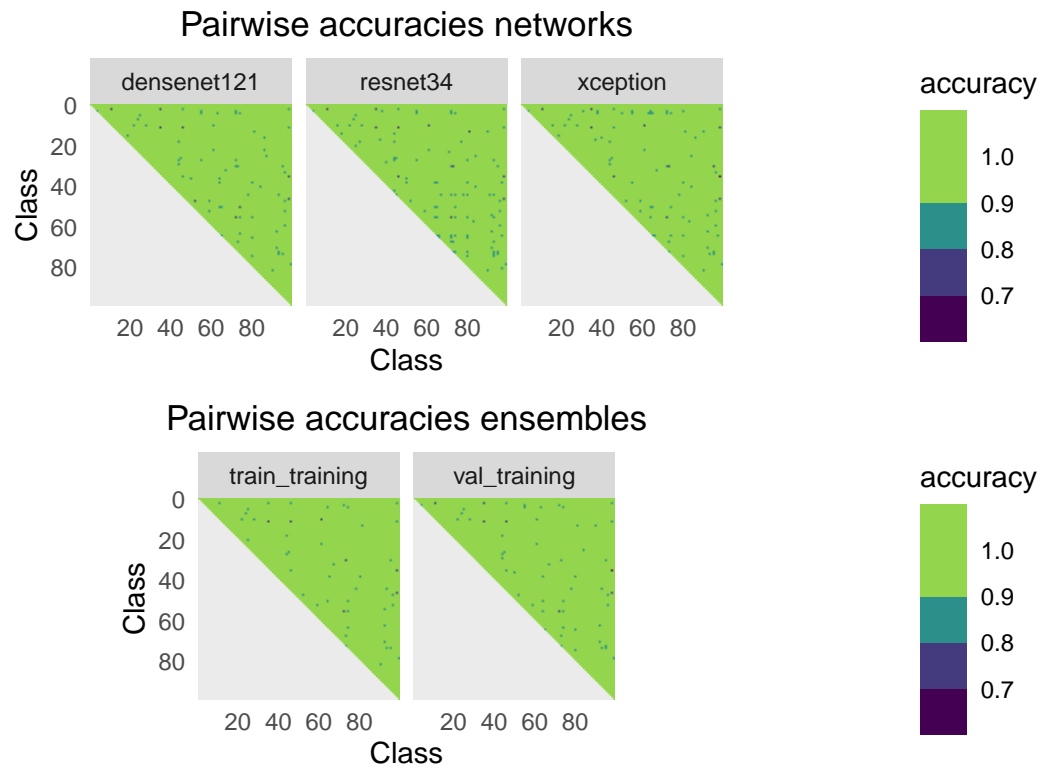
Replication 7 , fold 3



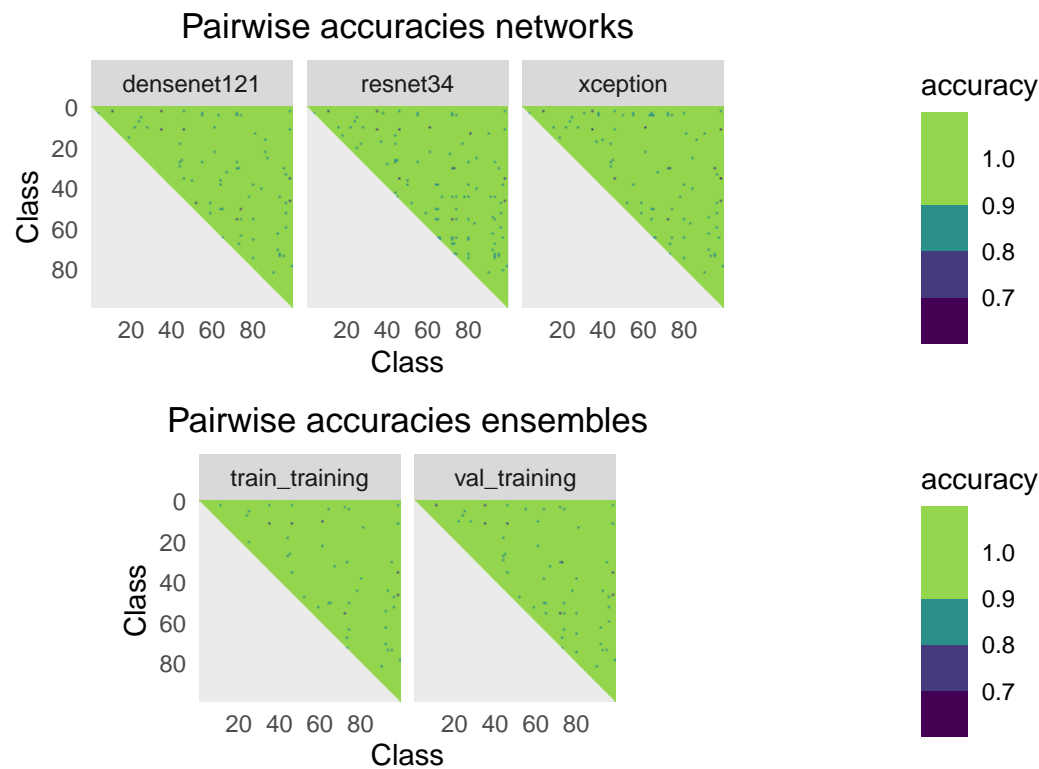
Replication 7 , fold 4



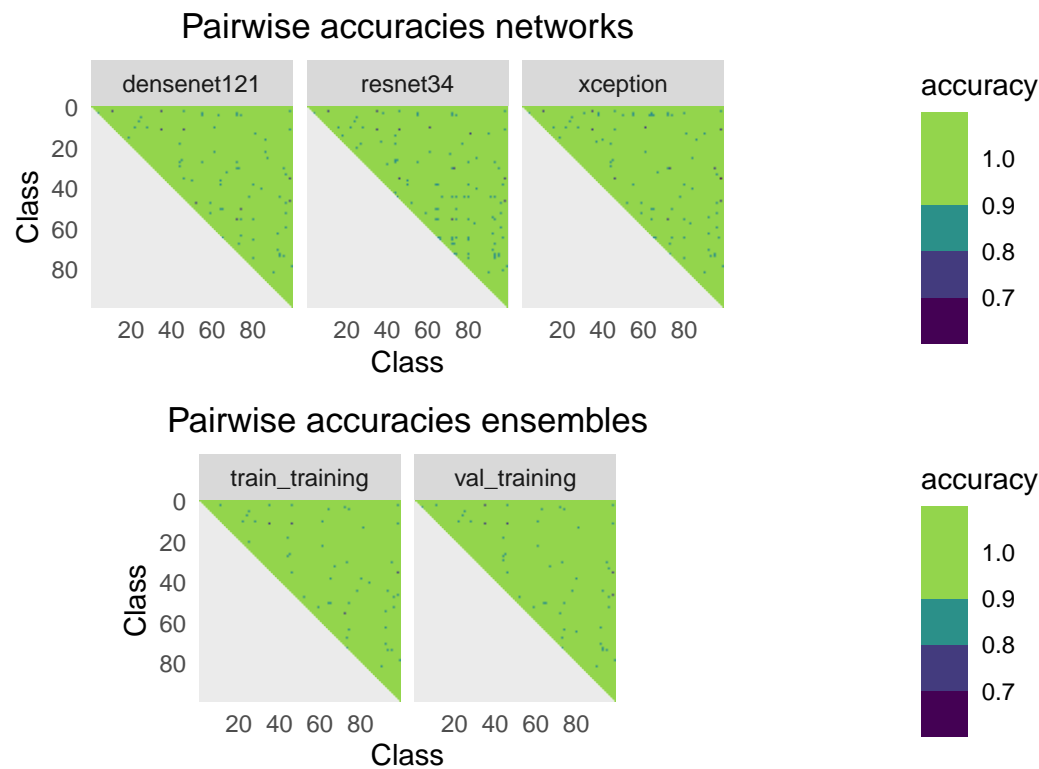
Replication 8 , fold 0



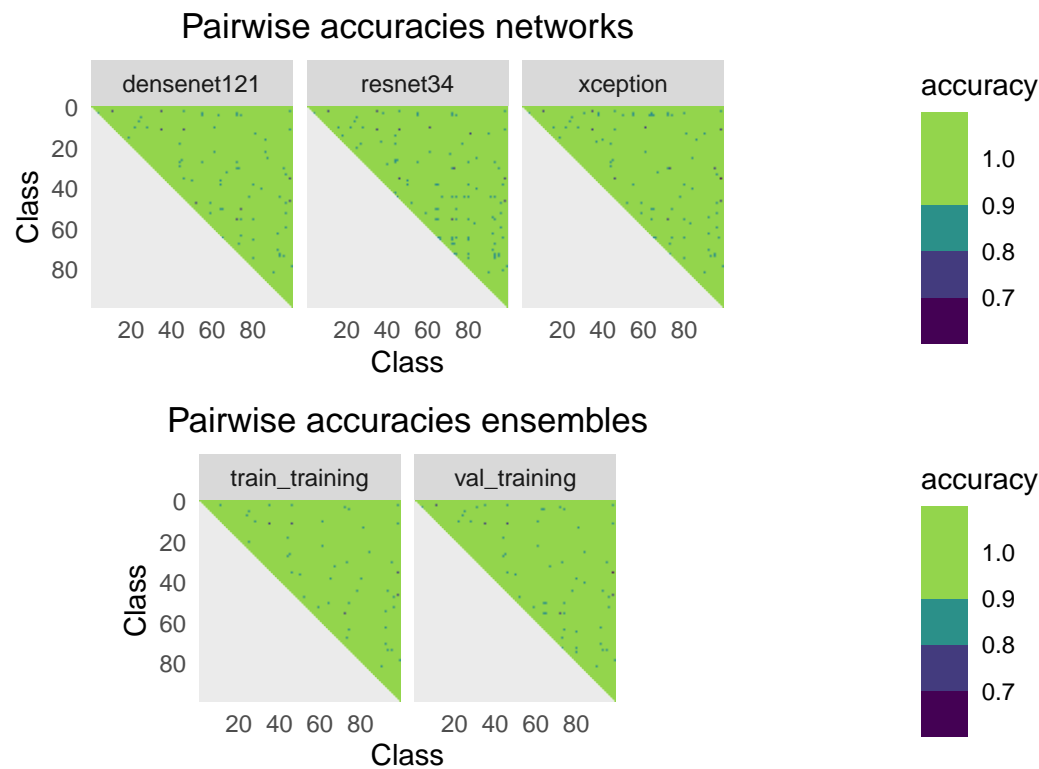
Replication 8 , fold 1



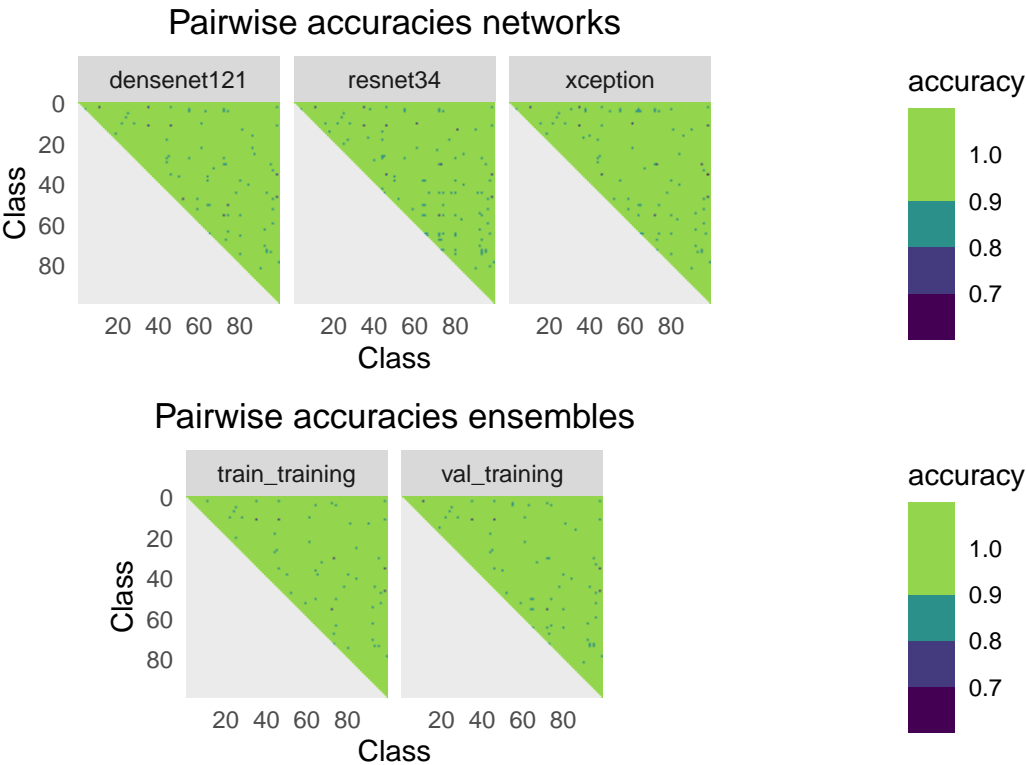
Replication 8 , fold 2



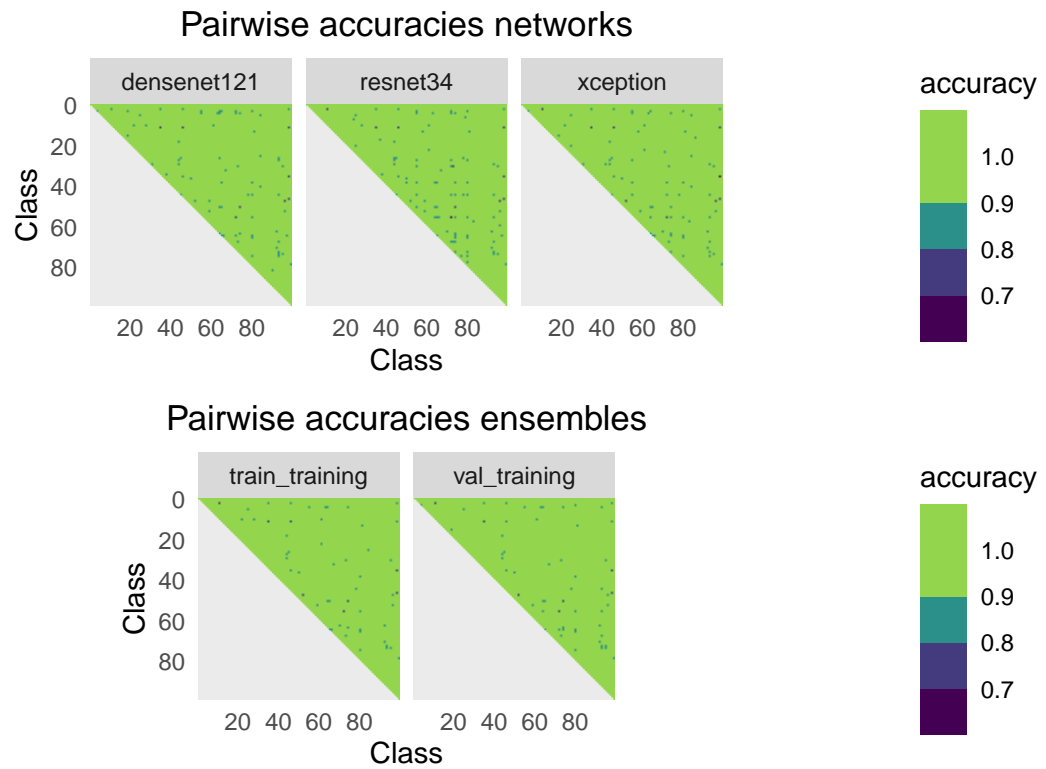
Replication 8 , fold 3



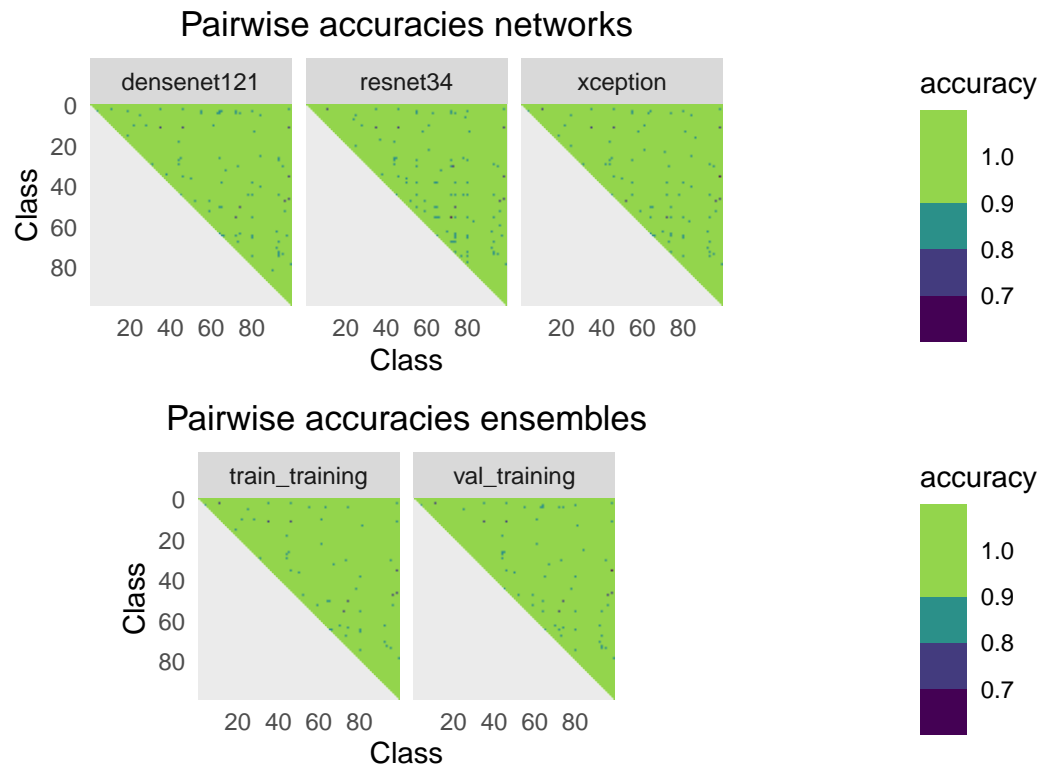
Replication 8 , fold 4



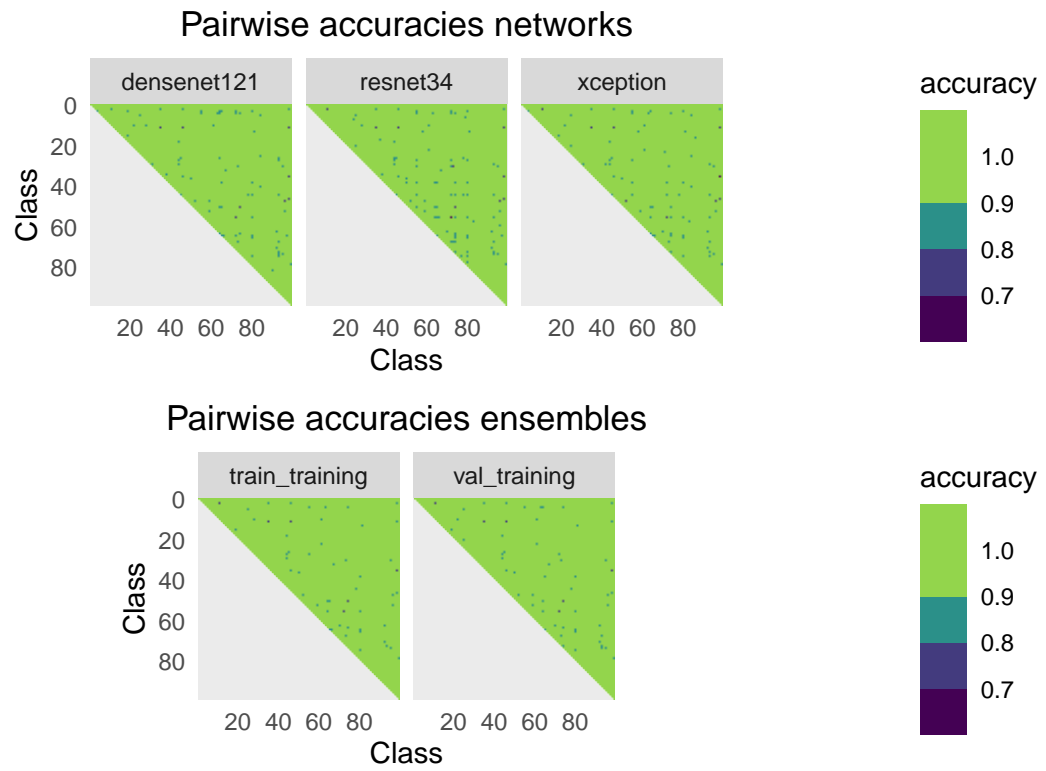
Replication 9 , fold 0



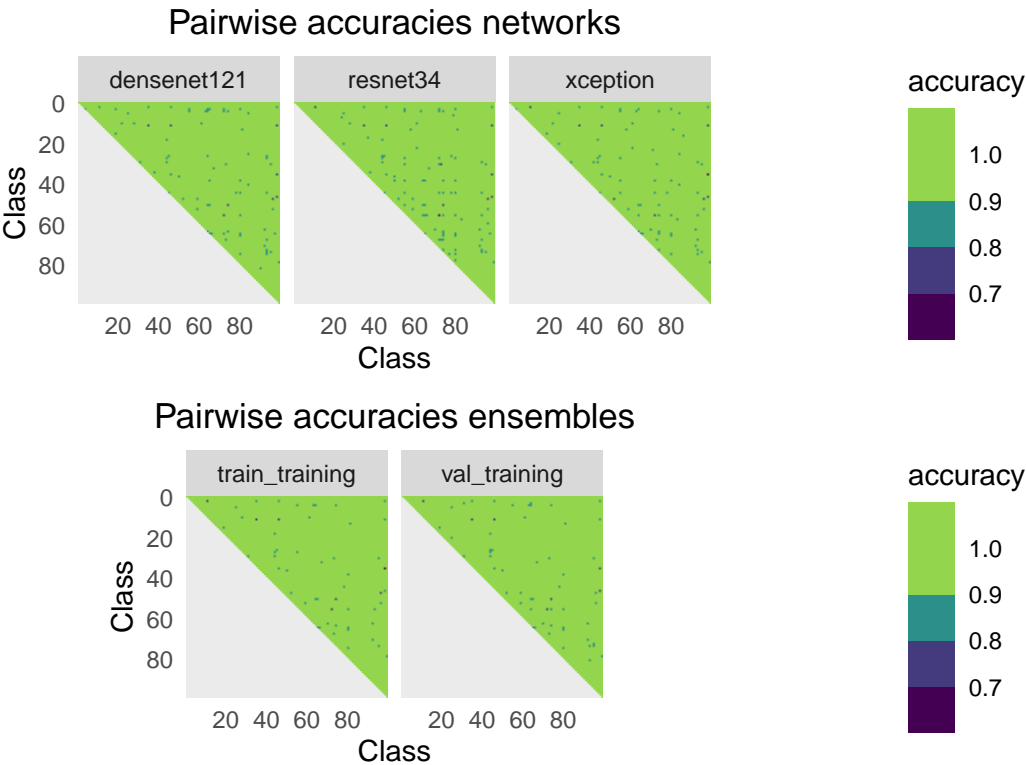
Replication 9 , fold 1



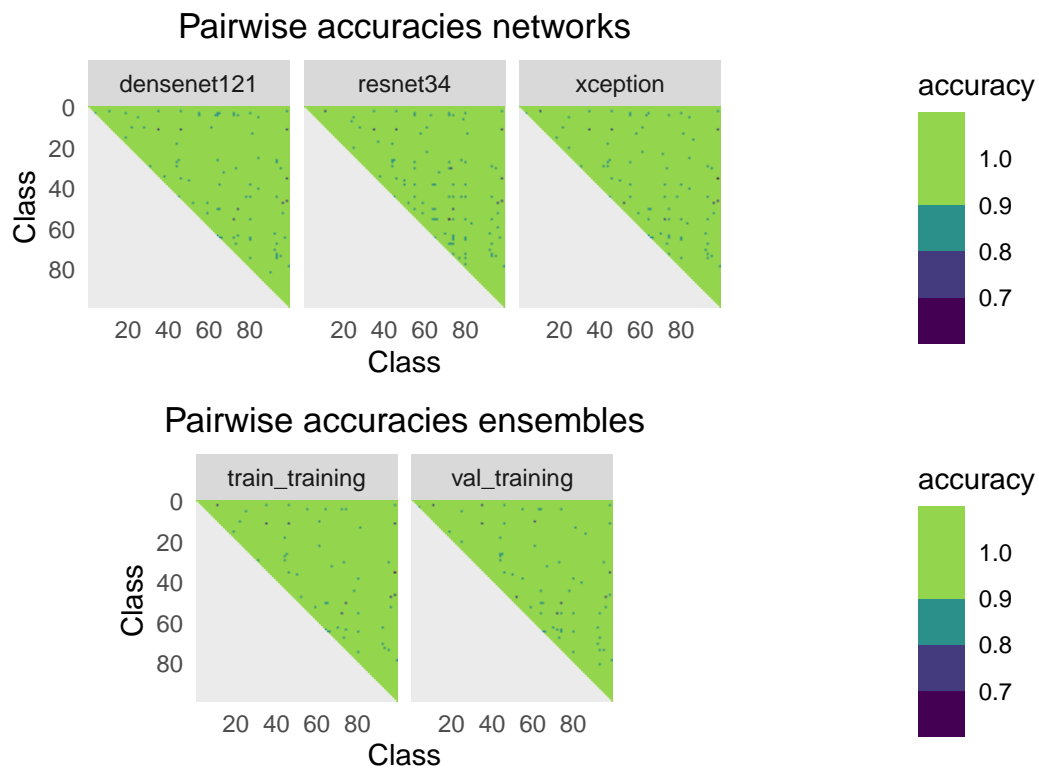
Replication 9 , fold 2



Replication 9 , fold 3



Replication 9 , fold 4



Need some other way to visualize this.